STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number 179466

TO: Sheridan Swope **Art Unit:** 1656 **Location:** rem/2B71/3C70 **Serial Number:** 10/758902 **Wednesday, February 22, 2006**	**From:** Beverly Shears **Location:** Biotech-Chem Library REM 1A54 **Phone:** 571-272-2528 beverly.shears@uspto.gov

Search Notes

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

Swope, S.
10/758902
Seq. IDs 1 & 9

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2006, 23:43:27 ; Search time 1211.06 Seconds
(without alignments)
1408.107 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/absa/ABSSWEB_spool/US10758902/runat_17022006_160759_3676/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10758902_@CGN_1_1_5142_@runat_17022006_160759_3676 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	100.0	1085	15	AY437531	AY437531 Bougainvi
2	160	100.0	1387	15	AF445416	AF445416 Bougainvi
3	111	69.4	65	6	A82770	A82770 Sequence 5
4	111	69.4	65	6	AR454120	AR454120 Sequence
5	72	45.0	363	6	A82773	A82773 Sequence 8
6	72	45.0	363	6	AR454123	AR454123 Sequence
7	70	43.8	1364	15	DQ013264	DQ013264 Bougainvi
8	64	40.0	167305	8	AP001527	AP001527 Homo sapi
9	64	40.0	189637	14	AC009765	AC009765 Homo sapi
10	62	38.8	1942	15	SNU66191	U66191 Sambucus ni
11	61	38.1	711	15	AF338910	AF338910 Phytolacc
12	61	38.1	714	15	AY603352	AY603352 Phytolacc
13	61	38.1	714	15	AY603353	AY603353 Phytolacc
14	61	38.1	939	15	AY327475	AY327475 Phytolacc
15	61	38.1	942	15	AY547315	AY547315 Phytolacc
16	61	38.1	942	15	AY572976	AY572976 Phytolacc
17	61	38.1	1164	15	PAPAP	X55383 P.americana
18	61	38.1	1195	6	A36639	A36639 Sequence 1
19	61	38.1	1195	6	A42103	A42103 Sequence 1
20	61	38.1	1195	6	I43835	I43835 Sequence 1
21	61	38.1	1195	6	I55866	I55866 Sequence 1
22	61	38.1	1379	6	AR009535	AR009535 Sequence
23	61	38.1	1379	6	AR136704	AR136704 Sequence
24	61	38.1	1379	6	AR141172	AR141172 Sequence
25	61	38.1	1379	6	AX427731	AX427731 Sequence
26	60.5	37.8	127037	8	AC011748	AC011748 Homo sapi
c 27	60	37.5	82369	9	AL929144	AL929144 Mouse DNA
28	60	37.5	110000	1	CP000082_05	Continuation (6 of
c 29	60	37.5	159553	14	AC142050	AC142050 Rattus no
30	60	37.5	196519	14	AC127834	AC127834 Rattus no
c 31	60	37.5	212628	14	AC097283	AC097283 Rattus no
32	60	37.5	227364	14	AC113732	AC113732 Rattus no
33	60	37.5	238457	14	AC114922	AC114922 Mus muscu
c 34	60	37.5	240406	14	AC095327	AC095327 Rattus no
35	59	36.9	783	15	AB071854	AB071854 Phytolacc
36	59	36.9	20509	15	AC074110	AC074110 Arabidops
37	59	36.9	191712	14	AC130247	AC130247 Rattus no
c 38	59	36.9	244211	14	AC111744	AC111744 Rattus no
39	58	36.2	1892	15	SEB400822	AJ400822 Sambucus
40	57.5	35.9	678	6	AR349037	AR349037 Sequence
c 41	57.5	35.9	167080	14	AC144371	AC144371 Felis cat
42	57	35.6	2392	15	AK110983	AK110983 Oryza sat
c 43	57	35.6	110000	15	AP008211_028	Continuation (29 o
c 44	57	35.6	116691	8	HSJ570012	AL121835 Human DNA
45	57	35.6	140234	15	AC016779	AC016779 Genomic s
c 46	57	35.6	164898	15	AC084218	AC084218 Oryza sat
47	57	35.6	166862	14	AC128043	AC128043 Rattus no
c 48	57	35.6	210209	14	AC164216	AC164216 Bos tauru
c 49	57	35.6	232723	14	AC129704	AC129704 Rattus no
50	56	35.0	465	6	AX427706	AX427706 Sequence
51	56	35.0	714	15	AY603354	AY603354 Phytolacc
52	56	35.0	792	6	AX427704	AX427704 Sequence
53	56	35.0	882	6	A67183	A67183 Sequence 1
54	56	35.0	945	1	AY705712	AY705712 Rhodococc
55	56	35.0	945	6	AX427702	AX427702 Sequence
56	56	35.0	1092	6	AX427720	AX427720 Sequence
57	56	35.0	1164	15	AY049785	AY049785 Phytolacc
58	56	35.0	1249	15	PAPAPSRIP	X98079 P.americana
59	56	35.0	1378	6	AX427732	AX427732 Sequence
60	56	35.0	1379	6	AR136705	AR136705 Sequence
61	56	35.0	1443	15	AY363053	AY363053 Emericell
62	56	35.0	61157	14	AC137956	AC137956 Mus muscu
c 63	56	35.0	154897	14	AC060762	AC060762 Homo sapi
64	56	35.0	164790	14	AC146381	AC146381 Pan trogl
65	56	35.0	171046	14	AC159681	AC159681 Bos tauru
66	56	35.0	188802	9	AC090007	AC090007 Mus Muscu
c 67	56	35.0	189279	8	AC005028	AC005028 Homo sapi
68	56	35.0	192006	8	AC142328	AC142328 Pan trogl
c 69	56	35.0	197191	5	BX294377	BX294377 Zebrafish
70	55.5	34.7	2429	6	CQ845813	CQ845813 Sequence
71	55.5	34.7	2429	8	AK131518	AK131518 Homo sapi
72	55.5	34.7	3260	8	AY498712	AY498712 Homo sapi
73	55.5	34.7	35187	15	AB046434	AB046434 Arabidops
74	55.5	34.7	38844	6	AR203509	AR203509 Sequence
75	55.5	34.7	38844	6	AX451954	AX451954 Sequence
76	55.5	34.7	88126	15	F3D18	AF296829 Arabidops

	77	55.5	34.7	110000	15	AP008208_113	Continuation (114
c	78	55.5	34.7	113404	8	AC096653	AC096653 Homo sapi
	79	55.5	34.7	128520	15	AP004123	AP004123 Oryza sat
	80	55.5	34.7	162391	15	AP005414	AP005414 Oryza sat
c	81	55	34.4	1935	6	CQ714738	CQ714738 Sequence
c	82	55	34.4	2558	6	AX392932	AX392932 Sequence
c	83	55	34.4	3154	8	AK172794	AK172794 Homo sapi
c	84	55	34.4	3621	8	BC064930	BC064930 Homo sapi
c	85	55	34.4	3857	8	AF216833	AF216833 Homo sapi
c	86	55	34.4	3873	8	AB013380	AB013380 Homo sapi
	87	55	34.4	7005	15	AF355103	AF355103 Pleurotus
c	88	55	34.4	145111	14	AL390245	AL390245 Homo sapi
	89	55	34.4	147913	8	HSDJ613A2	AL121990 Human DNA
	90	55	34.4	148679	8	AC099788	AC099788 Homo sapi
	91	55	34.4	150077	5	AL928881	AL928881 Zebrafish
c	92	55	34.4	153860	14	AC016301	AC016301 Homo sapi
c	93	55	34.4	169293	8	AC024601	AC024601 Homo sapi
	94	55	34.4	183745	14	AC150693	AC150693 Bos tauru
c	95	55	34.4	189224	14	AC164234	AC164234 Bos tauru
	96	55	34.4	194982	14	AC156751	AC156751 Otolemur
c	97	55	34.4	215416	14	AC153228	AC153228 Bos tauru
c	98	55	34.4	222520	14	AC120336	AC120336 Rattus no
	99	55	34.4	226021	14	AC094545	AC094545 Rattus no
c	100	55	34.4	255257	14	AC114472	AC114472 Rattus no

ALIGNMENTS

RESULT 1
AY437531
LOCUS AY437531 1085 bp mRNA linear PLN 20-JAN-2005
DEFINITION Bougainvillea spectabilis antiviral protein (Ap1) mRNA, complete cds.
ACCESSION AY437531
VERSION AY437531.1 GI:40890052
KEYWORDS .
SOURCE Bougainvillea spectabilis
ORGANISM Bougainvillea spectabilis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE 1 (bases 1 to 1085)
AUTHORS Balasaraswathi,R., Suguna Rani,K. and Bansal,V.
TITLE A full length antiviral cDNA sequence from Bougainvillea spectabilis Willd.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1085)
AUTHORS Balasaraswathi,R., Suguna Rani,K. and Bansal,V.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-2003) Centre For Plant Molecular Biology, Tamil Nadu Agricultural University, Lawley Road, Coimbatore, Tamil Nadu 641003, India
FEATURES Location/Qualifiers
source 1. .1085
/organism="Bougainvillea spectabilis"
/mol_type="mRNA"
/db_xref="taxon:146096"
/ecotype="Coimbatore region"
/country="India"
/note="biotype: red flower trait; authority: Bougainvillea spectabilis Willd."
gene 1. .1085
/gene="Ap1"
5'UTR 1. .25
/gene="Ap1"
CDS 26. .943
/gene="Ap1"
/note="crop antiviral and ribosome-inactivating protein; BAP; BAP1; antiviral activity against tospo group of crop viruses"
/codon_start=1
/product="antiviral protein"
/protein_id="AAR97371.1"
/db_xref="GI:40890053"
/translation="MGWWAIIVEPMLVMPSIVNKETTSLGYNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADAKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEAIHGKTINGQEIAKFFLITIQMVSEAARFKYIETEVVDRGLYGSFKPNFKVLNLENNWGDISDAIHKSSPQCTTINPALQLISPSNDPWVVNKVSQISPDMGILKFKSSKLTQFATMIRSAIAEDLDGDELEILEPNIA"
3'UTR 944. .1085
/gene="Ap1"
polyA_signal 984. .989
/gene="Ap1"
ORIGIN

Alignment Scores:

Pred. No.:	1.1e-15	Length:	1085
Score:	160.00	Matches:	30
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	15	Gaps:	0

US-10-758-902-1 (1-30) x AY437531 (1-1085)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 TACAACACTGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 163

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        164 TTGCGCAATGAATTGGCTAAGGGCACACCA 193
```

RESULT 2
AF445416
LOCUS AF445416 1387 bp mRNA linear PLN 29-NOV-2001
DEFINITION Bougainvillea spectabilis bouganin mRNA, complete cds.
ACCESSION AF445416
VERSION AF445416.1 GI:17149253
KEYWORDS .
SOURCE Bougainvillea spectabilis
ORGANISM Bougainvillea spectabilis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE 1 (bases 1 to 1387)
AUTHORS den Hartog,M.T., Lubelli,C., Boon,L., Heerkens,S., Ortiz Buijsse,A.P., de Boer,M. and Stirpe,F.
TITLE Cloning and expression of cDNA coding for bouganin: A type I ribosome-inactivating protein from Bougainvillea spectabilis Willd
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1387)
AUTHORS den Hartog,M.T.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Meibergdreef 45, Amsterdam 1105 BA, The Netherlands
FEATURES Location/Qualifiers
source 1. .1387
/organism="Bougainvillea spectabilis"
/mol_type="mRNA"
/db_xref="taxon:146096"
/note="authority: Bougainvillea spectabilis Willd"
CDS 238. .1155
/note="ribosome-inactivating protein"
/codon_start=1
/product="bouganin"
/protein_id="AAL35962.1"
/db_xref="GI:17149254"
/translation="MGWWAIIVEPMLVMPSIVNKETTSLGYNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEAIHGKTINGQEIAKFFLIVIQMVSEAARFKYIETEVVDRGLYGSFKPNFKVLNLENNWGDISDAIHKSSPQCTTINPALQLISPSNDPWVVNKVSQISPDMGILKFKSSKLTQFATMIRSAIVEDLDGDELEILEPNIA"
ORIGIN

```
Alignment Scores:
Pred. No.:              1.41e-15        Length:         1387
Score:                  160.00          Matches:        30
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     15              Gaps:           0

US-10-758-902-1 (1-30) x AF445416 (1-1387)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 375

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        376 TTGCGCAACGAATTGGCTAAGGGCACACCA 405

RESULT 3
A82770
LOCUS       A82770                    65 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 5 from Patent WO9855623.
ACCESSION   A82770
VERSION     A82770.1  GI:6732460
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     TYPE-1 RIBOSOME-INACTIVATING PROTEIN
  JOURNAL   Patent: WO 9855623-A 5 10-DEC-1998;
            STIRPE FIORENZO (IT); BOLOGNESI ANDREA (IT)
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              4.35e-09        Length:         65
Score:                  111.00          Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            69.4%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x A82770 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 4
AR454120
LOCUS       AR454120                  65 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 5 from patent US 6680296.
ACCESSION   AR454120
VERSION     AR454120.1  GI:42687049
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     Type-1 ribosome-inactivating protein
  JOURNAL   Patent: US 6680296-A 5 20-JAN-2004;
            Tanox Pharma B.V.; Amsterdam;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.35e-09        Length:         65
Score:                  111.00          Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            69.4%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x AR454120 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 5
A82773
LOCUS       A82773                   363 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 8 from Patent WO9855623.
ACCESSION   A82773
VERSION     A82773.1  GI:6732463
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     TYPE-1 RIBOSOME-INACTIVATING PROTEIN
  JOURNAL   Patent: WO 9855623-A 8 10-DEC-1998;
            STIRPE FIORENZO (IT); BOLOGNESI ANDREA (IT)
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              0.0434          Length:         363
Score:                  72.00           Matches:        14
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            45.0%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x A82773 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 6
AR454123
LOCUS       AR454123                 363 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 8 from patent US 6680296.
ACCESSION   AR454123
VERSION     AR454123.1  GI:42687052
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 363)
```

```
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     Type-1 ribosome-inactivating protein
  JOURNAL   Patent: US 6680296-A 8 20-JAN-2004;
            Tanox Pharma B.V.; Amsterdam;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              0.0434          Length:         363
Score:                  72.00           Matches:        14
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            45.0%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x AR454123 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 7
DQ013264
LOCUS       DQ013264               1364 bp    mRNA    linear   PLN 20-JUL-2005
DEFINITION  Bougainvillea x buttiana antiviral protein 1 mRNA, complete cds.
ACCESSION   DQ013264
VERSION     DQ013264.2  GI:68342547
KEYWORDS    .
SOURCE      Bougainvillea x buttiana
  ORGANISM  Bougainvillea x buttiana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Choudhary,N. and Lodha,M.L.
  TITLE     cDNA Sequence of Bougainvillea Antiviral Protein (BAP1)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1364)
  AUTHORS   Choudhary,N. and Lodha,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2005) Division of Biochemistry, Indian
            Agricultural Research Institute, Pusa, New Delhi 110012, India
REFERENCE   3  (bases 1 to 1364)
  AUTHORS   Choudhary,N. and Lodha,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-2005) Division of Biochemistry, Indian
            Agricultural Research Institute, Pusa, New Delhi 110012, India
  REMARK    Sequence update by submitter
COMMENT     On Jun 30, 2005 this sequence version replaced gi:63147983.
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="Bougainvillea x buttiana"
                     /mol_type="mRNA"
                     /cultivar="Mahara"
                     /db_xref="taxon:328062"
                     /tissue_type="leaves"
     5'UTR           1. .120
     CDS             121. .1080
                     /note="BAP1"
                     /codon_start=1
                     /product="antiviral protein 1"
                     /protein_id="AAY34283.2"
                     /db_xref="GI:68342548"
                     /translation="MKPLGGLVITCIWWAIIVELVVIKPSIITKETASLGHNTVSFNL
                     EDATEQVYRSVIKSLRNELQTSTLVCKIPVTPQSLAVDKNQFVVVSLTWKSKEVQLGI
                     DVTNAYVVGYQDKLKNQDYRAFLLKDAPPLAKDKLFPGVKSETLPFGGTYPNLVKAGN
                     VDRREQFELGVEKLGHAIDSIFGKPKNDQNVARFFLNAIQIVSEAARFKYIENEVVRG
                     GLNSGLSKPNGKMLNLENSWGHISDAIHNSNQKYKCETISPALELQNADYSKWVVNKV
                     SEISPDLGILKYKSSKLTQSTTIMRSIVVEDSDELEKLETIIG"
     3'UTR           1081. .1364
ORIGIN

Alignment Scores:
Pred. No.:              0.348           Length:         1364
Score:                  70.00           Matches:        17
Percent Similarity:     67.7%           Conservative:   4
Best Local Similarity:  54.8%           Mismatches:     8
Query Match:            43.8%           Indels:         2
DB:                     15              Gaps:           1

US-10-758-902-1 (1-30) x DQ013264 (1-1364)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIle 18
              :::||||||||||||||||||||||   :::|||   |||      |||   :::   |||
Db        229 CACAACACTGTGTCATTTAACCTGGAAGATGCTACTGAACAAGTGTACCGCTCTGTTATA 288

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              :::   ||||||||||||||||        |||
Db        289 AAATCTTTGCGCAACGAATTACAAACTAGCACA 321

RESULT 8
AP001527
LOCUS       AP001527               167305 bp    DNA     linear   PRI 17-JUN-2003
DEFINITION  Homo sapiens genomic DNA, chromosome 11 clone:RP11-732A21, complete
            sequence.
ACCESSION   AP001527
VERSION     AP001527.5  GI:31790725
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA
  JOURNAL   Published Only in Database (2000)
REFERENCE   2  (bases 1 to 167305)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-2000) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     On Jun 16, 2003 this sequence version replaced gi:17425230.
FEATURES             Location/Qualifiers
     source          1. .167305
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="11q"
                     /clone="RP11-732A21"
ORIGIN

Alignment Scores:
Pred. No.:              421             Length:         167305
Score:                  64.00           Matches:        16
Percent Similarity:     60.6%           Conservative:   4
Best Local Similarity:  48.5%           Mismatches:     7
Query Match:            40.0%           Indels:         6
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x AP001527 (1-167305)

Qy          2 AsnThrValSerPheAsn----------------LeuGlyGluAlaTyrGluTyrPro 15
              |||:::||||||   |||                |||||||||||   |||
Db      78150 AACTCCGTCTCAATAAATAAATAAGAATGTGGACTGCTTGGAGAGGCTTCAGAAGTCTGT 78209
```

```
Qy         16 ThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
                ||||||:|||||||||   |||:::||||||
Db      78210 GAGATGATTGAAGAGTTGAGAAACAGACTGAGTAAAGGT 78248

RESULT 9
AC009765
LOCUS       AC009765               189637 bp    DNA     linear   HTG 21-SEP-2001
DEFINITION  Homo sapiens clone RP11-400E19, WORKING DRAFT SEQUENCE, 4 unordered
            pieces.
ACCESSION   AC009765
VERSION     AC009765.5  GI:15706127
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 189637)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome, clone RP11-400E19
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 189637)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
            Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Depayre,E., Devon,K., Dewar,K.,
            Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
            Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
            Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
            Karatas,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P.,
            Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
            Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
            Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
            Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
            Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
            Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Sep 20, 2001 this sequence version replaced gi:10334912.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L2177
                Center clone name: 400_E_19
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 36% of reads
                Sequencing vector: Plasmid; n/a; 64% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 188074 bases at least Q40
                Consensus quality: 188849 bases at least Q30
                Consensus quality: 189137 bases at least Q20
                Insert size: 180000; agarose-fp
                Insert size: 189337; sum-of-contigs
                Quality coverage: 12.4 in Q20 bases; agarose-fp
                Quality coverage: 11.8 in Q20.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1   148407: contig of 148407 bp in length
            *  148408   148507: gap of 100 bp
            *  148508   149627: contig of 1120 bp in length
            *  149628   149727: gap of 100 bp
            *  149728   175731: contig of 26004 bp in length
            *  175732   175831: gap of 100 bp
            *  175832   189637: contig of 13806 bp in length.
FEATURES             Location/Qualifiers
     source          1. .189637
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="RP11-400E19"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .148407
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
     gap             148408. .148507
                     /estimated_length=100
     misc_feature    148508. .149627
                     /note="assembly_fragment"
     gap             149628. .149727
                     /estimated_length=100
     misc_feature    149728. .175731
                     /note="assembly_fragment"
     gap             175732. .175831
                     /estimated_length=100
     misc_feature    175832. .189637
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
ORIGIN

Alignment Scores:
Pred. No.:              478          Length:         189637
Score:                  64.00        Matches:        16
Percent Similarity:     60.6%        Conservative:   4
Best Local Similarity:  48.5%        Mismatches:     7
Query Match:            40.0%        Indels:         6
DB:                     14           Gaps:           1

US-10-758-902-1 (1-30) x AC009765 (1-189637)

Qy          2 AsnThrValSerPheAsn----------------LeuGlyGluAlaTyrGluTyrPro 15
              |||:::||||||   |||                ||||||||||||   |||
Db      28174 AACTCCGTCTCAATAAATAAATAAGAATGTGGACTGCTTGGAGAGGCTTCAGAAGTCTGT 28233

Qy         16 ThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
                ||||||:|||||||||   |||:::||||||
Db      28234 GAGATGATTGAAGAGTTGAGAAACAGACTGAGTAAAGGT 28272

RESULT 10
SNU66191
LOCUS       SNU66191               1942 bp    mRNA    linear   PLN 12-JUL-1997
DEFINITION  Sambucus nigra Neu5Ac alpha-2,6-gal/galNAc-binding type 2
            ribosome-inactivating protein precursor, mRNA, complete cds.
ACCESSION   U66191
VERSION     U66191.1  GI:1755081
KEYWORDS    .
SOURCE      Sambucus nigra (European elder)
  ORGANISM  Sambucus nigra
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
REFERENCE   1  (bases 1 to 1942)
  AUTHORS   Van Damme,E.J., Roy,S., Barre,A., Citores,L., Mostafapous,K.,
            Rouge,P., Van Leuven,F., Girbes,T., Goldstein,I.J. and Peumans,W.J.
  TITLE     Elderberry (Sambucus nigra) bark contains two structurally
            different Neu5Ac(alpha2,6)Gal/GalNAc-binding type 2
            ribosome-inactivating proteins
  JOURNAL   Eur. J. Biochem. 245 (3), 648-655 (1997)
   PUBMED   9183001
REFERENCE   2  (bases 1 to 1942)
```

```
  AUTHORS   Van Damme,E.J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-AUG-1996) E.J.M. Van Damme, Catholic University of
            Leuven, Lab Phytopathology and Plant Protection, Willem De Croylaan
            42, Leuven Heverlee, Brabant 3001, Belgium
FEATURES             Location/Qualifiers
     source          1. .1942
                     /organism="Sambucus nigra"
                     /mol_type="mRNA"
                     /db_xref="taxon:4202"
                     /clone="LECSNAI'"
                     /tissue_type="bark"
     5'UTR           1. .31
     CDS             32. .1741
                     /note="lectin"
                     /codon_start=1
                     /product="Neu5Ac alpha-2,6-gal/galNAc-binding type 2
                     ribosome-inactivating protein precusor"
                     /protein_id="AAC49754.1"
                     /db_xref="GI:1755082"
                     /translation="MKVVATILYLVVLAICGLGIHGAHPTHSAPPTVYPSVSFNLTEA
                     NSNEYRHFLQELRGKVILGSHRAFDLPVLNPESKVSDSDRFVLVRLTNPSRKKVTLAI
                     DVVTFYVVAPAQNDRSYFFSGSSEVQRENLFVDTTQEDLNFKGDYTSLEHQVGFGRVY
                     IPLGPKSLAQSISSLSTYKSSAGDNKRLARSLLVVIQMVSEAARFRYIQLRIQASITD
                     AKEFTPDLLMLSMENKWSSMSSEIQQAQPGGAFAQVVKLLDQRNHPIDVTNFRRLFQL
                     TSVAVLLHGCPTVTKMPAYIIKMPVFNGGEDEERCSVVEEVTRRIGGRDGFCAEVKNG
                     DEKDGTPVQLSSCGEQSNQQWTFSTDGTIQSLGKCLTTSSSVMIYNCKVVPPESTKWV
                     VSIDGTITNPRSGLVLTAPKAAEGTLVSLEKNVHAARQGWIVGNVEPLVTFIVGYEQM
                     CLETNPGNNDVSLGDCSVKSASKVDQKWALYGDGTIRVNNDRSLCVTSEGKSSNEPII
                     ILKCLGWANQRWVFNTDGTISNPDSKLVMHVDQNDVPLRKIILSHPSGTSNQQWIAST
                     HPA"
     sig_peptide     32. .115
     mat_peptide     116. .1738
                     /product="Neu5Ac alpha-2,6-gal/galNAc-binding type 2
                     ribosome-inactivating protein"
                     /note="lectin A chain"
     3'UTR           1742. .1942
     polyA_site      1891. .1896
     polyA_signal    1933. .1942
ORIGIN

Alignment Scores:
Pred. No.:              9.51          Length:        1942
Score:                  62.00         Matches:       15
Percent Similarity:     67.7%         Conservative:  6
Best Local Similarity:  48.4%         Mismatches:    8
Query Match:            38.8%         Indels:        2
DB:                     15            Gaps:          1

US-10-758-902-1 (1-30) x SNU66191 (1-1942)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||   :::|||||||||||||||   ||||||        ||||||      |||:::
Db        131 TATCCCTCGGTTTCCTTTAATTTGACGGAGGCCAACTCGAACGAATACAGACACTTCCTA 190

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              |||:::||||||   ::::::      |||:::
Db        191 CAGGAACTGCGAGGGAAAGTGATACTGGGAAGC 223

RESULT 11
AF338910
LOCUS       AF338910                711 bp    mRNA    linear   PLN 21-MAR-2001
DEFINITION  Phytolacca americana antiviral protein (mPAP) mRNA, partial cds.
ACCESSION   AF338910
VERSION     AF338910.1  GI:13398616
KEYWORDS    .
SOURCE      Phytolacca americana (American pokeweed)
  ORGANISM  Phytolacca americana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1  (bases 1 to 711)
  AUTHORS   Chen,D., Wang,X. and Zhou,G.
  TITLE     Pokeweed antiviral protein gene,partical cds
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 711)
  AUTHORS   Wang,X., Chen,D. and Zhou,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JAN-2001) Plant Pathology, Institute of Plant
            Protection, Chinese Academy of Agriculture Sciences,
            Yuanmingyuanxilu No.2, Beijing 100094, China
FEATURES             Location/Qualifiers
     source          1. .711
                     /organism="Phytolacca americana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3527"
     gene            <1. .>711
                     /gene="mPAP"
     CDS             <1. .>711
                     /gene="mPAP"
                     /note="AVP"
                     /codon_start=1
                     /product="antiviral protein"
                     /protein_id="AAK21951.1"
                     /db_xref="GI:13398617"
                     /translation="VNTIIYNVGSTTISKYATFLNDLRNEAKDPSLKCYGIPMLPNTN
                     TNPKYVLVELQGSNKKTITLMLRRNNLYVMGYSDPFEANKCRYHIFNDISGTERQDVE
                     TTLCPNANSRVSKNINFDSRYPTLESKAGVKSRSQVQLGIQILDSNIGKISGVMSFTE
                     KTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAFNPNPKVLNLQETWGKISTAIHGA
                     KNGVLPKPLELVDASGAKW"
ORIGIN

Alignment Scores:
Pred. No.:              4.95          Length:        711
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     15            Gaps:          1

US-10-758-902-1 (1-30) x AF338910 (1-711)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db          4 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 63

Qy         20 AspLeuArgAsnGlu 24
              |||||||||||||
Db         64 GATCTTCGTAATGAA 78

RESULT 12
AY603352
LOCUS       AY603352                714 bp    DNA     linear   PLN 17-MAY-2004
DEFINITION  Phytolacca americana antiviral protein PAP (pap) gene, pap-s
            allele, partial cds.
ACCESSION   AY603352
VERSION     AY603352.1  GI:47175554
KEYWORDS    .
SOURCE      Phytolacca americana (American pokeweed)
  ORGANISM  Phytolacca americana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1  (bases 1 to 714)
  AUTHORS   Chen,G., Lei,J., Cao,B. and Zeng,G.
  TITLE     Phytolacca americana antiviral protein (PAP) DNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 714)
  AUTHORS   Chen,G., Lei,J., Cao,B. and Zeng,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2004) Horticultural College, South China
            Agricultural University, Wushan, Guangzhou, Guangdong 510642, PR
            China
FEATURES             Location/Qualifiers
     source          1. .714
                     /organism="Phytolacca americana"
```

```
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3527"
                     /tissue_type="spring leaves"
     gene            <1. .>714
                     /gene="pap"
                     /allele="s"
     mRNA            <1. .>714
                     /gene="pap"
                     /allele="s"
                     /product="antiviral protein PAP"
     CDS             <1. .714
                     /gene="pap"
                     /allele="s"
                     /note="resistance to virus"
                     /codon_start=1
                     /product="antiviral protein PAP"
                     /protein_id="AAT12447.1"
                     /db_xref="GI:47175555"
                     /translation="VNTIIYNVGSTTISKYATFLNDLRNEAKDPSLKCYGIPMLPNTN
                     TNPKYVLVELQGSNKKTITLMLRRNNLYVMGYSDPFETNKCRYHIFNDISGTERQDVE
                     TTLCPNANSRVSKNINFDSRYPTLESKAGVKSRSQVQLGIQILDSNIGKISGVMSFTE
                     KTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAFNPNPKVLNLQETWGKISTAIHDA
                     KNGVLPKPLELVDASGAKW"
ORIGIN

Alignment Scores:
Pred. No.:              4.97          Length:         714
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     15            Gaps:           1

US-10-758-902-1 (1-30) x AY603352 (1-714)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db          4 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 63

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db         64 GATCTTCGTAATGAA 78

RESULT 13
AY603353
LOCUS       AY603353                714 bp    DNA     linear   PLN 17-MAY-2004
DEFINITION  Phytolacca acinosa antivral protein PAPa1 (papa1) gene, papa1-s
            allele, partial cds.
ACCESSION   AY603353
VERSION     AY603353.1  GI:47175556
KEYWORDS    .
SOURCE      Phytolacca acinosa (food pokeweed)
  ORGANISM  Phytolacca acinosa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1  (bases 1 to 714)
  AUTHORS   Chen,G., Lei,J., Cao,B. and Zeng,G.
  TITLE     Phytolacca acinosa anti-viral protein PAP (PAPa1) DNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 714)
  AUTHORS   Chen,G., Lei,J., Cao,B. and Zeng,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2004) Horticultural College, South China
            Agricultural University, Wushan, Guangzhou, Guangdong 510642, PR
            China
FEATURES             Location/Qualifiers
     source          1. .714
                     /organism="Phytolacca acinosa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3528"
                     /tissue_type="summer leaves"
     gene            <1. .>714
                     /gene="papa1"
                     /allele="s"
     mRNA            <1. .>714
                     /gene="papa1"
                     /allele="s"
                     /product="antivral protein PAPa1"
     CDS             <1. .714
                     /gene="papa1"
                     /allele="s"
                     /codon_start=1
                     /product="antivral protein PAPa1"
                     /protein_id="AAT12448.1"
                     /db_xref="GI:47175557"
                     /translation="MNTIIYNVGSTTISKYATFLNDLRNEAKDPSLKCYGIPMLPNTN
                     TNPKYVLVELQGSNKKTITLMLRRNNLYVMGYSDPFETNKCRYHIFNDISGTERQDVE
                     TTLCPNANSRVSRNINFDSRYPTLESKAGVKSRSQVQLGIQILDSNIGKISGVMSFTE
                     KTEAEFLLVAIQMVSEAARFKYIENQVRTNFNRAFNPNPKVLNLQETWGKISTAIHDA
                     KNGVLPKPLELVDASGAKW"
ORIGIN

Alignment Scores:
Pred. No.:              4.97          Length:         714
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     15            Gaps:           1

US-10-758-902-1 (1-30) x AY603353 (1-714)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db          4 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 63

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db         64 GATCTTCGTAATGAA 78

RESULT 14
AY327475
LOCUS       AY327475                939 bp    mRNA    linear   PLN 01-JUL-2004
DEFINITION  Phytolacca heterotepala anti-viral protein PAP (RIP1) mRNA,
            complete cds.
ACCESSION   AY327475
VERSION     AY327475.1  GI:37625511
KEYWORDS    .
SOURCE      Phytolacca heterotepala
  ORGANISM  Phytolacca heterotepala
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Delli Bovi,P. and Corrado,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUN-2003) Department of Soil, Plants and
            Environmental Sciences, University of Naples 'Federico II', via
            Universita' 100, Portici, Naples 80055, Italy
FEATURES             Location/Qualifiers
     source          1. .939
                     /organism="Phytolacca heterotepala"
                     /mol_type="mRNA"
                     /db_xref="taxon:248308"
     gene            1. .939
                     /gene="RIP1"
     CDS             1. .939
                     /gene="RIP1"
                     /note="PhRIP1; ribosome inactivating protein"
                     /codon_start=1
                     /product="anti-viral protein PAP"
                     /protein_id="AAQ95991.1"
                     /db_xref="GI:37625512"
                     /translation="MKSMLVVTISVWLILAPTSTWAVNTIIYNVGSTTISKYATFLDD
                     LRNEAKDPNLKCYGIPMLPNTNSNPKYVLVELQGSNKKTITLMLRRNNLYVMGYSDPF
```

```
                    DTSKCRYHIFNDISGTERQDVETTLCPNSNSRVSKNINYDSRYPTLESKVGVKSRSQV
                    QLGIQILDSDIGKISGVTSFSEKTEAEFLLVAIQISEAARFKYIENQVKTNFNRAFNP
                    NPKVLNLEETWGKISTAIHDAKNGVLPKPLELVDASGAKWIVLRVDEMKPDVALLNYV
                    SGSCQTTYNQNAMFPQLIMSTYYNYMANLGDLFEEF"
ORIGIN

Alignment Scores:
Pred. No.:              6.57          Length:        939
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     15            Gaps:          1

US-10-758-902-1 (1-30) x AY327475 (1-939)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||:::
Db         70 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGGAT 129

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        130 GATCTTCGTAATGAA 144

RESULT 15
AY547315
LOCUS       AY547315                942 bp    DNA     linear   PLN 13-JUL-2005
DEFINITION  Phytolacca americana antiviral protein gene, complete cds.
ACCESSION   AY547315
VERSION     AY547315.1  GI:44889055
KEYWORDS    .
SOURCE      Phytolacca americana (American pokeweed)
  ORGANISM  Phytolacca americana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1  (bases 1 to 942)
  AUTHORS   Zhao,Y., Wang,X., Zhou,G. and Li,H.
  TITLE     A pokeweed antiviral protein gene in roots of Phytolacca americana
  JOURNAL   Acta Virol. 48 (2), 131-132 (2004)
   PUBMED   15462289
REFERENCE   2  (bases 1 to 942)
  AUTHORS   Zhao,Y., Wang,X. and Li,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-FEB-2004) Plant Virology, Institute of Plant
            Protection, CAAS, No.2 Yuanmingyuan Road West, Beijing 100094, P.R.
            China
FEATURES             Location/Qualifiers
     source          1. .942
                     /organism="Phytolacca americana"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3527"
     mRNA            <1. .>942
                     /product="antiviral protein"
     CDS             1. .942
                     /codon_start=1
                     /product="antiviral protein"
                     /protein_id="AAS48199.1"
                     /db_xref="GI:44889056"
                     /translation="MKSMLVVTISIWLILAPTSTWAVNTIIYNVGSTTISKYATFLND
                     LRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKKTITLMLRRNNLYVMGYSDPF
                     ETNKCRYHIFNDISGTERQDVETTLCPNANSRVSKNINFDSRYPTLESKAGVKSRSQV
                     QLGIQILDSNIGKISGVMSFTEKTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAFN
                     PNPKVLNLQETWGKISTAIHDAKNGVLPKPLELVDASGAKWIVLRVDEIKPDVALLNY
                     VGGSCQTTYNQNAMFPQLIMSTYYNYMVNLGDLFEGF"
ORIGIN

Alignment Scores:
Pred. No.:              6.59          Length:        942
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     15            Gaps:          1

US-10-758-902-1 (1-30) x AY547315 (1-942)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||:::
Db         70 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 129

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        130 GATCTTCGTAATGAA 144

RESULT 16
AY572976
LOCUS       AY572976                942 bp    mRNA    linear   PLN 05-APR-2004
DEFINITION  Phytolacca americana antiviral protein (PAP) mRNA, complete cds.
ACCESSION   AY572976
VERSION     AY572976.1  GI:45826466
KEYWORDS    .
SOURCE      Phytolacca americana (American pokeweed)
  ORGANISM  Phytolacca americana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1  (bases 1 to 942)
  AUTHORS   Xiao,Z.A. and Jiang,Y.
  TITLE     A gene encoding the pokeweed antivirus protein in the leaf of
            Phytolacca americana
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 942)
  AUTHORS   Xiao,Z.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal
            University, No. 19 Xinjiekouwai Street, Haidian District, Beijing
            100875, China
FEATURES             Location/Qualifiers
     source          1. .942
                     /organism="Phytolacca americana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3527"
     gene            1. .942
                     /gene="PAP"
     CDS             1. .942
                     /gene="PAP"
                     /codon_start=1
                     /product="antiviral protein"
                     /protein_id="AAS77872.1"
                     /db_xref="GI:45826467"
                     /translation="MKVMLVVTISIWLILAPTSTWAVNTIIYNVGSTTISKYATFLND
                     LRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKKTITLMLRRNNLYVMGYSDPF
                     ETNKCRYHIFNDISGTERQDVETTLCPNANSRVSKNINFDSRYPTLESKAGVKSRSQV
                     QLGIQILDSNIGKISGVMSFTEKTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAFN
                     PNPKVLNLQETWGKISTAIHDAKNGVLPKPLELVDASGAKWIVLRVDEIKPDVALLNY
                     VGGSCQTTYNQNAMFPQLIMSTYYNYMVNLGDLFEGF"
ORIGIN

Alignment Scores:
Pred. No.:              6.59          Length:        942
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     15            Gaps:          1

US-10-758-902-1 (1-30) x AY572976 (1-942)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||:::
Db         70 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 129

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        130 GATCTTCGTAATGAA 144
```

```
RESULT 17
PAPAP
LOCUS       PAPAP                   1164 bp    mRNA    linear   PLN 18-NOV-1991
DEFINITION  P.americana PAP gene for anti-viral protein.
ACCESSION   X55383
VERSION     X55383.1  GI:20421
KEYWORDS    antiviral protein; cell wall protein; PAP gene; ribosome
            inactivating protein.
SOURCE      Phytolacca americana (American pokeweed)
  ORGANISM  Phytolacca americana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1  (bases 1 to 1164)
  AUTHORS   Lin,Q., Chen,Z.C., Antoniw,J.F. and White,R.F.
  TITLE     Isolation and characterization of a cDNA clone encoding the
            anti-viral protein from Phytolacca americana
  JOURNAL   Plant Mol. Biol. 17 (4), 609-614 (1991)
   PUBMED   1912488
REFERENCE   2  (bases 1 to 1164)
  AUTHORS   Antoniw,J.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-1990) Antoniw J.F., AFRC Inst of Arable Crops
            Research, Dept. of Plant Pathology, Rothamsted Experimental
            Station, Harpenden, Hert, AL5 2JQ, UK
FEATURES             Location/Qualifiers
     source          1. .1164
                     /organism="Phytolacca americana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3527"
                     /tissue_type="leaf"
                     /dev_stage="vegetative"
     gene            1. .1164
                     /gene="PAP"
     CDS             2. .943
                     /gene="PAP"
                     /codon_start=1
                     /product="anti-viral protein"
                     /protein_id="CAA39054.1"
                     /db_xref="GI:20422"
                     /db_xref="GOA:P10297"
                     /db_xref="UniProt/Swiss-Prot:P10297"
                     /translation="MKSMLVVTISIWLILAPTSTWAVNTIIYNVGSTTISKYATFLND
                     LRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKKTITLMLRRNNLYVMGYSDPF
                     ETNKCRYHIFNDISGTERQDVETTLCPNANSRVSKNINFDSRYPTLESKAGVKSRSQV
                     QLGIQILDSNIGKISGVMSFTEKTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAFN
                     PNPKVLNLQETWGKISTAIHDAKNGVLPKPLELVDASGAKWIVLRVDEIKPDVALLNY
                     VGGSCQTTYNQNAMFPQLIMSTYYNYMVNLGDLFEGF"
ORIGIN

Alignment Scores:
Pred. No.:              8.17          Length:        1164
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     15            Gaps:          1

US-10-758-902-1 (1-30) x PAPAP (1-1164)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db         71 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 130

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        131 GATCTTCGTAATGAA 145

RESULT 18
A36639
LOCUS       A36639                  1195 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 1 from Patent EP0585554.
ACCESSION   A36639
VERSION     A36639.1  GI:2293943
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Kim,M., Lee,K., Na,B., Jeong,H.S., Choi,K., Moon,Y. and Jeon,H.
  TITLE     Process for preparing a transgenic plant expressing phytolacca
            antiviral protein
  JOURNAL   Patent: EP 0585554-A 1 09-MAR-1994;
            JINRO LIMITED (KR)
COMMENT     Other publication JP 6078775 940322
            Other publication KR 9512900 951023.
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              8.39          Length:        1195
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     6             Gaps:          1

US-10-758-902-1 (1-30) x A36639 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 19
A42103
LOCUS       A42103                  1195 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 1 from Patent EP0637591.
ACCESSION   A42103
VERSION     A42103.1  GI:2297595
KEYWORDS    .
SOURCE      Phytolacca americana (American pokeweed)
  ORGANISM  Phytolacca americana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Moon,Y., Jeon,H., Choi,K., Lee,K. and Kim,M.
  TITLE     A novel expression vector for phytolacca antiviral protein
  JOURNAL   Patent: EP 0637591-A 1 08-FEB-1995;
            JINRO LIMITED (KR)
COMMENT     Other publication AU 662844 950914
            Other publication JP 7067660 950314
            Other publication CA 2102859 950103
            Other publication AU 5064293 950119.
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Phytolacca americana"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3527"
ORIGIN

Alignment Scores:
Pred. No.:              8.39          Length:        1195
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
```

```
DB:                    6              Gaps:          1

US-10-758-902-1 (1-30) x A42103 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 20
I43835
LOCUS       I43835                 1195 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5633155.
ACCESSION   I43835
VERSION     I43835.1  GI:2468933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Kim,M.-K., Lee,K.-H., Na,B.-K., Jeong,H.-S., Choi,K.-W., Moon,Y.-H.
            and Jeon,H.-S.
  TITLE     Expression vector for phytolacca antiviral protein and process for
            preparing transgenic plant transformed therewith
  JOURNAL   Patent: US 5633155-A 1 27-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:             8.39          Length:        1195
Score:                 61.00         Matches:       12
Percent Similarity:    68.0%         Conservative:  5
Best Local Similarity: 48.0%         Mismatches:    6
Query Match:           38.1%         Indels:        2
DB:                    6             Gaps:          1

US-10-758-902-1 (1-30) x I43835 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 21
I55866
LOCUS       I55866                 1195 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5648234.
ACCESSION   I55866
VERSION     I55866.1  GI:2476660
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Moon,Y.-H., Jeon,H.-S., Choi,K.-W., Lee,K.-H. and Kim,M.-K.
  TITLE     Expression vector for Phytolacca antiviral protein
  JOURNAL   Patent: US 5648234-A 1 15-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:             8.39          Length:        1195
Score:                 61.00         Matches:       12
Percent Similarity:    68.0%         Conservative:  5
Best Local Similarity: 48.0%         Mismatches:    6
Query Match:           38.1%         Indels:        2
DB:                    6             Gaps:          1

US-10-758-902-1 (1-30) x I55866 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 22
AR009535
LOCUS       AR009535               1379 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5756322.
ACCESSION   AR009535
VERSION     AR009535.1  GI:3968340
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1379)
  AUTHORS   Tumer,N.E.
  TITLE     Pokeweed antiviral protein mutants
  JOURNAL   Patent: US 5756322-A 1 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .1379
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:             9.7           Length:        1379
Score:                 61.00         Matches:       12
Percent Similarity:    68.0%         Conservative:  5
Best Local Similarity: 48.0%         Mismatches:    6
Query Match:           38.1%         Indels:        2
DB:                    6             Gaps:          1

US-10-758-902-1 (1-30) x AR009535 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 23
AR136704
LOCUS       AR136704               1379 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6137030.
ACCESSION   AR136704
VERSION     AR136704.1  GI:14477376
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1379)
  AUTHORS   Tumer,N.E.
  TITLE     Pap mutants that exhibit anti-viral and/or anti-fungal activity in
            plants
  JOURNAL   Patent: US 6137030-A 1 24-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .1379
                     /organism="unknown"
```

```
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              9.7             Length:         1379
Score:                  61.00           Matches:        12
Percent Similarity:     68.0%           Conservative:   5
Best Local Similarity:  48.0%           Mismatches:     6
Query Match:            38.1%           Indels:         2
DB:                     6               Gaps:           1

US-10-758-902-1 (1-30) x AR136704 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 24
AR141172
LOCUS       AR141172                1379 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6146628.
ACCESSION   AR141172
VERSION     AR141172.1  GI:15100689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1379)
  AUTHORS   Uckun,F.M. and Tumer,N.E.
  TITLE     Biotherapeutic agents comprising recombinant PAP and PAP mutants
  JOURNAL   Patent: US 6146628-A 1 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .1379
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              9.7             Length:         1379
Score:                  61.00           Matches:        12
Percent Similarity:     68.0%           Conservative:   5
Best Local Similarity:  48.0%           Mismatches:     6
Query Match:            38.1%           Indels:         2
DB:                     6               Gaps:           1

US-10-758-902-1 (1-30) x AR141172 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 25
AX427731
LOCUS       AX427731                1379 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 30 from Patent WO0233107.
ACCESSION   AX427731
VERSION     AX427731.1  GI:21537838
KEYWORDS    .
SOURCE      Phytolacca americana (American pokeweed)
  ORGANISM  Phytolacca americana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1
  AUTHORS   Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
  TITLE     Plant cell death system
  JOURNAL   Patent: WO 0233107-A 30 25-APR-2002;
            CAMBRIDGE ADVANCED TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .1379
                     /organism="Phytolacca americana"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3527"
ORIGIN

Alignment Scores:
Pred. No.:              9.7             Length:         1379
Score:                  61.00           Matches:        12
Percent Similarity:     68.0%           Conservative:   5
Best Local Similarity:  48.0%           Mismatches:     6
Query Match:            38.1%           Indels:         2
DB:                     6               Gaps:           1

US-10-758-902-1 (1-30) x AX427731 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 26
AC011748
LOCUS       AC011748              127037 bp    DNA     linear   PRI 21-APR-2005
DEFINITION  Homo sapiens BAC clone RP11-441M4 from 2, complete sequence.
ACCESSION   AC011748
VERSION     AC011748.7  GI:13435284
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 127037)
  AUTHORS   Harris,A., Abbott,A., Hawkins,M. and Glaser,E.
  TITLE     The sequence of Homo sapiens BAC clone RP11-441M4
  JOURNAL   Unpublished (2001)
REFERENCE   2  (bases 1 to 127037)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-OCT-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   3  (bases 1 to 127037)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAR-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 127037)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   5  (bases 1 to 127037)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-APR-2005) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Mar 23, 2001 this sequence version replaced gi:11415218.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu
                Contact: submissions@watson.wustl.edu
```

```
            ---------- Summary Statistics
                Center project name: H_NH0441M04
            ----------.

            NOTICE:

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. Wes Warren,
            Department of Genetics, Washington University, St. Louis MO. For
            additional information about the map position of this sequence, see
            http://genome.wustl.edu

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries. Genomics 51:1-8. The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at http://www.chori.org
            VECTOR:  pBACe3.6

            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-549J11; the clone sequenced
            to the right is RP11-257N21, 200 bp overlap.  Actual start of this
            clone is at base position 1 of RP11-441M4; actual end is at base
            position 40609 of RP11-257N21.
FEATURES             Location/Qualifiers
     source          1. .127037
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /clone="RP11-441M4"
                     /clone_lib="RPCI-11"
     misc_feature    32816. .33089
                     /note="CpG_island (%GC=62.8, o/e=0.93, #CpGs=26)"
     misc_feature    38989. .39254
                     /note="CpG_island (%GC=63.5, o/e=0.96, #CpGs=27)"
     misc_feature    45982. .46198
                     /note="CpG_island (%GC=60.4, o/e=0.86, #CpGs=18)"
     misc_feature    61200. .61433
                     /note="CpG_island (%GC=57.3, o/e=1.00, #CpGs=18)"
     misc_feature    62374. .62647
                     /note="CpG_island (%GC=60.9, o/e=0.75, #CpGs=21)"
     misc_feature    98611. .98888
                     /note="CpG_island (%GC=60.4, o/e=0.75, #CpGs=21)"
ORIGIN

Alignment Scores:
Pred. No.:              1.16e+03        Length:         127037
Score:                  60.50           Matches:        14
Percent Similarity:     40.9%           Conservative:   4
Best Local Similarity:  31.8%           Mismatches:     7
Query Match:            37.8%           Indels:         19
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x AC011748 (1-127037)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db     107269 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 107328

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||

Db     107329 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 107388

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db     107389 AGAAACTCCCTA 107400

RESULT 27
AL929144/c
LOCUS       AL929144               82369 bp    DNA     linear   ROD 20-FEB-2003
DEFINITION  Mouse DNA sequence from clone RP23-441D24 on chromosome 2, complete
            sequence.
ACCESSION   AL929144
VERSION     AL929144.10  GI:28445903
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 82369)
  AUTHORS   Tracey,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-FEB-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Feb 20, 2003 this sequence version replaced gi:27902020.
            Sequence from the Mouse Genome Sequencing Consortium whole genome
            shotgun may have been used to confirm this sequence.  Sequence data
            from the whole genome shotgun alone has only been used where it has
            a phred quality of at least 30.
            ---------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ----------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest, except on the rare
            occasion of the clone being a YAC.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-441D24 is
            from the RPCI-23 Mouse BAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .82369
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="2"
                     /clone="RP23-441D24"
                     /clone_lib="RPCI-23"
ORIGIN

Alignment Scores:
Pred. No.:              895             Length:         82369
Score:                  60.00           Matches:        11
Percent Similarity:     65.4%           Conservative:   6
```

```
Best Local Similarity:  42.3%          Mismatches:     9
Query Match:            37.5%          Indels:         0
DB:                     9              Gaps:           0

US-10-758-902-1 (1-30) x AL929144 (1-82369)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              :::|||||||||:::         :::   :::||||||:::||||||      :::|||
Db      36750 ATCTCCTTTAATATGTTTTTGGTTTTTGTCCACCCCACATACATACAAGCATTCAAAAAC 36691

Qy         24 GluLeuAlaLysGlyThr 29
                 |||||||||
Db      36690 AATAACATCAAAGGAACA 36673

RESULT 28
CP000082_05
WPCOMMENT
  Sequence split into 27 fragments  LOCUS CP000082 Accession CP000082
     Fragment Name      Begin     End
     CP000082_00            1    110000
     CP000082_01       100001    210000
     CP000082_02       200001    310000
     CP000082_03       300001    410000
     CP000082_04       400001    510000
     CP000082_05       500001    610000
     CP000082_06       600001    710000
     CP000082_07       700001    810000
     CP000082_08       800001    910000
     CP000082_09       900001   1010000
     CP000082_10      1000001   1110000
     CP000082_11      1100001   1210000
     CP000082_12      1200001   1310000
     CP000082_13      1300001   1410000
     CP000082_14      1400001   1510000
     CP000082_15      1500001   1610000
     CP000082_16      1600001   1710000
     CP000082_17      1700001   1810000
     CP000082_18      1800001   1910000
     CP000082_19      1900001   2010000
     CP000082_20      2000001   2110000
     CP000082_21      2100001   2210000
     CP000082_22      2200001   2310000
     CP000082_23      2300001   2410000
     CP000082_24      2400001   2510000
     CP000082_25      2500001   2610000
     CP000082_26      2600001   2650701
Continuation (6 of 27) of CP000082 from base 500001 (CP000082 Psychrobacter arcticum 273

Alignment Scores:
Pred. No.:              1.2e+03        Length:         110000
Score:                  60.00          Matches:        12
Percent Similarity:     68.4%          Conservative:   1
Best Local Similarity:  63.2%          Mismatches:     6
Query Match:            37.5%          Indels:         0
DB:                     1              Gaps:           0

US-10-758-902-1 (1-30) x CP000082_05 (1-110000)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||         ||||||  ||||||  ||||||:::||||||  |||||||||
Db      92548 TATAAACGACGCTCGTTTACTTTGGGCTAAGCCTATCAATACCCAATTTTTATACAA 92604

RESULT 29
AC142050/c
LOCUS       AC142050              159553 bp    DNA     linear   HTG 21-MAR-2003
DEFINITION  Rattus norvegicus clone CH230-334J11, *** SEQUENCING IN PROGRESS
            ***, 55 unordered pieces.
ACCESSION   AC142050
VERSION     AC142050.1  GI:29135521
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 159553)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., Mcleod,M., Mcneill,T., Meenen,E., Milosavljevic,A.,
            Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
            Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,
            Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G.,
            Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
            Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A.,
            Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E.,
            Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
            Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A.,
            Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,
            Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,
            Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E.,
            Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,
            Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
            Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,
            Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
            Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R.,
            Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
            Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
            Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
            Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 159553)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     -------------- Genome Center
               Center: Baylor College of Medicine
               Center code: BCM
               Web site: http://www.hgsc.bcm.tmc.edu/
               Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
               Center project name: GQMD
               Center clone name: CH230-334J11
            -------------- Summary Statistics
               Sequencing vector: Plasmid;
               Chemistry: Dye-terminator Big Dye: 100% of reads
               Assembly program: Phrap; version 0.990329
               Consensus quality: 131561 bases at least Q40
               Consensus quality: 138750 bases at least Q30
```

```
    Consensus quality: 144073 bases at least Q20
    Estimated insert size: 136832; sum-of-contigs estimation
    Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
--------------
* NOTE: Estimated insert size may differ from sequence length
*   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 55 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*        1     1050: contig of 1050 bp in length
*     1051     1150: gap of unknown length
*     1151     2793: contig of 1643 bp in length
*     2794     2893: gap of unknown length
*     2894     4413: contig of 1520 bp in length
*     4414     4513: gap of unknown length
*     4514     5714: contig of 1201 bp in length
*     5715     5814: gap of unknown length
*     5815     7065: contig of 1251 bp in length
*     7066     7165: gap of unknown length
*     7166     8324: contig of 1159 bp in length
*     8325     8424: gap of unknown length
*     8425     9951: contig of 1527 bp in length
*     9952    10051: gap of unknown length
*    10052    11308: contig of 1257 bp in length
*    11309    11408: gap of unknown length
*    11409    12893: contig of 1485 bp in length
*    12894    12993: gap of unknown length
*    12994    14260: contig of 1267 bp in length
*    14261    14360: gap of unknown length
*    14361    15896: contig of 1536 bp in length
*    15897    15996: gap of unknown length
*    15997    17677: contig of 1681 bp in length
*    17678    17777: gap of unknown length
*    17778    19743: contig of 1966 bp in length
*    19744    19843: gap of unknown length
*    19844    21898: contig of 2055 bp in length
*    21899    21998: gap of unknown length
*    21999    23676: contig of 1678 bp in length
*    23677    23776: gap of unknown length
*    23777    25744: contig of 1968 bp in length
*    25745    25844: gap of unknown length
*    25845    27883: contig of 2039 bp in length
*    27884    27983: gap of unknown length
*    27984    29124: contig of 1141 bp in length
*    29125    29224: gap of unknown length
*    29225    30722: contig of 1498 bp in length
*    30723    30822: gap of unknown length
*    30823    32060: contig of 1238 bp in length
*    32061    32160: gap of unknown length
*    32161    33716: contig of 1556 bp in length
*    33717    33816: gap of unknown length
*    33817    35256: contig of 1440 bp in length
*    35257    35356: gap of unknown length
*    35357    37116: contig of 1760 bp in length
*    37117    37216: gap of unknown length
*    37217    39072: contig of 1856 bp in length
*    39073    39172: gap of unknown length
*    39173    40905: contig of 1733 bp in length
*    40906    41005: gap of unknown length
*    41006    42288: contig of 1283 bp in length
*    42289    42388: gap of unknown length
*    42389    44475: contig of 2087 bp in length
*    44476    44575: gap of unknown length
*    44576    46729: contig of 2154 bp in length
*    46730    46829: gap of unknown length
*    46830    48457: contig of 1628 bp in length
*    48458    48557: gap of unknown length
*    48558    50390: contig of 1833 bp in length
*    50391    50490: gap of unknown length
*    50491    51882: contig of 1392 bp in length
*    51883    51982: gap of unknown length
*    51983    54369: contig of 2387 bp in length
*    54370    54469: gap of unknown length
*    54470    56448: contig of 1979 bp in length
*    56449    56548: gap of unknown length
*    56549    59347: contig of 2799 bp in length
*    59348    59447: gap of unknown length
*    59448    61987: contig of 2540 bp in length
*    61988    62087: gap of unknown length
*    62088    63574: contig of 1487 bp in length
*    63575    63674: gap of unknown length
*    63675    66606: contig of 2932 bp in length
*    66607    66706: gap of unknown length
*    66707    69996: contig of 3290 bp in length
*    69997    70096: gap of unknown length
*    70097    72964: contig of 2868 bp in length
*    72965    73064: gap of unknown length
*    73065    75978: contig of 2914 bp in length
*    75979    76078: gap of unknown length
*    76079    79925: contig of 3847 bp in length
*    79926    80025: gap of unknown length
*    80026    83115: contig of 3090 bp in length
*    83116    83215: gap of unknown length
*    83216    86362: contig of 3147 bp in length
*    86363    86462: gap of unknown length
*    86463    90320: contig of 3858 bp in length
*    90321    90420: gap of unknown length
*    90421    94926: contig of 4506 bp in length
*    94927    95026: gap of unknown length
*    95027    98428: contig of 3402 bp in length
*    98429    98528: gap of unknown length
*    98529   103394: contig of 4866 bp in length
*   103395   103494: gap of unknown length
*   103495   108744: contig of 5250 bp in length
*   108745   108844: gap of unknown length
*   108845   113802: contig of 4958 bp in length
*   113803   113902: gap of unknown length
*   113903   118843: contig of 4941 bp in length
*   118844   118943: gap of unknown length
*   118944   124305: contig of 5362 bp in length
*   124306   124405: gap of unknown length
*   124406   129275: contig of 4870 bp in length
*   129276   129375: gap of unknown length

Alignment Scores:
Pred. No.:              1.75e+03        Length:         159553
Score:                  60.00           Matches:        10
Percent Similarity:     65.2%           Conservative:   5
Best Local Similarity:  43.5%           Mismatches:     8
Query Match:            37.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC142050 (1-159553)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              :::|||:::     |||||||||   |||:::   ||||||   |||   ::::::|||
Db      78691 ATGGGGCAGAAGCAAGAGTATCCCAGATTCTTGGCTGACCTGGGGAACAGAGTGAGCAAA 78632

Qy         28 GlyThrPro 30
                 |||
Db      78631 AGCCAGCCT 78623

RESULT 30
AC127834
LOCUS       AC127834               196519 bp    DNA     linear   HTG 20-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-310P20, WORKING DRAFT SEQUENCE, 2
            unordered pieces.
ACCESSION   AC127834
VERSION     AC127834.3  GI:25139816
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
```

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 196519)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 196519)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 196519)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 20, 2002 this sequence version replaced gi:23913725.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
---------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
---------- Project Information
Center project name: GZYH
Center clone name: CH230-310P20
---------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 178081 bases at least Q40
Consensus quality: 179853 bases at least Q30
Consensus quality: 181198 bases at least Q20
Estimated insert size: 180567; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 195390: contig of 195390 bp in length
* 195391 195490: gap of unknown length
* 195491 196519: contig of 1029 bp in length.

FEATURES Location/Qualifiers
source 1. .196519
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-310P20"
misc_feature 1. .1015
/note="wgs_end_extension
clone_end:T7"
misc_feature 5736. .7657
/note="wgs_end_extension
clone_end:T7"
misc_feature 9092. .9650
/note="clone_boundary
clone_end:T7
site:
end_sequence:BZ149095"
misc_feature 189761. .190699
/note="clone_boundary
clone_end:Sp6
site:
end_sequence:BZ149098"
misc_feature 191015. .192248
/note="wgs_end_extension
clone_end:Sp6"
misc_feature 194316. .195390
/note="wgs_end_extension
clone_end:Sp6"
gap 195391. .195490
/estimated_length=unknown
ORIGIN

Alignment Scores:
Pred. No.: 2.17e+03 Length: 196519
Score: 60.00 Matches: 10
Percent Similarity: 76.0% Conservative: 9

```
Best Local Similarity:  40.0%          Mismatches:    6
Query Match:            37.5%          Indels:        0
DB:                     14             Gaps:          0

US-10-758-902-1 (1-30) x AC127834 (1-196519)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::||||||:::|||   :::      |||:::::|||||||||   :::|||
Db      63260 TTCCATACTGTGACATTCATGATGGAGATGGCTTTTCAGTACCCTACTGAGTTGCAGAGC 63319

Qy         21 LeuArgAsnGluLeu 25
                |||||:::::
Db      63320 AAGAGAZACAAGATT 63334

RESULT 31
AC097283/c
LOCUS       AC097283               212628 bp    DNA     linear   HTG 10-MAY-2003
DEFINITION  Rattus norvegicus clone CH230-167D17, WORKING DRAFT SEQUENCE, 2
            unordered pieces.
ACCESSION   AC097283
VERSION     AC097283.7  GI:30522850
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 212628)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 212628)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 212628)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On May 10, 2003 this sequence version replaced gi:25009237.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GGIR
                Center clone name: CH230-167D17
            -------------- Summary Statistics
                Assembly program: Atlas 3.0;
                Consensus quality: 206134 bases at least Q40
                Consensus quality: 207427 bases at least Q30
                Consensus quality: 208728 bases at least Q20
                Estimated insert size: 216264; sum-of-contigs estimation
                Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1   211427: contig of 211427 bp in length
            *  211428   211527: gap of unknown length
            *  211528   212628: contig of 1101 bp in length.
FEATURES             Location/Qualifiers
     source          1. .212628
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-167D17"
     misc_feature    complement(3559. .4319)
                     /note="clone_boundary
                     clone_end:T7
                     site:EcoRI
                     end_sequence:BH303628"
     gap             211428. .211527
                     /estimated_length=unknown
```

```
ORIGIN

Alignment Scores:
Pred. No.:              2.35e+03        Length:         212628
Score:                  60.00           Matches:        10
Percent Similarity:     76.0%           Conservative:   9
Best Local Similarity:  40.0%           Mismatches:     6
Query Match:            37.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC097283 (1-212628)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::||||||:::|||   :::      |||::::::|||||||||   :::|||
Db      61098 TTCCATACTGTGACATTCATGATGGAGATGGCTTTTCAGTACCCTACTGAGTTGCAGAGC 61039

Qy         21 LeuArgAsnGluLeu 25
                 ||||||::::::
Db      61038 AAGAGAAACAAGATT 61024

RESULT 32
AC113732
LOCUS       AC113732               227364 bp    DNA     linear   HTG 20-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-210M17, WORKING DRAFT SEQUENCE.
ACCESSION   AC113732
VERSION     AC113732.8  GI:25138760
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 227364)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 227364)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 227364)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 20, 2002 this sequence version replaced gi:22856683.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GSDO
                Center clone name: CH230-210M17
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 220390 bases at least Q40
                Consensus quality: 221613 bases at least Q30
                Consensus quality: 222427 bases at least Q20
                Estimated insert size: 224125; sum-of-contigs estimation
                Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *         1   227364: contig of 227364 bp in length.
FEATURES             Location/Qualifiers
     source          1. .227364
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-210M17"
     misc_feature    1. .1005
                     /note="wgs_contig"
     misc_feature    225547. .227364
```

```
                     /note="wgs_contig"
ORIGIN

Alignment Scores:
Pred. No.:              2.51e+03        Length:         227364
Score:                  60.00           Matches:        10
Percent Similarity:     76.0%           Conservative:   9
Best Local Similarity:  40.0%           Mismatches:     6
Query Match:            37.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC113732 (1-227364)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::||||||:::|||   :::     |||::::::|||||||||   :::|||
Db     130831 TTCCATACTGTGACATTCATGATGGAGATGGCTTTTCAGTACCCTACTGAGTTGCAGAGC 130890

Qy         21 LeuArgAsnGluLeu 25
                ||||||::::::
Db     130891 AAGAGAAACAAGATT 130905

RESULT 33
AC114922
LOCUS       AC114922               238457 bp    DNA     linear   HTG 08-NOV-2003
DEFINITION  Mus musculus chromosome UNK clone RP23-206O17, WORKING DRAFT
            SEQUENCE, 8 unordered pieces.
ACCESSION   AC114922
VERSION     AC114922.5  GI:38229422
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 238457)
  AUTHORS   Wilson,R.K.
  TITLE     The sequence of Mus musculus clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 238457)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAR-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
REFERENCE   3  (bases 1 to 238457)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-NOV-2003) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
COMMENT     On Nov 8, 2003 this sequence version replaced gi:34495077.

            ----------------- Genome Center ----------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu
            Contact: submissions@watson.wustl.edu
            -------------- Project Information -------------------
            Center project name: M_BA0206O17
            ------------------------------------------------------
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 0%
            Sequencing vector: plasmid; 100%
            Chemistry: Dye-primer ET; 0% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 234575 bases at least Q40
            Consensus quality: 235087 bases at least Q30
            Consensus quality: 235374 bases at least Q20
            Insert size: 194000; agarose-fp
            Insert size: 236818; sum-of-contigs
            Quality coverage: 14.14 in Q20 bases; agarose-fp
            Quality coverage: 11.17 in Q20 bases; sum-of-contigs
            ------------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1      117: contig of 117 bp in length
            *      118      217: gap of unknown length
            *      218     1039: contig of 822 bp in length
            *     1040     1139: gap of unknown length
            *     1140    10438: contig of 9299 bp in length
            *    10439    10538: gap of unknown length
            *    10539    17369: contig of 6831 bp in length
            *    17370    17469: gap of unknown length
            *    17470    31212: contig of 13743 bp in length
            *    31213    31312: gap of unknown length
            *    31313    58819: contig of 27507 bp in length
            *    58820    58919: gap of unknown length
            *    58920   104268: contig of 45349 bp in length
            *   104269   104368: gap of unknown length
            *   104369   238457: contig of 134089 bp in length.
FEATURES             Location/Qualifiers
     source          1. .238457
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="UNK"
                     /clone="RP23-206O17"
     misc_feature    1. .117
                     /note="assembly_name:Contig26"
     gap             118. .217
                     /estimated_length=unknown
     misc_feature    218. .1039
                     /note="assembly_name:Contig20"
     gap             1040. .1139
                     /estimated_length=unknown
     misc_feature    1140. .10438
                     /note="assembly_name:Contig31"
     gap             10439. .10538
                     /estimated_length=unknown
     misc_feature    10539. .17369
                     /note="assembly_name:Contig32"
     gap             17370. .17469
                     /estimated_length=unknown
     misc_feature    17470. .31212
                     /note="assembly_name:Contig33"
     gap             31213. .31312
                     /estimated_length=unknown
     misc_feature    31313. .58819
                     /note="assembly_name:Contig34"
     gap             58820. .58919
                     /estimated_length=unknown
     misc_feature    58920. .104268
                     /note="assembly_name:Contig35"
     gap             104269. .104368
                     /estimated_length=unknown
     misc_feature    104369. .238457
                     /note="assembly_name:Contig36"
ORIGIN

Alignment Scores:
Pred. No.:              2.64e+03        Length:         238457
Score:                  60.00           Matches:        11
Percent Similarity:     65.4%           Conservative:   6
Best Local Similarity:  42.3%           Mismatches:     9
Query Match:            37.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC114922 (1-238457)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              :::|||||||||:::         :::   :::|||||:::||||||      :::|||
```

```
Db      28063 ATCTCCTTTAATATGTTTTTGGTTTTTGTCCACCCCACATACATACAAGCATTCAAAAAC 28122

Qy         24 GluLeuAlaLysGlyThr 29
                  |||||||||
Db      28123 AATAACATCAAAGGAACA 28140

RESULT 34
AC095327/c
LOCUS       AC095327               240406 bp    DNA     linear   HTG 10-MAY-2003
DEFINITION  Rattus norvegicus clone CH230-89H22, *** SEQUENCING IN PROGRESS
            ***, 2 unordered pieces.
ACCESSION   AC095327
VERSION     AC095327.6  GI:30522069
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 240406)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 240406)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-SEP-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 240406)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On May 10, 2003 this sequence version replaced gi:23264460.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GGBN
                Center clone name: CH230-89H22
            -------------- Summary Statistics
                Assembly program: Atlas 3.0;
                Consensus quality: 215532 bases at least Q40
                Consensus quality: 218102 bases at least Q30
                Consensus quality: 219920 bases at least Q20
                Estimated insert size: 228525; sum-of-contigs estimation
                Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1   238917: contig of 238917 bp in length
            *  238918   239017: gap of unknown length
            *  239018   240406: contig of 1389 bp in length.
FEATURES             Location/Qualifiers
     source          1. .240406
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-89H22"
     misc_feature    1. .1904
                     /note="wgs_end_extension
                     clone_end:Sp6"
     misc_feature    16214. .16757
                     /note="clone_boundary
                     clone_end:Sp6
                     site:EcoRI
                     end_sequence:BH340076"
     misc_feature    complement(234581. .235409)
                     /note="clone_boundary
                     clone_end:T7
                     site:EcoRI
                     end_sequence:BH340075"
     misc_feature    235988. .238917
                     /note="wgs_end_extension
```

```
                clone_end:T7"
    gap         238918. .239017
                /estimated_length=unknown
ORIGIN

Alignment Scores:
Pred. No.:              2.66e+03        Length:         240406
Score:                  60.00           Matches:        10
Percent Similarity:     65.2%           Conservative:   5
Best Local Similarity:  43.5%           Mismatches:     8
Query Match:            37.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC095327 (1-240406)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              :::|||:::      |||||||||   |||:::   ||||||   |||   ::::::|||
Db      88378 ATGGGGCAGAAGCAAGAGTATCCCAGATTCTTGGCTGACCTGGGGAACAGAGTGAGCAAA 88319

Qy         28 GlyThrPro 30
                 |||
Db      88318 AGCCAGCCT 88310

RESULT 35
AB071854
LOCUS       AB071854                 783 bp    DNA     linear   PLN 19-MAR-2002
DEFINITION  Phytolacca americana paps1 gene for PAP-S1, partial cds.
ACCESSION   AB071854
VERSION     AB071854.1  GI:19570837
KEYWORDS    .
SOURCE      Phytolacca americana (American pokeweed)
  ORGANISM  Phytolacca americana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE   1
  AUTHORS   Honjo,E. and Watanabe,K.
  TITLE     Cloning of genomic DNA encoding two types of pokeweed antiviral
            protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
            their recombinant proteins with other PAP isofoms
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 783)
  AUTHORS   Watanabe,K. and Honjo,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
            Department of Applied Biological Sciences; Honjo-machi, Saga city,
            Saga 840-8502, Japan (E-mail:watakei@cc.saga-u.ac.jp,
            Tel:81-952-28-8774, Fax:81-952-28-8774)
FEATURES            Location/Qualifiers
     source         1. .783
                    /organism="Phytolacca americana"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:3527"
     gene           1. .783
                    /gene="paps1"
     CDS            <1. .>783
                    /gene="paps1"
                    /note="mature pokeweed antiviral protein-S1"
                    /codon_start=1
                    /product="PAP-S1"
                    /protein_id="BAB86349.1"
                    /db_xref="GI:19570838"
                    /translation="INTITFDAGNATINKYATFMESLRNEAKDPSLKCYGIPMLPNTN
                    STIKYLLVKLQGASLKTITLMLRRNNLYVMGYSDPYDNKCRYHIFNDIKGTEYSDVEN
                    TLCPSSNPRVAKPINYNGLYPTLEKKAGVTSRNQVQLGIQILSSDIGKISGQGSFTEK
                    IEAKPLLVAIQMVSEAARFKYIENQVKTNFNRDFSPNDKVLDLEENWGKISTAIHNSK
                    NGALPKPLELKNADGTKWIVLRVDEIKPDVGLLNYVNGTCQAT"
ORIGIN

Alignment Scores:
Pred. No.:              11.4            Length:         783
Score:                  59.00           Matches:        12
Percent Similarity:     72.0%           Conservative:   6
Best Local Similarity:  48.0%           Mismatches:     5
Query Match:            36.9%           Indels:         2
DB:                     15              Gaps:           1

US-10-758-902-1 (1-30) x AB071854 (1-783)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          4 AATACGATAACGTTCGACGCTGGAAATGCAACCATTAACAAGTATGCTACCTTTATGGAA 63

Qy         20 AspLeuArgAsnGlu 24
                ||||||||||||
Db         64 TCTCTTCGTAATGAA 78

RESULT 36
AC074110
LOCUS       AC074110                 20509 bp    DNA     linear   PLN 30-JAN-2001
DEFINITION  Arabidopsis thaliana chromosome 1 BAC T18C15 genomic sequence,
            complete sequence.
ACCESSION   AC074110
VERSION     AC074110.5  GI:11072070
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 20509)
  AUTHORS   Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
            Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
            Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
  TITLE     Arabidopsis thaliana chromosome 1 BAC T18C15 genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 20509)
  AUTHORS   Town,C.D. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUL-2000) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
REFERENCE   3  (bases 1 to 20509)
  AUTHORS   Town,C.D. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-2000) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
REFERENCE   4  (bases 1 to 20509)
  AUTHORS   Town,C.D. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-2001) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
COMMENT     On Nov 2, 2000 this sequence version replaced gi:11024897.
            Address all correspondence to:at@tigr.org

            BAC clone T18C15 is from Arabidopsis thaliana chromosome 1
            The orientation of the sequence is from SP6 to T7 end of the BAC
            clone.
            Genes were identified by a combination of several methods: Gene
            prediction programs including Genscan+ (Chris Burge,
            http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
            http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
            of GlimmerM, see Mihaela Pertea,
            http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
            GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
            mpertea@tigr.org), searches of the complete sequence against a
            peptide database and the plant EST database at TIGR
            (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
            indicate the level of evidence for their annotation. Genes with
            similarity to other proteins are named after the database hits.
            Genes without significant peptide similarity but with EST
            similarity are named as  unknown  proteins. Genes without protein
            or EST similarity, that are predicted by more than two gene
            prediction programs over most of their length are annotated as
            hypothetical  proteins. Genes encoding tRNAs are predicted by
            tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
            Simple repeats are identified by repeatmasker (Arian Smit,
```

```
          http://ftp.genome.washington.edu/RM/RepeatMasker.html).
FEATURES             Location/Qualifiers
     source          1. .20509
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3702"
                     /chromosome="I"
                     /clone="T18C15"
                     /ecotype="Columbia"
     misc_feature    1
                     /note="14845 nt beyond this point were not included in the
                     submitted sequence due to an overlap with another BAC
                     (F2J10)"
     repeat_region   1923. .1996
                     /rpt_family="(CATA)n"
     repeat_region   2189. .2242
                     /rpt_family="(CATA)n"
     repeat_region   2248. .2426
                     /rpt_family="(CATA)n"
     gene            complement(3293. .4000)
                     /gene="T18C15_5"
                     /note="predicted by genemark hmm"
     mRNA            complement(join(<3293. .3351,3479. .3543,3640. .3812,
                     3893. .>4000))
                     /gene="T18C15_5"
     CDS             complement(join(3293. .3351,3479. .3543,3640. .3812,
                     3893. .4000))
                     /gene="T18C15_5"
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="AAG60163.1"
                     /db_xref="GI:12597853"
                     /translation="MDDTDADSLKSAAEHLISTLDDPVVVVLGSSPEKDKLCGGGGGG
                     KKARKSLKCLRESSGRSRGNSIRKARVKHNFKSELHVQREGRAHSLILDKTMFRFALL
                     IERRPNGFGRITKHDRALTVLGCVTGVTDAVI"
     gene            4699. .7134
                     /gene="T18C15_1"
                     /note="contains similarity to mutator like transposase
                     GB:AAD25847 GI:4587619 from (Arabidopsis thaliana)"
     mRNA            join(<4699. .6910,6989. .>7134)
                     /gene="T18C15_1"
     CDS             join(4699. .6910,6989. .7134)
                     /gene="T18C15_1"
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="AAG60164.1"
                     /db_xref="GI:12597854"
                     /translation="MAEREVVVLCYWNCHIKHGPDGVYFEGSTPKEMRVKKNADFSRF
                     LDELYLITGFDKQKSKLEIVARYPVVQSPNKFRYLLHPVANDIHWEKMLEVPSNHPCI
                     NSVEFYLEAKPKPNDPPPAPWSLLPMGMNPQKRQKSRHQVVGKRQKSTQQEVGDTNSG
                     SGSGSTPTLVSGLWLEGDTMRVGLCFKDLAEMKKAVDWCSIKRRQKCLLRETEKDVYV
                     VECERWHCKWSICASRREEDGLFEITECSGPHDCYPEHLNDFDAECIPFQIERVVRVQ
                     PTLSTAELDKWWEKKFGFALDQVVEHCSEGLVEDAKVKAIKRFFGDWDQSFRLIPKLM
                     SVLHSSNGLLVDWQYDSLTHDPEHASFRGLFWAFSQSIQGFQHCRPLIVVDTKNLGGK
                     YKMKLMIASAFDATNQYFPLAFAVTKEVSVDSWRWFLTRIREKVTQRQGICLISSPDP
                     DILAVINEPGSQWKEPWAYHRFCLYHLCSKLCSVSPGFDYNMHFLVDEAGSSSQKEEF
                     DSYMKEIKERNPEAWKWLDQFPPHQWALAHDDGRRYGIMRIDTEALFAVCKRFRKVAM
                     AGGVMLLFGQLKDAFAESFKLSRGSLKHGDVYTEHVMEKLEEFETDSDTWVITITPLE
                     RDAYQVSMAPKKKTRLMGQSNDSTSGIVQLNDTTCTCGEFQKNKFPCLHALAVCDELK
                     INPLQYVDDCYTVERYHKTYSAKFSPVPELSAWPEAYGVPTLIPPVIEPPPPKVSGKG
                     KEKDTEDDHLEEDEDGDDDEEEEDDDVDDDEEDDDDVDDDEDDEW"
     repeat_region   complement(7033. .7139)
                     /rpt_family="(CAT)n"
     gene            complement(7457. .9907)
                     /gene="T18C15_2"
                     /note="similar to mitotic checkpoint protein GB:BAB02543
                     GI:9294423 from (Arabidopsis thaliana)"
     mRNA            complement(join(<7457. .7748,7961. .8061,8138. .8216,
                     8531. .8611,8764. .8839,8976. .9242,9336. .9418,9573. .9703,
                     9794. .>9907))
                     /gene="T18C15_2"
     CDS             complement(join(7661. .7748,7961. .8061,8138. .8216,
                     8531. .8611,8764. .8839,8976. .9242,9336. .9418,9573. .9703,
                     9794. .9907))
                     /gene="T18C15_2"
                     /codon_start=1
                     /product="mitotic checkpoint protein, putative"
                     /protein_id="AAG60165.1"
                     /db_xref="GI:12597855"
                     /translation="MTLVPAIGRELSNPPSDGISNLRFSNNSDHLLVSSWDKSVRLYD
                     ANGDLMRGEPKHGGAVLDCCFHDDSSGFSVCADTKVRRIDFNAGKEDVLGTHEKPVRC
                     VEYSYAAGQVITGSWDKTIKCWDPRGASGTERTQIGTYMQPERVNSLSLVGNRLVVAT
                     AGRHVNIYDLRNMSQPEQRRESSLKYQTRCVRCYPNGTGYALSSVEGRVSMEFFDLSE
                     AAQAKKYAFKCHRKSEDGRDIVYPVNAIAFHPIYGTFASGGCDGFVNIWDGNNKKRLY
                     QYSKYPTSIAALSFSRDGGLLAVASSYTFEEGDKPHEPDAIFVRSVNEIEVKPKPKVY
                     PNPPV"
     repeat_region   complement(10745. .10806)
                     /rpt_family="AT_rich"
     gene            11289. .14824
                     /gene="T18C15_3"
                     /note="similar to Cys2 His2 type zinc finger protein 2
                     GB:BAA85107 GI:6009885 from (Arabidopsis thaliana)"
     mRNA            join(<11289. .12519,13302. .>14824)
                     /gene="T18C15_3"
     CDS             join(11289. .12519,13302. .14824)
                     /gene="T18C15_3"
                     /codon_start=1
                     /product="Cys2/His2-type zinc finger protein, putative"
                     /protein_id="AAG60166.1"
                     /db_xref="GI:12597856"
                     /translation="MDLKTLNQFSPLTKLTVPNHRDVQVRTDQLITYERSKRKSSLHD
                     DEDLISKRRCLDFQRKIEDNECANDGVFVAPPRFKSGQVSIRQRSDAPLSSQAVKHDE
                     FANDAFYKPWLDSFRLKRQRLGDDEDPSSSSSPSEVDIAALTLLQFSCDRRHPQTQTL
                     TRPQPQTHKTQLQRPPPQLQSQTQTAPPKSDLFKCSICEKVFTSYQALGGHKASHSIK
                     AAQLENAGADAGEKTRSKMLSPSGKIHKCDICHVLFPTGQALGGHKRRHYEGLLGGHK
                     RGNDEAVLKLSPNSNKSVVTKVLDAEQSLRASDNIHKRNQDEVVPSRDKWSLSNVSVV
                     KNVLDLKLSLGESDGGHKDSQDEVVVHEDKCSPSSNGSIVTNVSDPEQSVRRLIDLNN
                     PPSLEFDQSRGGDVEEVEKEVVLALSSQMKQPSKDVSALIKRLEFAMQERKDGLLADD
                     NVLIEMIMELEGNISTTNGDDEDPYSEGRLIKVIEPIGLDEDDECVEIGLGSCEQEPI
                     QERFGDDKDPSSDHGNVESIRLEEEDAVLPEPWLKSRLKSRDREQSQRQGFGEYEDCF
                     SERRFLQEEEEECFGDDEDSFSDQISFLESNRLEEEFEEEKEAARFSNDNDFVELLFQ
                     GIEQSKSKPKPKSCSYYDDDDDDDDDGDEDDDDDDDDVDPSSKDIRLEEENECENRAV
                     IRPSLNSVAPNQQRFGDDEVPSSSSSLSKDETAALCPTPHSQTQPQSQTQLQKVTQPQ
                     TQMLPKSDSYQCNVCGRELPSYQALGGHKASHRTKPPVENATGEKMRPKKLAPSGKIH
                     KCSICHREFSTGQSLGGHKRLHYEGVLRGHKRSQEKEAVSQGDKLSPSGNGSVVTHVP
                     DPKQSRKGLIVINKVPSPEFNDPGDKDILEGESALLANKLEQDRGITSTRMINGLKFF
                     NFL"
     repeat_region   complement(13144. .13188)
                     /rpt_family="(TA)n"
     repeat_region   complement(13987. .14059)
                     /rpt_family="Rf:ATCOPIA24I|ATCOPIA24I Internal region of
                     ATCOPIA24 copia-like LTR-retrotransposon."
     repeat_region   complement(13989. .14059)
                     /rpt_family="Rf:ATCOPIA24I|ATCOPIA24I Internal region of
                     ATCOPIA24 copia-like LTR-retrotransposon."
     repeat_region   complement(13989. .14057)
                     /rpt_family="Rf:ATCOPIA24I|ATCOPIA24I Internal region of
                     ATCOPIA24 copia-like LTR-retrotransposon."
     repeat_region   complement(13989. .14048)
                     /rpt_family="Rf:ATCOPIA24I|ATCOPIA24I Internal region of
                     ATCOPIA24 copia-like LTR-retrotransposon."
     repeat_region   complement(13992. .14059)
                     /rpt_family="(CAT)n"
     repeat_region   complement(13992. .14051)
                     /rpt_family="Rf:ATCOPIA24I|ATCOPIA24I Internal region of
                     ATCOPIA24 copia-like LTR-retrotransposon."
     repeat_region   complement(13994. .14059)
                     /rpt_family="Rf:ATCOPIA24I|ATCOPIA24I Internal region of
                     ATCOPIA24 copia-like LTR-retrotransposon."
     repeat_region   complement(13994. .14057)
                     /rpt_family="Rf:ATCOPIA24I|ATCOPIA24I Internal region of
                     ATCOPIA24 copia-like LTR-retrotransposon."
     repeat_region   complement(13997. .14059)

Alignment Scores:
Pred. No.:          315          Length:          20509
```

```
Score:                  59.00          Matches:       13
Percent Similarity:     62.5%          Conservative:  2
Best Local Similarity:  54.2%          Mismatches:    9
Query Match:            36.9%          Indels:        0
DB:                     15             Gaps:          0

US-10-758-902-1 (1-30) x AC074110 (1-20509)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              |||   ||||||:::|||||||||          |||:::         |||   |||
Db       4517 TTCCTCCTAGGTCAAGCATATGAAAAGGCAGTTATCATCAAACCACCGGAGAATTCCTTA 4576

Qy         26 AlaLysGlyThr 29
              ||||||||||||
Db       4577 GCGAAAGGTACA 4588

RESULT 37
AC130247
LOCUS       AC130247               191712 bp    DNA     linear   HTG 12-OCT-2002
DEFINITION  Rattus norvegicus clone CH230-376M13, WORKING DRAFT SEQUENCE.
ACCESSION   AC130247
VERSION     AC130247.3  GI:23915322
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 191712)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 191712)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-AUG-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 191712)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-OCT-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Oct 12, 2002 this sequence version replaced gi:22538509.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: KARJ
                Center clone name: CH230-376M13
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 174170 bases at least Q40
                Consensus quality: 176032 bases at least Q30
                Consensus quality: 177089 bases at least Q20
                Estimated insert size: 178148; sum-of-contigs estimation
                Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1   191712: contig of 191712 bp in length.
FEATURES             Location/Qualifiers
     source          1. .191712
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-376M13"
     misc_feature    1. .1616
                     /note="wgs_end_extension
                     clone_end:Sp6"
     misc_feature    4223. .5101
                     /note="clone_boundary
                     clone_end:Sp6
                     site:MboI
```

```
                     end_sequence:RXAWM79TV"
     misc_feature    183618. .184593
                     /note="clone_boundary
                     clone_end:T7
                     site:MboI
                     end_sequence:RXAWM79TJ"
     misc_feature    188079. .189078
                     /note="wgs_end_extension
                     clone_end:T7"
     misc_feature    190496. .191712
                     /note="wgs_end_extension
                     clone_end:T7"
ORIGIN
```

Alignment Scores:

Pred. No.:	3.05e+03	Length:	191712
Score:	59.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	3
Best Local Similarity:	76.9%	Mismatches:	0
Query Match:	36.9%	Indels:	0
DB:	14	Gaps:	0

US-10-758-902-1 (1-30) x AC130247 (1-191712)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyr 14
              |||||||:::|||||||||||||||||:::|||||||:::|||
Db      66733 AATACTCTTTCCTTTAATTTAGGAAAAGCTTACCAGTAC 66771
```

```
RESULT 38
AC111744/c
LOCUS       AC111744.               244211 bp    DNA     linear   HTG 15-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-153O4, *** SEQUENCING IN PROGRESS
            ***, 6 unordered pieces.
ACCESSION   AC111744
VERSION     AC111744.5  GI:25007029
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 244211)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 244211)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 244211)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 15, 2002 this sequence version replaced gi:23270098.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GOAC
                Center clone name: CH230-153O4
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 221486 bases at least Q40
                Consensus quality: 224228 bases at least Q30
                Consensus quality: 226263 bases at least Q20
                Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    17797: contig of 17797 bp in length
            *    17798    17897: gap of unknown length
            *    17898    56390: contig of 38493 bp in length
```

```
            *    56391    56490: gap of unknown length
            *    56491   237087: contig of 180597 bp in length
            *   237088   237187: gap of unknown length
            *   237188   240543: contig of 3356 bp in length
            *   240544   240643: gap of unknown length
            *   240644   242172: contig of 1529 bp in length
            *   242173   242272: gap of unknown length
            *   242273   244211: contig of 1939 bp in length.
FEATURES             Location/Qualifiers
     source          1. .244211
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-153O4"
     misc_feature    1. .1744
                     /note="wgs_contig"
     misc_feature    15907. .17797
                     /note="wgs_contig"
     gap             17798. .17897
                     /estimated_length=unknown
     misc_feature    17898. .19957
                     /note="wgs_contig"
     gap             56391. .56490
                     /estimated_length=unknown
     misc_feature    56491. .59283
                     /note="wgs_contig"
     gap             237088. .237187
                     /estimated_length=unknown
     misc_feature    237188. .238796
                     /note="wgs_contig"
     gap             240544. .240643
                     /estimated_length=unknown
     gap             242173. .242272
                     /estimated_length=unknown
ORIGIN

Alignment Scores:
Pred. No.:              3.9e+03         Length:         244211
Score:                  59.00           Matches:        10
Percent Similarity:     100.0%          Conservative:   3
Best Local Similarity:  76.9%           Mismatches:     0
Query Match:            36.9%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC111744 (1-244211)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyr 14
              ||||||:::|||||||||||||||:::||||||:::|||
Db      22813 AATACTCTTTCCTTTAATTTAGGAAAAGCTTACCAGTAC 22775

RESULT 39
SEB400822
LOCUS       SEB400822               1892 bp    mRNA    linear   PLN 27-FEB-2001
DEFINITION  Sambucus ebulus mRNA for ribosome-inactivating protein precursor
            (ebu1 gene).
ACCESSION   AJ400822
VERSION     AJ400822.1  GI:13171072
KEYWORDS    ebu1 gene; ribosome-inactivating protein precursor.
SOURCE      Sambucus ebulus
  ORGANISM  Sambucus ebulus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
REFERENCE   1
  AUTHORS   Girbes,T., Iglesias,R., Perez,Y., Ferreras,J.M. and Citores,L.
  TITLE     Molecular cloning of ebulin 1
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1892)
  AUTHORS   Girbes,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2000) Girbes T., Bioquimica, Biologia Molecular y
            Fisiologia, Universidad de Valladolid, Dr. Mergelina s/n,
            Valladolid, 47005, SPAIN
```

```
FEATURES             Location/Qualifiers
     source          1. .1892
                     /organism="Sambucus ebulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:28503"
                     /tissue_type="leaves"
                     /country="Spain:Palencia"
     gene            1. .1892
                     /gene="ebu1"
     5'UTR           1. .33
                     /gene="ebu1"
     CDS             34. .1728
                     /gene="ebu1"
                     /EC_number="3.2.2.22"
                     /function="unknown"
                     /codon_start=1
                     /product="ribosome-inactivating protein precursor"
                     /protein_id="CAC33178.1"
                     /db_xref="GI:13171073"
                     /db_xref="GOA:Q9AVR2"
                     /db_xref="UniProt/TrEMBL:Q9AVR2"
                     /translation="MRVVKAAMLYLHIVVLAIYSVGIQGIDYPSVSFNLAGAKSTTYR
                     DFLKNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLVRLTNYNGDTVTSAVDVTNLY
                     LVAFSANGNSYFFKDATELQKSNLFLGTTQHTLSFTGNYDNLETAAGTRRESIELGPN
                     PLDGAITSLWYDGGVARSLLVLIQMVPEAARFRYIEQEVRRSLQQLTSFTPNALMLSM
                     ENNWSSMSLEVQLSGDNVSPFSGTVQLQNYDHTPRLVDNFEELYKITGIAILLFRCVA
                     TKTTHNAIRMPHVLVGEDNKFNDGETCAIPAPFTRRIVGRDGLCVDVRNGYDTDGTPI
                     QLWPCGTQRNQQWTFYNDKTIRSMGKCMTANGLNSGSYIMITDCSTAAEDATKWEVLI
                     DGSIINPSSGLVMTAPSGASRTTLLLENNIHAASQGWTVSNDVQPIATLIVGYNEMCL
                     QANGENNNVWMEDCDVTSVQQQWALFDDRTIRVNNSRGLCVTSNGYVSKDLIVIRKCQ
                     GLATQRWFFNSDGSVVNLKSTRVMDVKESDVSLQEVIIFPATGNPNQQWRTQVPQI"
     sig_peptide     34. .108
                     /gene="ebu1"
     mat_peptide     109. .927
                     /gene="ebu1"
                     /product="ebulin 1 A-chain"
                     /EC_number="3.2.2.22"
     mat_peptide     928. .1725
                     /gene="ebu1"
                     /product="ebulin 1 B-chain"
                     /EC_number="3.2.2.22"
     misc_feature    109. .1728
                     /gene="ebu1"
                     /note="encodes transition peptide that is
                     post-translationally processed into mature peptides A an
                     B"
     3'UTR           1729. .1872
                     /gene="ebu1"
     polyA_signal    1771. .1776
                     /gene="ebu1"
     polyA_site      1872
                     /gene="ebu1"
ORIGIN

Alignment Scores:
Pred. No.:              40.4            Length:         1892
Score:                  58.00           Matches:        14
Percent Similarity:     64.5%           Conservative:   6
Best Local Similarity:  45.2%           Mismatches:     9
Query Match:            36.2%           Indels:         2
DB:                     15              Gaps:           1

US-10-758-902-1 (1-30) x SEB400822 (1-1892)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIle 18
              |||   :::|||||||||||||||      |||             |||      |||:::
Db        115 TATCCCTCCGTCTCCTTCAATTTGGCGGGAGCCAAGTCGACTACATACAGGGACTTCTTA 174

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              ::::::||||||:::   :::|||   ||||||
Db        175 AAGAACCTGCGAGATAGGGTCGCAACTGGCACC 207

RESULT 40
```

```
AR349037
LOCUS       AR349037                678 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3648 from patent US 6583275.
ACCESSION   AR349037
VERSION     AR349037.1  GI:33746082
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Doucette-Stamm,L.A. and Bush,D.
  TITLE     Nucleic acid sequences and expression system relating to
            Enterococcus faecium for diagnostics and therapeutics
  JOURNAL   Patent: US 6583275-A 3648 24-JUN-2003;
            Genome Therapeutics Corporation; Waltham, MA
FEATURES             Location/Qualifiers
     source          1. .678
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              17.1          Length:         678
Score:                  57.50         Matches:        11
Percent Similarity:     62.9%         Conservative:   11
Best Local Similarity:  31.4%         Mismatches:     8
Query Match:            35.9%         Indels:         5
DB:                     6             Gaps:           1

US-10-758-902-1 (1-30) x AR349037 (1-678)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::      |||   :::|||||||||   |||::::::      |||::::::|||
Db        112 TTCTCAAAAACTTCTATGGATTTGGGAGAAAGATATGATTTTAAGGGGTTTATGGAAGAT 171

Qy         21 LeuArgAsnGluLeuAla----------LysGlyThrPro 30
                 :::|||::::::          :::|||||||||
Db        172 AAAATGGACGAGGTATCAAGTAGGGAAATTCCAGAAGGCACACCT 216


Search completed: February 20, 2006, 13:14:20
Job time : 1260.06 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2006, 23:33:13 ; Search time 147.989 Seconds
(without alignments)
1351.053 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160757_3660/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h
-USER=US10758902_@CGN_1_1_900_@runat_17022006_160757_3660 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	111	69.4	65	2	AAV81465	Aav81465 Ribosome-
2	72	45.0	363	2	AAV81468	Aav81468 Ribosome-
3	61	38.1	1195	2	AAQ56672	Aaq56672 Sequence
4	61	38.1	1195	2	AAQ81457	Aaq81457 Phytolacc
5	61	38.1	1378	12	ADG76061	Adg76061 American
6	61	38.1	1379	3	AAZ45197	Aaz45197 Wild-type
7	61	38.1	1379	3	AAZ59220	Aaz59220 Pokeweed
8	61	38.1	1379	4	AAC87929	Aac87929 P. americ
9	61	38.1	1379	6	AAD42738	Aad42738 Pokeweed
10	61	38.1	1379	10	ADI05787	Adi05787 DNA encod
11	57.5	35.9	678	10	ADC94021	Adc94021 E. faeciu
12	56	35.0	465	6	AAD42717	Aad42717 Pokeweed
13	56	35.0	792	6	AAD42716	Aad42716 Pokeweed
14	56	35.0	882	2	AAT99556	Aat99556 Phytolacc
15	56	35.0	945	6	AAD42715	Aad42715 Pokeweed
16	56	35.0	945	10	AAD48802	Aad48802 Rhodococc
17	56	35.0	1092	6	AAD42729	Aad42729 Pokeweed
18	56	35.0	1164	11	ADM74751	Adm74751 HIV-1 inh
19	56	35.0	1164	11	ADM74765	Adm74765 HIV-1 inh
20	56	35.0	1378	6	AAD42739	Aad42739 Pokeweed
21	56	35.0	1379	3	AAZ59221	Aaz59221 Variant p
22	56	35.0	2197	13	ADX60777	Adx60777 Plant ful
23	55.5	34.7	2429	12	ADQ67299	Adq67299 Novel hum
24	55.5	34.7	38844	6	AAL40255	Aal40255 Genomic D
c 25	55	34.4	2139	5	AAS82218	Aas82218 DNA encod
c 26	55	34.4	2558	6	AAD33649	Aad33649 Human TRI
c 27	55	34.4	2840	12	ADJ27234	Adj27234 Human TRI
c 28	55	34.4	2950	12	ADJ27233	Adj27233 Human TRI
c 29	53	33.1	903	5	AAC84981	Aac84981 Myxoma vi
30	53	33.1	962	2	AAQ89874	Aaq89874 Bryodin-2
31	53	33.1	5366	4	ABL28589	Abl28589 Drosophil
32	53	33.1	31068	4	ABL28588	Abl28588 Drosophil
33	52	32.5	1040	11	ACN90027	Acn90027 Breast ca
34	52	32.5	1364	8	ABX13666	Abx13666 Piromyces
35	52	32.5	1380	14	ACL66796	Acl66796 M. xanthu
c 36	52	32.5	1467	14	ADW07610	Adw07610 GTase cDN
37	52	32.5	1689	13	ADX50786	Adx50786 Plant ful
38	52	32.5	1692	13	ADX34957	Adx34957 Plant ful
39	52	32.5	19954	14	ACL64687	Acl64687 M. xanthu
40	52	32.5	110000	14	ADZ45062_06	Continuation (7 of
41	51.5	32.2	258	12	ACH83280	Ach83280 Human gen
42	51.5	32.2	543	12	ACH69580	Ach69580 Human gen
c 43	51.5	32.2	549	4	AAF87195	Aaf87195 Human ion
44	51.5	32.2	717	14	ACL72405	Acl72405 M. xanthu
c 45	51.5	32.2	1341	12	ADN61734	Adn61734 Human cDN
c 46	51.5	32.2	1356	8	ABZ68498	Abz68498 Nucleotid
c 47	51.5	32.2	1398	6	ABA96143	Aba96143 Human gam
c 48	51.5	32.2	1446	6	AAD36319	Aad36319 Human tra
c 49	51.5	32.2	1455	6	ABX97011	Abx97011 Human NOV
c 50	51.5	32.2	1455	12	ADN61738	Adn61738 Human cDN
c 51	51.5	32.2	1457	6	ABX97009	Abx97009 Human NOV
c 52	51.5	32.2	1568	6	ABA96145	Aba96145 Human gam
c 53	51.5	32.2	1672	10	ADB78729	Adb78729 Human GAB
c 54	51.5	32.2	1672	10	ADB78728	Adb78728 Human GAB
55	51.5	32.2	2106	6	ABV76598	Abv76598 Signal pe
c 56	51.5	32.2	2819	6	ABV72622	Abv72622 Human tra
57	51.5	32.2	12028	14	ACL64608	Acl64608 M. xanthu
c 58	51.5	32.2	82938	6	ABV72623	Abv72623 Human tra
59	51.5	32.2	109973	3	AAF22298	Aaf22298 BAC conta
60	51	31.9	542	12	ACH73191	Ach73191 Human gen
c 61	51	31.9	1981	4	AAI14937	Aai14937 Probe #48
c 62	51	31.9	1981	4	ABA56674	Aba56674 Human foe
c 63	51	31.9	1981	4	AAI36292	Aai36292 Probe #49
c 64	51	31.9	1981	4	ABA46128	Aba46128 Human bre
c 65	51	31.9	1981	4	ABA26279	Aba26279 Probe #47
c 66	51	31.9	1981	4	AAK30333	Aak30333 Human bon
c 67	51	31.9	1981	4	AAK04811	Aak04811 Human bra
c 68	51	31.9	1981	4	ABS29973	Abs29973 Human liv
c 69	51	31.9	1981	5	AAI04714	Aai04714 Probe #47
c 70	51	31.9	1981	6	ABS04920	Abs04920 Human gen
71	51	31.9	2746	2	AAQ07044	Aaq07044 Gene enco
c 72	51	31.9	3005	4	AAK70293	Aak70293 Human imm
c 73	51	31.9	3387	4	AAK70291	Aak70291 Human imm
74	51	31.9	3702	10	ADH83681	Adh83681 Enterococ
75	51	31.9	4249	2	AAX20201	Aax20201 Enterococ
76	51	31.9	4249	6	ABN98186	Abn98186 E faecali
77	51	31.9	4249	8	ACA88150	Aca88150 E. faecal

	78	51	31.9	4249	8	ABX61756 Abx61756 Enterococ
	79	51	31.9	4249	14	ADY39137 Ady39137 Novel Ent
	80	51	31.9	4359	2	AAX20200 Aax20200 Enterococ
	81	51	31.9	4359	6	ABN98185 Abn98185 E faecali
	82	51	31.9	4359	8	ACA88149 Aca88149 E. faecal
	83	51	31.9	4359	8	ABX61755 Abx61755 Enterococ
	84	51	31.9	4359	14	ADY39135 Ady39135 Novel Ent
	85	51	31.9	6449	6	ABZ12264 Abz12264 Arabidops
	86	51	31.9	12445	2	AAX13179 Aax13179 Enterococ
	87	51	31.9	12445	6	ABS98974 Abs98974 Enterococ
	88	51	31.9	13222	4	AAH25109 Aah25109 Nucleotid
	89	51	31.9	50000	10	ADC56844 Adc56844 Human ATP
c	90	51	31.9	110000	14	ADZ59507_3 Continuation (4 of
c	91	51	31.9	110459	14	AEB44581 Aeb44581 Sleep dis
	92	51	31.9	194534	12	ADQ97481 Adq97481 Human can
	93	50.5	31.6	1830	10	ADB58699 Adb58699 Toxicity-
	94	50.5	31.6	3632	6	ABN67289 Abn67289 Streptoco
	95	50.5	31.6	42360	13	ABD32640 Abd32640 Mouse can
	96	50	31.2	495	12	ADK16596 Adk16596 Nanoarcha
c	97	50	31.2	598	13	ACN54798 Acn54798 Cotton an
	98	50	31.2	670	3	AAZ88227 Aaz88227 Misgurnus
	99	50	31.2	816	13	ADY79692 Ady79692 G. pentap
	100	50	31.2	1002	13	ADS56955 Ads56955 Bacterial

ALIGNMENTS

RESULT 1
AAV81465
ID AAV81465 standard; DNA; 65 BP.
XX
AC AAV81465;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE Ribosome-inactivating protein coding sequence fragment.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; ss.
XX
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX
PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 22; 39pp; English.
XX
CC This sequence encodes a fragment of the ribosome-inactivating protein
CC (RIP) of the invention. The RIP is designated bouganin, and comprises a
CC linear polypeptide (26 kDa) with a pI of 9.0, where the amino-terminal
CC end exhibits 50 % homology with the sequence shown in AAW67752. The
CC proteins and conjugates form compositions in treating various human
CC diseases or conditions, including cancer, graft-versus-host disease,
CC organ transplant rejection, type I diabetes, multiple sclerosis,
CC rheumatoid arthritis, systemic lupus erythematosus, and myasthenia
CC gravis. The proteins are also useful as therapeutic anti-viral agents in
CC plants and mammals. Compositions containing the polynucleotide encoding
CC bouganin are useful in gene therapy. Bouganin possesses low non-specific
CC toxicity, which makes it very suitable for use as the toxic agent in
CC various immunotoxins. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 65 BP; 19 A; 18 C; 15 G; 13 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.55e-10	Length:	65
Score:	111.00	Matches:	21
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	69.4%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-1 (1-30) x AAV81465 (1-65)

```
Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63
```

RESULT 2
AAV81468
ID AAV81468 standard; DNA; 363 BP.
XX
AC AAV81468;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE Ribosome-inactivating protein, coding sequence fragment.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; ss.
XX
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX
PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 24; 39pp; English.
XX
CC This sequence represents a fragment of the DNA encoding the ribosome-
CC inactivating protein (RIP) of the invention. The RIP is designated
CC bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,
CC where the amino-terminal end exhibits 50 % homology with the sequence
CC shown in AAW67752. The proteins and conjugates form compositions in
CC treating various human diseases or conditions, including cancer, graft-
CC versus-host disease, organ transplant rejection, type I diabetes,
CC multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC viral agents in plants and mammals. Compositions containing the
CC polynucleotide encoding bouganin are useful in gene therapy. Bouganin

```
CC   possesses low non-specific toxicity, which makes it very suitable for use
CC   as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC   correct OS field.)
XX
SQ   Sequence 363 BP; 110 A; 68 C; 85 G; 100 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.00927        Length:         363
Score:                  72.00          Matches:        14
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            45.0%          Indels:         0
DB:                     2              Gaps:           0

US-10-758-902-1 (1-30) x AAV81468 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 3
AAQ56672
ID   AAQ56672 standard; cDNA; 1195 BP.
XX
AC   AAQ56672;
XX
DT   16-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   04-SEP-1994  (first entry)
XX
DE   Sequence of Phytolacca antiviral protein (PAP) cDNA.
XX
KW   Antiviral protein; PAP; virus-resistance; transgenic plant; ss.
XX
OS   Phytolacca americana; L.
XX
FH   Key             Location/Qualifiers
FT   CDS             33. .974
FT                   /*tag=  a
XX
PN   EP585554-A1.
XX
PD   09-MAR-1994.
XX
PF   30-JUN-1993;   93EP-00110445.
XX
PR   16-AUG-1992;   92KR-00014895.
XX
PA   (JINR-) JIN RO LTD.
XX
PI   Kim M,  Lee K,  Na B,  Jeong H,  Choi K,  Moon Y,  Jeon H;
XX
DR   WPI; 1994-076002/10.
DR   P-PSDB; AAR48548.
XX
PT   Expression vector for phytolacca antiviral protein - used for producing
PT   transgenic virus-resistant plants and for producing the antiviral agent.
XX
PS   Disclosure; Fig 1; 15pp; English.
XX
CC   To isolate PAP gene, total cellular mRNA was purified from leaves of
CC   Phytolacca americana L. obtd. in Korea. A cDNA library was constructed.
CC   The PAP gene was selected by immunoscreening employing anti-PAP antibody.
CC   A deletion mutant was prepd. from the isolated PAP gene, and the DNA
CC   sequence of the PAP genomewas determined. (Updated on 25-MAR-2003 to
CC   correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.03           Length:         1195
Score:                  61.00          Matches:        12
Percent Similarity:     68.0%          Conservative:   5
Best Local Similarity:  48.0%          Mismatches:     6
Query Match:            38.1%          Indels:         2
DB:                     2              Gaps:           1

US-10-758-902-1 (1-30) x AAQ56672 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla-----TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::||||               :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              |||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 4
AAQ81457
ID   AAQ81457 standard; cDNA; 1195 BP.
XX
AC   AAQ81457;
XX
DT   16-OCT-2003  (revised)
DT   25-AUG-1995  (first entry)
XX
DE   Phytolacca antiviral protein (PAP) cDNA.
XX
KW   Antiviral protein; vector pMJ12; KCCM 10037; PAP; ss.
XX
OS   Phytolacca americana; L.
XX
PN   AU9350642-A.
XX
PD   19-JAN-1995.
XX
PF   11-NOV-1993;   93AU-00050642.
XX
PR   02-JUL-1993;   93KR-00012360.
XX
PA   (JINR-) JIN RO LTD.
XX
PI   Lee K,  Choi K,  Jeon H,  Kim M,  Moon Y;
XX
DR   WPI; 1995-067518/10.
XX
PT   Recombinant vector for producing Phytolacca anti-viral protein - and
PT   transformed E. coli useful for making immunoconjugates for treatment of
PT   AIDS.
XX
PS   Claim 1; Fig 1; 27pp; English.
XX
CC   Total cellular mRNA from leaves of P. americana was used to produce a
CC   cDNA library and this screened with anti-PAP antibody raised in rabbits
CC   against purified PAP. Inserts were isolated from 2 clones and sequenced
CC   to identify a 1195 ORF (AAQ81457) that encodes a 313 AA PAP including a
CC   22 AA signal peptide. The mature PAP gene was sugjected to PCR
CC   amplification using primers AAQ81458 and AAQ81459. The amplification
CC   product was cut with Hind III and inserted into the commercial FLAG (RTM)
CC   vector cut with the same enzyme to form pMJ12. pMJ12 is deposited with
CC   the Korean Collection of Culture and Microorganism (KCCM), an
CC   International Depository Authoritory, on June 30 1993, ad deposition No.
CC   KCCM 10037, and claimed. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1195 BP; 420 A; 203 C; 229 G; 343 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.03           Length:         1195
Score:                  61.00          Matches:        12
Percent Similarity:     68.0%          Conservative:   5
Best Local Similarity:  48.0%          Mismatches:     6
Query Match:            38.1%          Indels:         2
DB:                     2              Gaps:           1

US-10-758-902-1 (1-30) x AAQ81457 (1-1195)
```

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 5
ADG76061
ID   ADG76061 standard; DNA; 1378 BP.
XX
AC   ADG76061;
XX
DT   11-MAR-2004  (first entry)
XX
DE   American pokeweed antiviral protein (PAP) DNA SeqID 1.
XX
KW   gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
KW   nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
KW   american pokeweed; retroviral.
XX
OS   Phytolacca americana.
XX
PN   WO2003106479-A2.
XX
PD   24-DEC-2003.
XX
PF   17-JUN-2003; 2003WO-US019141.
XX
PR   17-JUN-2002; 2002US-0389649P.
XX
PA   (PARK-) PARKER HUGHES INST.
XX
PI   Uckun FM;
XX
DR   WPI; 2004-082156/08.
DR   P-PSDB; ADG76064.
XX
PT   Novel modified pokeweed antiviral protein useful for inhibiting viral
PT   replication, for inducing depurination of viral RNA, or for treating
PT   viral infection in subject.
XX
PS   Example 2; SEQ ID NO 1; 62pp; English.
XX
CC   This invention relates to novel modified pokeweed antiviral proteins
CC   (PAPs). Specifically, it refers to modifications relative to wild-type
CC   PAP that confer increased activity towards viral RNA, particularly
CC   retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
CC   modified PAP also exhibits decreased activity towards ribosomal RNA
CC   relative to wild-type PAP. The present invention describes a molecular
CC   model of PAP-HIV RNA interactions that have been used for the rational
CC   redesign of PAP mutants with potent anti-HIV activity, where
CC   modifications have been introduced in regions other than the active site.
CC   Accordingly, these mutants represent antiviral agents that can work as
CC   nucleoside analogue inhibitors of reverse transcriptase, as well as viral
CC   protease inhibitors that can be used for treating viral infections. As
CC   such, they are useful for inhibiting viral replication and for
CC   depurinating viral RNA. This polynucleotide sequence is the DNA encoding
CC   the wild type american pokeweed antiviral protein (PAP) of the invention.
XX
SQ   Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.62          Length:          1378
Score:                  61.00         Matches:         12
Percent Similarity:     68.0%         Conservative:    5
Best Local Similarity:  48.0%         Mismatches:      6
Query Match:            38.1%         Indels:          2
DB:                     12            Gaps:            1

US-10-758-902-1 (1-30) x ADG76061 (1-1378)
```

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        293 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 352

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        353 GATCTTCGTAATGAA 367

RESULT 6
AAZ45197
ID   AAZ45197 standard; DNA; 1379 BP.
XX
AC   AAZ45197;
XX
DT   29-FEB-2000  (first entry)
XX
DE   Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
XX
KW   Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
KW   ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
KW   potato virus X; cucumber mosaic virus; CMV; ss;
KW   tomato yellow leaf curl virus.
XX
OS   Phytolacca americana.
XX
FH   Key             Location/Qualifiers
FT   CDS             225. .1166
FT                   /*tag=  a
FT                   /product= "PAP"
FT                   /note= "Pokeweed antiviral protein"
XX
PN   WO9960843-A1.
XX
PD   02-DEC-1999.
XX
PF   21-MAY-1999;   99WO-US011301.
XX
PR   22-MAY-1998;   98US-0086374P.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Tumer NE,  Wang P;
XX
DR   WPI; 2000-062555/05.
DR   P-PSDB; AAY58025.
XX
PT   New antiviral DNA useful for generating transgenic plants resistant to
PT   viruses and/or fungi.
XX
PS   Example; Page 4-5; 43pp; English.
XX
CC   This is the Pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
CC   a type I ribosome-inhibiting protein (RIP) found in the cell walls of
CC   Phytolacca americana (pokeweed). It is a single polypeptide chain that
CC   catalytically removes a specific adenine residue from a highly conserved
CC   stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
CC   antiviral protein II (PAP II) protein confers antiviral and or antifungal
CC   activities to plants. A DNA molecule encoding a PAP II protein with an
CC   intact catalytic active site amino acid residue (E172) is useful for
CC   generating transgenic plants. PAP II DNA is useful for generating
CC   transgenic plants (especially cereal crops) through transforming a
CC   protoplast or introducing the DNA directly into a plant part prior to
CC   regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
CC   activity thus have increased resistance to viruses and/or fungi. Viruses
CC   include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
CC   yellow leaf curl virus, and fungi include Pythium, Phytophthora,
CC   Scleropora and Aspergillus. PAP II proteins also confer resistance to
CC   other plants pests including insects, bacteria and nematodes. PAP II DNA
CC   is also useful for identifying a PAP II protein having reduced
CC   cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
CC   unlike PAP transgenic plants which are stunted and sterile, PAP II
CC   transgenic plants have a normal and fertile phenotype
XX
```

```
SQ   Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.63          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x AAZ45197 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 7
AAZ59220
ID   AAZ59220 standard; cDNA; 1379 BP.
XX
AC   AAZ59220;
XX
DT   20-APR-2000  (first entry)
XX
DE   Pokeweed antiviral protein coding sequence spring leaf form.
XX
KW   Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
KW   resistance; potato virus X; potato virus Y; potato leaf roll virus;
KW   tuber; ss.
XX
OS   Phytolacca americana.
XX
PN   US6015940-A.
XX
PD   18-JAN-2000.
XX
PF   07-APR-1992;   92US-00865169.
XX
PR   07-APR-1992;   92US-00865169.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Kaniewski WK,  Tumer NE,  Lodge JK;
XX
DR   WPI; 2000-126326/11.
XX
PT   Production of transgenic potato plants or tubers expressing pokeweed
PT   antiviral protein which are resistant to potato virus X or Y.
XX
PS   Claim 6; Fig 4; 30pp; English.
XX
CC   This is the coding sequence for the spring leaf form of the pokeweed
CC   antiviral protein (PAP) which is used to generate transgenic potato
CC   plants. PAP is able to confer resistance to infection by potato virus X
CC   (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
CC   potato plant or tuber expressing PAP
XX
SQ   Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.63          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x AAZ59220 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 8
AAC87929
ID   AAC87929 standard; DNA; 1379 BP.
XX
AC   AAC87929;
XX
DT   06-MAR-2001  (first entry)
XX
DE   P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.
XX
KW   Phytolacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
KW   biotherapeutic; fusion protein; immunoconjugate; mutant; cytostatic;
KW   anti-HIV; human immunodeficiency virus; AIDS; leukaemia; lymphoma;
KW   brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; ss.
XX
OS   Phytolacca americana.
XX
FH   Key             Location/Qualifiers
FT   CDS             225. .1166
FT                   /*tag= a
FT                   /product= "pokeweed antiviral protein (PAP)"
XX
PN   US6146628-A.
XX
PD   14-NOV-2000.
XX
PF   11-JUL-1995;   95US-00501253.
XX
PR   11-JUL-1995;   95US-00501253.
XX
PA   (MINU ) UNIV MINNESOTA & RUTGERS.
PA   (UYNE-) UNIV STATE NEW JERSEY.
XX
PI   Uckun FM,  Tumer NE;
XX
DR   WPI; 2001-040422/05.
DR   P-PSDB; AAB36500.
XX
PT   Immunoconjugates useful for treating cancer and acquired immunodeficiency
PT   syndrome, comprises mutant pokeweed anti-viral protein and a targeting
PT   moiety that binds a cell surface receptor.
XX
PS   Disclosure; Col 47-50; 32pp; English.
XX
CC   The present invention describes a fusion protein or an immunoconjugate
CC   (I), comprising mutant Pokeweed Anti-viral Protein (PAP) having an amino
CC   acid substitution at residue 75, 97 or 176 of native PAP and a targeting
CC   moiety that binds a cell surface receptor. (I) can have cytostatic and
CC   anti-HIV activities, and is an inhibitor of cellular RNA or protein
CC   synthesis. (I) is useful for treating AIDS and cancers including
CC   leukaemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
CC   tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
CC   colon cancer. Immunoconjugates prepared using PAP mutants exhibit an
CC   improved therapeutic index over immunoconjugates containing either wild-
CC   type PAP or variant PAP. The present sequence encodes the wild-type PAP,
CC   which is given in the exemplification of the present invention
XX
SQ   Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.63          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
```

```
DB:                    4              Gaps:          1

US-10-758-902-1 (1-30) x AAC87929 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 9
AAD42738
ID   AAD42738 standard; DNA; 1379 BP.
XX
AC   AAD42738;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Pokeweed PAP' DNA #1.
XX
KW   Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
XX
OS   Phytolacca americana.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    290. .1076
FT                   /*tag=  a
FT                   /note= "Mature PAP' sequence"
XX
PN   WO200233107-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-GB004593.
XX
PR   14-OCT-2000; 2000GB-00025217.
XX
PA   (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI   Thomas CJR,  Mcpherson MJ,  Atkinson HJ,  Neelam A;
XX
DR   WPI; 2002-489891/52.
XX
PT   Inducing necrotic effect in specific cells of plant by transforming plant
PT   with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT   which acts in response to application of specific stimulus to plant.
XX
PS   Claim 5; Page 86; 87pp; English.
XX
CC   The invention relates to a method of inducing a necrotic effect in
CC   specific cells of a plant. The method involves transforming the plant
CC   with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC   PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC   in response to the application of a specific stimulus to the plant so as
CC   to facilitate expression of the pokeweed antiviral protein in specific
CC   cells of the plant. The method is useful for inducing a necrotic effect
CC   in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ   Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.63          Length:        1379
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     6             Gaps:          1

US-10-758-902-1 (1-30) x AAD42738 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 10
ADI05787
ID   ADI05787 standard; DNA; 1379 BP.
XX
AC   ADI05787;
XX
DT   15-APR-2004  (first entry)
XX
DE   DNA encoding the wild-type pokeweed antiviral protein.
XX
KW   ribosome depurination; antifungal; antiviral; virucide; anti-HIV;
KW   cytostatic; immunosuppressive; agricultural biotechnology; pharmaceutics;
KW   medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
KW   B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
KW   ds.
XX
OS   Phytolacca americana.
XX
FH   Key             Location/Qualifiers
FT   CDS             225. .1166
FT                   /*tag=  a
FT                   /product= "Wild-type pokeweed antiviral protein"
XX
PN   WO200262952-A2.
XX
PD   15-AUG-2002.
XX
PF   01-FEB-2002; 2002WO-US002792.
XX
PR   02-FEB-2001; 2001US-0266396P.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Tumer NE,  Hudak KA,  Parikh B;
XX
DR   WPI; 2003-156656/15.
DR   P-PSDB; ADI05788.
XX
PT   New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
PT   type PAP, useful in agricultural biotechnology or in the fields of
PT   pharmaceutics and medicine, e.g. treating cancer, AIDS, viral infection
PT   or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 1; 51pp; English.
XX
CC   The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
CC   that is less toxic than wild-type PAP and exhibits ribosome depurination
CC   activity, where the mutant is a central domain mutant or N-terminal
CC   domain mutant. The PAP mutants have the following activities: antifungal,
CC   antiviral, virucide, anti-HIV, cytostatic and immunosuppressive. The PAP
CC   mutants are useful in agricultural biotechnology as well as in the fields
CC   of pharmaceutics and medicine. The PAP mutants and methods are useful in
CC   treating mammals with cancer, AIDS, viral infection or autoimmune
CC   diseases associated with proliferations of unwanted T-cells or B-cells.
CC   The transgenic plants are useful in exhibiting resistance to a broad
CC   spectrum of plant pests e.g. viruses and fungi. This polynucleotide
CC   sequence represents the DNA encoding the wild-type pokeweed antiviral
CC   protein of the invention.
XX
SQ   Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.63          Length:        1379
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
```

```
Query Match:            38.1%       Indels:        2
DB:                     10          Gaps:          1

US-10-758-902-1 (1-30) x ADI05787 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   |||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 11
ADC94021
ID   ADC94021 standard; DNA; 678 BP.
XX
AC   ADC94021;
XX
DT   01-JAN-2004  (first entry)
XX
DE   E. faecium DNA sequence SEQ ID 3648.
XX
KW   ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;
KW   abdominal-pelvic infection.
XX
OS   Enterococcus faecium.
XX
PN   US6583275-B1.
XX
PD   24-JUN-2003.
XX
PF   30-JUN-1998;   98US-00107532.
XX
PR   02-JUL-1997;   97US-0051571P.
PR   14-MAY-1998;   98US-0085598P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Doucette-Stamm LA,  Bush D;
XX
DR   WPI; 2003-799836/75.
DR   P-PSDB; ADC97675.
XX
PT   New isolated nucleic acid derived from Enterococcus faecium encoding an
PT   Enterococcus faecium polypeptide useful for detection, prevention and
PT   treatment of a pathological condition resulting from a bacterial
PT   infection.
XX
PS   Example 1; SEQ ID NO 3648; 243pp; English.
XX
CC   The invention relates to an isolated nucleic acid derived from
CC   Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC   one of 10 fully defined sequences given in the (or comprising 40
CC   sequential nucleotides chosen from any of the nucleic acids, its
CC   complement or sequences hybridising to it). Also included are a
CC   recombinant vector comprising the nucleic acid operably linked to
CC   transcription regulatory element, a cell comprising the vector and a
CC   single-stranded probe comprising the nucleic acid. The nucleic acids are
CC   chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC   The nucleic acids is useful for diagnosing pathological conditions
CC   resulting from E. faecium bacterial infection (e.g. urinary tract
CC   infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC   infection) and for screening drugs such as agonists and antagonists. The
CC   nucleic acid is useful for recombinant production of Candida albicans -
CC   derived peptides or antisense polypeptides. Pharmaceutical compositions
CC   and vaccines containing the nucleic acid are useful for preventing or
CC   treating Enterococcus faecium infections. The present sequence represents
CC   one if the disclosed E. faecium nucleic acids.
XX
SQ   Sequence 678 BP; 269 A; 89 C; 127 G; 193 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.88        Length:        678
Score:                  57.50       Matches:       11
Percent Similarity:     62.9%       Conservative:  11
Best Local Similarity:  31.4%       Mismatches:    8
Query Match:            35.9%       Indels:        5
DB:                     10          Gaps:          1

US-10-758-902-1 (1-30) x ADC94021 (1-678)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::      |||   :::|||||||||   |||::::::      |||::::::|||
Db        112 TTCTCAAAAACTTCTATGGATTTGGGAGAAAGATATGATTTTAAGGGGTTTATGGAAGAT 171

Qy         21 LeuArgAsnGluLeuAla----------LysGlyThrPro 30
                 :::|||::::::              :::|||||||||
Db        172 AAAATGGACGAGGTATCAAGTAGGGAAATTCCAGAAGGCACACCT 216

RESULT 12
AAD42717
ID   AAD42717 standard; DNA; 465 BP.
XX
AC   AAD42717;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Pokeweed PAP-Salpha protein encoding DNA.
XX
KW   Necrotic effect; transgenic plant; antiviral protein; pokeweed; gene;
KW   PAP-Salpha; ds.
XX
OS   Phytolacca americana.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .465
FT                   /*tag= a
FT                   /product= "PAP-Salpha protein"
XX
PN   WO200233107-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-GB004593.
XX
PR   14-OCT-2000; 2000GB-00025217.
XX
PA   (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI   Thomas CJR,  Mcpherson MJ,  Atkinson HJ,  Neelam A;
XX
DR   WPI; 2002-489891/52.
DR   P-PSDB; AAE25920.
XX
PT   Inducing necrotic effect in specific cells of plant by transforming plant
PT   with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT   which acts in response to application of specific stimulus to plant.
XX
PS   Claim 3; Page 77; 87pp; English.
XX
CC   The invention relates to a method of inducing a necrotic effect in
CC   specific cells of a plant. The method involves transforming the plant
CC   with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC   PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC   in response to the application of a specific stimulus to the plant so as
CC   to facilitate expression of the pokeweed antiviral protein in specific
CC   cells of the plant. The method is useful for inducing a necrotic effect
CC   in specific cells of a plant. The present sequence is pokeweed PAP-Salpha
CC   protein encoding DNA
XX
SQ   Sequence 465 BP; 165 A; 97 C; 76 G; 127 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.61        Length:        465
Score:                  56.00       Matches:       11
```

```
Percent Similarity:     72.0%          Conservative:  7
Best Local Similarity:  44.0%          Mismatches:    5
Query Match:            35.0%          Indels:        2
DB:                     6              Gaps:          1

US-10-758-902-1 (1-30) x AAD42717 (1-465)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                ||||||||||:::
Db         67 TCTCTTCGTAATCAA 81

RESULT 13
AAD42716
ID   AAD42716 standard; DNA; 792 BP.
XX
AC   AAD42716;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Pokeweed mature PAP-S protein encoding DNA.
XX
KW   Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW   gene; ds.
XX
OS   Phytolacca americana.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .792
FT                   /*tag=  a
FT                   /product= "Mature PAP-S protein"
FT   primer_bind     1. .29
FT                   /*tag=  b
FT                   /bound_moiety= "Primer PS1BF"
FT   primer_bind     complement(436. .462)
FT                   /*tag=  c
FT                   /bound_moiety= "Primer PS1SR"
FT   primer_bind     463. .492
FT                   /*tag=  d
FT                   /bound_moiety= "Primer PS2BF"
FT   misc_feature    681. .686
FT                   /*tag=  e
FT                   /note= "Sequence replacing removed XbaI site"
FT   primer_bind     complement(765. .792)
FT                   /*tag=  f
FT                   /bound_moiety= "Primer PS2SR"
XX
PN   WO200233107-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-GB004593.
XX
PR   14-OCT-2000; 2000GB-00025217.
XX
PA   (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI   Thomas CJR,  Mcpherson MJ,  Atkinson HJ,  Neelam A;
XX
DR   WPI; 2002-489891/52.
DR   P-PSDB; AAE25919.
XX
PT   Inducing necrotic effect in specific cells of plant by transforming plant
PT   with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT   which acts in response to application of specific stimulus to plant.
XX
PS   Claim 2; Page 76; 87pp; English.
XX
CC   The invention relates to a method of inducing a necrotic effect in
CC   specific cells of a plant. The method involves transforming the plant
CC   with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC   PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC   in response to the application of a specific stimulus to the plant so as
CC   to facilitate expression of the pokeweed antiviral protein in specific
CC   cells of the plant. The method is useful for inducing a necrotic effect
CC   in specific cells of a plant. The present sequence is pokeweed mature PAP
CC   -S protein encoding DNA
XX
SQ   Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              12.8           Length:        792
Score:                  56.00          Matches:       11
Percent Similarity:     72.0%          Conservative:  7
Best Local Similarity:  44.0%          Mismatches:    5
Query Match:            35.0%          Indels:        2
DB:                     6              Gaps:          1

US-10-758-902-1 (1-30) x AAD42716 (1-792)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                ||||||||||:::
Db         67 TCTCTTCGTAATCAA 81

RESULT 14
AAT99556
ID   AAT99556 standard; DNA; 882 BP.
XX
AC   AAT99556;
XX
DT   17-OCT-2003  (revised)
DT   08-JUN-1998  (first entry)
XX
DE   Phytolacca insularis antiviral protein gPIP2 gene.
XX
KW   Antiviral protein; gPIP2 gene; virucide; transgenic plant;
KW   virus resistance; immunoconjugate; AIDS; cancer; therapy; ss.
XX
OS   Phytolacca insularis; Nakai.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .882
FT                   /*tag=  a
FT                   /transl_except= (pos:715. .717, aa:Ile)
XX
PN   EP808902-A2.
XX
PD   26-NOV-1997.
XX
PF   30-SEP-1996;   96EP-00307159.
XX
PR   22-MAY-1996;   96KR-00017404.
XX
PA   (JINR-) JIN RO LTD.
XX
PI   Moon Y,  Choi J,  Yun Y,  Jin J,  Hong E,  Lee J,  Choi K,  Lee J;
PI   Song S,  Choi Y,  Kim C,  Kim M;
XX
DR   WPI; 1998-001788/01.
DR   P-PSDB; AAW26773.
XX
PT   Antiviral proteins of Phytolacca insularis Nakai and their genes - useful
PT   in plant antiviral agents and immunoconjugates for the treatment of AIDS
PT   and cancer.
XX
PS   Claim 2; Page 10-12; 26pp; English.
XX
CC   This polynucleotide comprises the coding region of the Phytolacca
CC   insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
```

```
CC   designated gPIP2 (see AAW26773). The gPIP2 gene was isolated from leaf
CC   genomic DNA by PCR amplification (see AAT99558-59). Another gene (see
CC   AAT99557), encoding a 35.7 kDa protein (see AAW26774) designated gPIP50,
CC   has also been isolated from P. insularis Nakai. Also claimed are vectors
CC   encoding these antiviral proteins and host cells transformed or
CC   transfected with these vectors. E. coli XL1-Blue MRF' gPIP2 (KCCM-10080)
CC   host cells are claimed, as is a process for preparing antiviral protein
CC   by cultivating these cells and purifying the protein from inclusion
CC   bodies. The antiviral proteins and recombinant proteins inhibit protein
CC   synthesis. They can be used as active ingredients of antiviral agents of
CC   plant viruses, and employed in the manufacture of immunoconjugates for
CC   the treatment of AIDS and cancer. The isolated genes can be used in the
CC   breeding of transgenic plants having viral resistance. (Updated on 17-OCT
CC   -2003 to standardise OS field)
XX
SQ   Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              14.7          Length:         882
Score:                  56.00         Matches:        11
Percent Similarity:     68.0%         Conservative:   6
Best Local Similarity:  44.0%         Mismatches:     6
Query Match:            35.0%         Indels:         2
DB:                     2             Gaps:           1

US-10-758-902-1 (1-30) x AAT99556 (1-882)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db          7 AATACCATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGGAT 66

Qy         20 AspLeuArgAsnGlu 24
              :::|||||||||||||
Db         67 AATCTTCGTAATGAA 81

RESULT 15
AAD42715
ID   AAD42715 standard; DNA; 945 BP.
XX
AC   AAD42715;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Pokeweed pro-PAP-S protein encoding DNA.
XX
KW   Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW   gene; ds.
XX
OS   Phytolacca americana.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .945
FT                   /*tag=  a
FT                   /product= "Pro-PAP-S protein"
FT   primer_bind     1. .24
FT                   /*tag=  b
FT                   /bound_moiety= "Primer PPS1BF"
FT   primer_bind     complement(735. .776)
FT                   /*tag=  c
FT                   /bound_moiety= "Primer PSXDR"
FT   primer_bind     736. .777
FT                   /*tag=  d
FT                   /bound_moiety= "Primer PSXDF"
FT   misc_feature    750. .759
FT                   /*tag=  e
FT                   /note= "Sequence replacing removed XbaI site"
FT   primer_bind     complement(922. .945)
FT                   /*tag=  f
FT                   /bound_moiety= "Primer PPS2BR"
XX
PN   WO200233107-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-GB004593.
XX
PR   14-OCT-2000; 2000GB-00025217.
XX
PA   (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI   Thomas CJR,  Mcpherson MJ,  Atkinson HJ,  Neelam A;
XX
DR   WPI; 2002-489891/52.
DR   P-PSDB; AAE25918.
XX
PT   Inducing necrotic effect in specific cells of plant by transforming plant
PT   with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT   which acts in response to application of specific stimulus to plant.
XX
PS   Claim 24; Page 73-74; 87pp; English.
XX
CC   The invention relates to a method of inducing a necrotic effect in
CC   specific cells of a plant. The method involves transforming the plant
CC   with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC   PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC   in response to the application of a specific stimulus to the plant so as
CC   to facilitate expression of the pokeweed antiviral protein in specific
CC   cells of the plant. The method is useful for inducing a necrotic effect
CC   in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
CC   protein encoding DNA
XX
SQ   Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              16            Length:         945
Score:                  56.00         Matches:        11
Percent Similarity:     72.0%         Conservative:   7
Best Local Similarity:  44.0%         Mismatches:     5
Query Match:            35.0%         Indels:         2
DB:                     6             Gaps:           1

US-10-758-902-1 (1-30) x AAD42715 (1-945)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||          :::|||   ||||||::::::
Db         76 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 135

Qy         20 AspLeuArgAsnGlu 24
                ||||||||||:::
Db        136 TCTCTTCGTAATCAA 150

RESULT 16
AAD48802
ID   AAD48802 standard; DNA; 945 BP.
XX
AC   AAD48802;
XX
DT   07-MAR-2003  (first entry)
XX
DE   Rhodococcus erythropolis crtB gene.
XX
KW   Isoprenoid biosynthesis; enzyme; crtB; gene; ds.
XX
OS   Rhodococcus erythropolis.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .945
FT                   /*tag=  a
FT                   /product= "Rhodococcus erythropolis crtB protein"
XX
PN   WO200286094-A2.
XX
PD   31-OCT-2002.
XX
PF   24-APR-2002; 2002WO-US015033.
XX
```

```
PR   24-APR-2001; 2001US-0285910P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Bramucci MG,  Brzostowicz PC,  Cheng Q,  Kostichka KN,  Nagarajan V;
PI   Rouviere PE,  Tao L,  Thomas SM;
XX
DR   WPI; 2003-067638/06.
DR   P-PSDB; AAE31689.
XX
PT   New nucleic acid molecule from Rhodococcus erythropolis AN12 strain,
PT   useful for obtaining nucleic acid encoding isoprenoid compound
PT   biosynthetic enzyme, and for producing gene products having enhanced or
PT   altered activity.
XX
PS   Claim 2; Page 77-78; 85pp; English.
XX
CC   The present invention relates to novel Rhodococcus erythropolis AN12
CC   strain isoprenoid biosynthetic enzymes and polynucleotides encoding such
CC   proteins. Sequences of the invention are useful for regulating isoprenoid
CC   biosynthesis in an organism. They are useful for producing isoprenoid
CC   compounds and gene products having enhanced or altered activity. The
CC   present sequence is Rhodococcus erythropolis crtB gene
XX
SQ   Sequence 945 BP; 166 A; 308 C; 287 G; 184 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              16          Length:         945
Score:                  56.00       Matches:        10
Percent Similarity:     72.7%       Conservative:   6
Best Local Similarity:  45.5%       Mismatches:     6
Query Match:            35.0%       Indels:         0
DB:                     10          Gaps:           0

US-10-758-902-1 (1-30) x AAD48802 (1-945)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||:::::         ||||||:::|||:::     :::|||
Db        520 AATCTCGGTGAGGCGTTTCAGCTGACCAACTTCATCCGCGACGTCGGTGAAGACCTCGAC 579

Qy         27 LysGly 28
              :::|||
Db        580 CGGGGA 585

RESULT 17
AAD42729
ID   AAD42729 standard; DNA; 1092 BP.
XX
AC   AAD42729;
XX
DT   29-AUG-2003  (revised)
DT   15-NOV-2002  (first entry)
XX
DE   Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.
XX
KW   Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW   chimeric; rice; cystatin delta D86; NIa protease cleavage site; PCS; ds.
XX
OS   Phytolacca americana.
OS   Oryza sativa.
OS   Tobacco; Etch virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     1. .29
FT                   /*tag=  a
FT                   /bound_moiety= "Primer PS1BF"
FT   misc_feature    681. .686
FT                   /*tag=  b
FT                   /note= "Modified XbaI site"
FT   primer_bind     complement(742. .786)
FT                   /*tag=  c
FT                   /bound_moiety= "Primer PCS-PAPSR"
FT   primer_bind     766. .806
FT                   /*tag=  d
FT                   /bound_moiety= "Primer PCS-Delta86F"
FT   misc_feature    766. .786
FT                   /*tag=  e
FT                   /note= "TEV NIa protease cleavage site"
FT   primer_bind     complement(1066. .1092)
FT                   /*tag=  f
FT                   /bound_moiety= "Primer SYNPOTDelta86R"
XX
PN   WO200233107-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-GB004593.
XX
PR   14-OCT-2000; 2000GB-00025217.
XX
PA   (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI   Thomas CJR,  Mcpherson MJ,  Atkinson HJ,  Neelam A;
XX
DR   WPI; 2002-489891/52.
XX
PT   Inducing necrotic effect in specific cells of plant by transforming plant
PT   with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT   which acts in response to application of specific stimulus to plant.
XX
PS   Disclosure; Page 83; 87pp; English.
XX
CC   The invention relates to a method of inducing a necrotic effect in
CC   specific cells of a plant. The method involves transforming the plant
CC   with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC   PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC   in response to the application of a specific stimulus to the plant so as
CC   to facilitate expression of the pokeweed antiviral protein in specific
CC   cells of the plant. The method is useful for inducing a necrotic effect
CC   in specific cells of a plant. The present sequence is a fusion DNA. This
CC   sequence comprises pokeweed pro-PAP-S DNA, rice cystatin delta D86 DNA
CC   and Tobacco Etch virus (TEV) NIa protease cleavage site (PCS). (Updated
CC   on 29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              19.2        Length:         1092
Score:                  56.00       Matches:        11
Percent Similarity:     72.0%       Conservative:   7
Best Local Similarity:  44.0%       Mismatches:     5
Query Match:            35.0%       Indels:         2
DB:                     6           Gaps:           1

US-10-758-902-1 (1-30) x AAD42729 (1-1092)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                 |||||||||:::
Db         67 TCTCTTCGTAATCAA 81

RESULT 18
ADM74751
ID   ADM74751 standard; cDNA; 1164 BP.
XX
AC   ADM74751;
XX
DT   03-JUN-2004  (first entry)
XX
DE   HIV-1 inhibition activity related cDNA.
XX
KW   human immunodeficiency virus; HIV-1; tumour; plant;
```

```
KW   Chinese phytolacca leaf; trans-acting activation factor; Tat; mutant;
KW   gene; ss.
XX
OS   Human immunodeficiency virus 1.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1164
FT                   /*tag=  a
FT                   /product= "HIV-1 related protein"
XX
PN   CN1400220-A.
XX
PD   05-MAR-2003.
XX
PF   02-AUG-2001; 2001CN-00123911.
XX
PR   02-AUG-2001; 2001CN-00123911.
XX
PA   (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
PI   Peng X,  Bai L,  Yin B;
XX
DR   WPI; 2003-469263/45.
DR   P-PSDB; ADM74752.
XX
PT   Two kinds of cDNA with activity capable of extensively inhibiting HIV and
PT   its expression, separation and purification method in protokaryon.
XX
PS   Example 8; Page 9-10; 17pp; Chinese.
XX
CC   The present invention relates to two kinds of cDNA which can inhibit
CC   human immunodeficiency virus (HIV-1) activity, including separation clone
CC   of two kinds of cDNA, external mutation, fusion expression in prokaryons
CC   and application of the cDNA in preparation of preparation for curing the
CC   virus and tumours. One of the described cDNAs is obtained by separation
CC   and cloned from a plant Chinese phytolacca leaf, and one from the trans-
CC   acting activation factor (Tat) mutant coded by human immunodeficiency
CC   virus HIV-1 gene. This polynucleotide sequence represents a cDNA used in
CC   the HIV-1 inhibition activity of the invention.
XX
SQ   Sequence 1164 BP; 379 A; 239 C; 248 G; 298 T; 0 U; 0 Other;
```

Alignment Scores:			
Pred. No.:	20.8	Length:	1164
Score:	56.00	Matches:	11
Percent Similarity:	68.0%	Conservative:	6
Best Local Similarity:	44.0%	Mismatches:	6
Query Match:	35.0%	Indels:	2
DB:	11	Gaps:	1

US-10-758-902-1 (1-30) x ADM74751 (1-1164)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||:::
Db        292 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGGAT 351

Qy         20 AspLeuArgAsnGlu 24
              :::|||||||||||||
Db        352 AATCTTCGTAATGAA 366
```

```
RESULT 19
ADM74765
ID   ADM74765 standard; cDNA; 1164 BP.
XX
AC   ADM74765;
XX
DT   03-JUN-2004  (first entry)
XX
DE   HIV-1 inhibition activity related Tat cDNA.
XX
KW   human immunodeficiency virus; HIV-1; tumour; plant;
KW   Chinese phytolacca leaf; trans-acting activation factor; Tat; mutant;
KW   gene; ss.
XX
OS   Human immunodeficiency virus 1.
XX
FH   Key             Location/Qualifiers
FT   CDS             2. .943
FT                   /*tag=  a
FT                   /product= "Tat HIV-1 protein"
XX
PN   CN1400220-A.
XX
PD   05-MAR-2003.
XX
PF   02-AUG-2001; 2001CN-00123911.
XX
PR   02-AUG-2001; 2001CN-00123911.
XX
PA   (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
PI   Peng X,  Bai L,  Yin B;
XX
DR   WPI; 2003-469263/45.
DR   P-PSDB; ADM74766.
XX
PT   Two kinds of cDNA with activity capable of extensively inhibiting HIV and
PT   its expression, separation and purification method in protokaryon.
XX
PS   Example 9; Page 11-12; 17pp; Chinese.
XX
CC   The present invention relates to two kinds of cDNA which can inhibit
CC   human immunodeficiency virus (HIV-1) activity, including separation clone
CC   of two kinds of cDNA, external mutation, fusion expression in prokaryons
CC   and application of the cDNA in preparation of preparation for curing the
CC   virus and tumours. One of the described cDNAs is obtained by separation
CC   and cloned from a plant Chinese phytolacca leaf, and one from the trans-
CC   acting activation factor (Tat) mutant coded by human immunodeficiency
CC   virus HIV-1 gene. This polynucleotide sequence represents the Tat cDNA
CC   used in the HIV-1 inhibition activity of the invention.
XX
SQ   Sequence 1164 BP; 403 A; 203 C; 218 G; 340 T; 0 U; 0 Other;
```

Alignment Scores:			
Pred. No.:	20.8	Length:	1164
Score:	56.00	Matches:	11
Percent Similarity:	68.0%	Conservative:	6
Best Local Similarity:	44.0%	Mismatches:	6
Query Match:	35.0%	Indels:	2
DB:	11	Gaps:	1

US-10-758-902-1 (1-30) x ADM74765 (1-1164)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||:::
Db         71 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGGAT 130

Qy         20 AspLeuArgAsnGlu 24
              :::|||||||||||||
Db        131 AATCTTCGTAATGAA 145
```

```
RESULT 20
AAD42739
ID   AAD42739 standard; DNA; 1378 BP.
XX
AC   AAD42739;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Pokeweed PAP' DNA #2.
XX
KW   Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
XX
OS   Phytolacca americana.
XX
FH   Key             Location/Qualifiers
```

```
FT   misc_feature    290. .1076
FT                   /*tag= a
FT                   /note= "Mature PAP' sequence"
XX
PN   WO200233107-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-GB004593.
XX
PR   14-OCT-2000; 2000GB-00025217.
XX
PA   (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI   Thomas CJR,  Mcpherson MJ,  Atkinson HJ,  Neelam A;
XX
DR   WPI; 2002-489891/52.
XX
PT   Inducing necrotic effect in specific cells of plant by transforming plant
PT   with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT   which acts in response to application of specific stimulus to plant.
XX
PS   Claim 5; Page 86-87; 87pp; English.
XX
CC   The invention relates to a method of inducing a necrotic effect in
CC   specific cells of a plant. The method involves transforming the plant
CC   with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC   PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC   in response to the application of a specific stimulus to the plant so as
CC   to facilitate expression of the pokeweed antiviral protein in specific
CC   cells of the plant. The method is useful for inducing a necrotic effect
CC   in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ   Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              25.6          Length:         1378
Score:                  56.00         Matches:        12
Percent Similarity:     64.0%         Conservative:   4
Best Local Similarity:  48.0%         Mismatches:     7
Query Match:            35.0%         Indels:         2
DB:                     6             Gaps:           1

US-10-758-902-1 (1-30) x AAD42739 (1-1378)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCGGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 21
AAZ59221
ID   AAZ59221 standard; cDNA; 1379 BP.
XX
AC   AAZ59221;
XX
DT   20-APR-2000  (first entry)
XX
DE   Variant pokeweed antiviral protein spring leaf form coding sequence.
XX
KW   Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
KW   resistance; potato virus X; potato virus Y; potato leaf roll virus;
KW   tuber; ss.
XX
OS   Phytolacca americana.
XX
PN   US6015940-A.
XX
PD   18-JAN-2000.
XX
PF   07-APR-1992;   92US-00865169.
XX
PR   07-APR-1992;   92US-00865169.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Kaniewski WK,  Tumer NE,  Lodge JK;
XX
DR   WPI; 2000-126326/11.
XX
PT   Production of transgenic potato plants or tubers expressing pokeweed
PT   antiviral protein which are resistant to potato virus X or Y.
XX
PS   Claim 7; Fig 5; 30pp; English.
XX
CC   This is the coding sequence for a variant spring leaf form of the
CC   pokeweed antiviral protein (PAP') which is used to generate transgenic
CC   potato plants. PAP' is able to confer resistance to infection by potato
CC   virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in
CC   the potato plant or tuber expressing PAP'. PAP' varies from PAP
CC   (AAZ59220) by mutations L20R and Y49H
XX
SQ   Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              25.6          Length:         1379
Score:                  56.00         Matches:        12
Percent Similarity:     64.0%         Conservative:   4
Best Local Similarity:  48.0%         Mismatches:     7
Query Match:            35.0%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x AAZ59221 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCGGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 22
ADX60777
ID   ADX60777 standard; cDNA; 2197 BP.
XX
AC   ADX60777;
XX
DT   21-APR-2005  (first entry)
XX
DE   Plant full length insert polynucleotide seqid 31620.
XX
KW   plant protectant; plant growth regulant; gene therapy; plant;
KW   recombinant DNA construct; physical array; plant breeding marker;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW   extreme osmotic condition; pathogen tolerance; pest tolerance;
KW   growth rate; cell cycle pathway; disease resistance;
KW   galactomannan production; lignin production; plant growth regulator;
KW   yield; plant growth; plant development; seed oil; protein yield;
KW   protein content; gene; ss.
XX
OS   Unidentified.
XX
PN   US2004034888-A1.
XX
PD   19-FEB-2004.
XX
PF   28-APR-2003; 2003US-00425114.
XX
PR   06-MAY-1999;   99US-00304517.
PR   05-NOV-2001; 2001US-00985678.
XX
PA   (LIUJ/) LIU J.
```

```
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
XX
PI   Liu J,  Zhou Y,  Kovalic DK,  Screen SE,  Tabaska JE,  Cao Y;
XX
DR   WPI; 2004-180133/17.
XX
PT   New recombinant DNA construct, useful for improving plant tolerance to
PT   cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT   pests, for conferring increased resistance to plant disease, or for
PT   improving yield.
XX
PS   Claim 1; SEQ ID NO 31620; 15pp; English.
XX
CC   The invention describes a recombinant DNA construct comprising a
CC   polynucleotide consisting of a sequence encoding an amino acid sequence
CC   available in electronic form from the US patent office at
CC   ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC   of the invention are also useful in physical arrays of molecules and as
CC   plant breeding markers. The recombinant DNA construct is useful for
CC   improving plant tolerance to cold, heat, drought, herbicides, extreme
CC   osmotic conditions, pathogens or pests, for manipulating growth rate in
CC   plant cells by modification of the cell cycle pathway, for conferring
CC   increased resistance to plant disease, for producing galactomannan,
CC   lignin or plant growth regulators, for increasing the rate of homologous
CC   recombination in plants, for improving yield by modification of
CC   photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC   or by providing improved plant growth and development under at least one
CC   stress condition or for modifying seed oil or protein yield and/or
CC   content. This sequence represents a plant full length insert
CC   polynucleotide that can be used in the recombinant DNA construct of the
CC   invention.
XX
SQ   Sequence 2197 BP; 536 A; 578 C; 523 G; 560 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              45.8          Length:         2197
Score:                  56.00         Matches:        16
Percent Similarity:     48.7%         Conservative:   3
Best Local Similarity:  41.0%         Mismatches:     8
Query Match:            35.0%         Indels:         12
DB:                     13            Gaps:           2

US-10-758-902-1 (1-30) x ADX60777 (1-2197)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db        464 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 520

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                             |||||||||:::|||      |||
Db        521 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 577

RESULT 23
ADQ67299
ID   ADQ67299 standard; cDNA; 2429 BP.
XX
AC   ADQ67299;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Novel human cDNA sequence #2272.
XX
KW   ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW   cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
KW   neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   EP1440981-A2.
XX
PD   28-JUL-2004.
XX
PF   21-JAN-2004; 2004EP-00001196.
XX
PR   21-JAN-2003; 2003JP-00102206.
PR   09-MAY-2003; 2003JP-00131392.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Nagai K,  Irie R;
XX
DR   WPI; 2004-535376/52.
DR   P-PSDB; ADQ67606.
XX
PT   Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT   Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS   Claim 1; SEQ ID NO 4460; 2449pp; English.
XX
CC   The invention relates to 2495 novel polynucleotides (I) and their encoded
CC   polypeptides, sequences hybridizing to these nucleotides, sequences
CC   encoding partial polypeptides and sequences having 70% or 90% identity to
CC   the nucleotide and protein sequences. The nucleotides and polypeptides
CC   are useful as diagnostic markers or therapeutic target for the diseases
CC   or morbid states. They are also useful for treating osteoporosis,
CC   neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC   dementia and various cancers. This sequence corresponds to a nucleotide
CC   sequence of the invention.
XX
SQ   Sequence 2429 BP; 810 A; 453 C; 466 G; 700 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              63.2          Length:         2429
Score:                  55.50         Matches:        10
Percent Similarity:     48.7%         Conservative:   9
Best Local Similarity:  25.6%         Mismatches:     11
Query Match:            34.7%         Indels:         9
DB:                     12            Gaps:           1

US-10-758-902-1 (1-30) x ADQ67299 (1-2429)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr------------------------ 12
              ||||||::::::   |||:::            |||
Db       1773 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 1832

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 :::::::|||   ::::::      :::|||||||||   :::         ||||||
Db       1833 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 1889

RESULT 24
AAL40255
ID   AAL40255 standard; DNA; 38844 BP.
XX
AC   AAL40255;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Genomic DNA encoding human protease.
XX
KW   Human protease; transgenic animal; transgenic non-human animal; enzyme;
KW   tissue typing; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(72,G)
FT                   /*tag=  s
FT   variation       replace(1894,T)
FT                   /*tag=  t
FT   variation       replace(1897,T)
```

```
FT                   /*tag= u
FT   variation       replace(2123,C)
FT                   /*tag= v
FT   variation       replace(2124,A)
FT                   /*tag= w
FT   variation       replace(2648,C)
FT                   /*tag= x
FT   variation       replace(2805,T)
FT                   /*tag= y
FT   CDS             3000. .38206
FT                   /*tag= a
FT                   /product= "Human protease protein"
FT                   /note= "This coding region contains 8 introns"
FT   exon            3000. .3093
FT                   /*tag= b
FT                   /number= 1
FT   intron          3094. .4905
FT                   /*tag= c
FT                   /number= 1
FT   variation       replace(4036,G)
FT                   /*tag= z
FT   exon            4906. .5024
FT                   /*tag= d
FT                   /number= 2
FT   intron          5025. .17485
FT                   /*tag= e
FT                   /number= 2
FT   variation       replace(5445,T)
FT                   /*tag= aa
FT   variation       replace(5608,C)
FT                   /*tag= ab
FT   variation       replace(6243,A)
FT                   /*tag= ac
FT   variation       replace(6273,G)
FT                   /*tag= ad
FT   variation       replace(6294,G)
FT                   /*tag= ae
FT   variation       replace(6312,G)
FT                   /*tag= af
FT   variation       replace(6714,G)
FT                   /*tag= ag
FT   variation       replace(6815,C)
FT                   /*tag= ah
FT   variation       replace(6994,G)
FT                   /*tag= ai
FT   variation       replace(12478,C)
FT                   /*tag= aj
FT   variation       replace(13916,C)
FT                   /*tag= ak
FT   variation       replace(13974,G)
FT                   /*tag= al
FT   variation       replace(15081,A)
FT                   /*tag= am
FT   variation       replace(15907,G)
FT                   /*tag= an
FT   exon            17486. .17553
FT                   /*tag= f
FT                   /number= 3
FT   intron          17554. .19507
FT                   /*tag= g
FT                   /number= 3
FT   variation       replace(17884,A)
FT                   /*tag= ao
FT   variation       replace(17908,T)
FT                   /*tag= ap
FT   exon            19508. .19668
FT                   /*tag= h
FT                   /number= 4
FT   intron          19669. .25382
FT                   /*tag= i
FT                   /number= 4
FT   variation       replace(20551,S)
FT                   /*tag= aq
FT   variation       replace(21222,W)
FT                   /*tag= ar
FT   variation       replace(21232,W)
FT                   /*tag= as
FT   variation       replace(21353,W)
FT                   /*tag= at
FT   variation       replace(21904,W)
FT                   /*tag= au
FT   variation       replace(22132,S)
FT                   /*tag= av
FT   variation       replace(22882,T)
FT                   /*tag= aw
FT   variation       replace(23867,S)
FT                   /*tag= ax
FT   variation       replace(23954,G)
FT                   /*tag= ay
FT   exon            25383. .25421
FT                   /*tag= j
FT                   /number= 5
FT   intron          25422. .26622
FT                   /*tag= k
FT                   /number= 5
FT   variation       replace(26548,A)
FT                   /*tag= az
FT   exon            26623. .26794
FT                   /*tag= l
FT                   /number= 6
FT   intron          26795. .30319
FT                   /*tag= m
FT                   /number= 6
FT   variation       replace(27400,S)
FT                   /*tag= ba
FT   variation       replace(28069,R)
FT                   /*tag= bb
FT   variation       replace(29269,G)
FT                   /*tag= bc
FT   variation       replace(29537,A)
FT                   /*tag= bd
FT   variation       replace(29726,S)
FT                   /*tag= be
FT   exon            30320. .30579
FT                   /*tag= n
FT                   /number= 7
FT   variation       replace(30496,W)
FT                   /*tag= bf
FT   intron          30580. .34817
FT                   /*tag= o
FT                   /number= 7
FT   variation       replace(30695,S)
FT                   /*tag= bg
FT   variation       replace(30752,S)
FT                   /*tag= bh
FT   variation       replace(30849,T)
FT                   /*tag= bi
FT   variation       replace(30900,A)
FT                   /*tag= bj
FT   variation       replace(30904,T)
FT                   /*tag= bk
FT   variation       replace(31664,C)
FT                   /*tag= bl
FT   variation       replace(32014,S)
FT                   /*tag= bm
FT   variation       replace(32197,G)
FT                   /*tag= bn
FT   variation       replace(33505,W)
FT                   /*tag= bo
FT   variation       replace(33551,T)
FT                   /*tag= bp
FT   variation       replace(34648,S)
FT                   /*tag= bq
FT   variation       replace(34754,T)
FT                   /*tag= br
FT   exon            34818. .34960
```

```
FT                   /*tag=  p
FT                   /number= 8
FT   variation       replace(34867,C)
FT                   /*tag=  bs
FT   intron          34961. .38044
FT                   /*tag=  q
FT                   /number= 8
FT   variation       replace(35013,T)
FT                   /*tag=  bt
FT   variation       replace(36885,G)
FT                   /*tag=  bu
FT   exon            38045. .38206
FT                   /*tag=  r
FT                   /number= 9
FT   variation       replace(38527,A)
FT                   /*tag=  bv
XX
PN   WO200226947-A2.
XX
PD   04-APR-2002.
XX
PF   26-SEP-2001; 2001WO-US029960.
XX
PR   27-SEP-2000; 2000US-0235557P.
PR   13-DEC-2000; 2000US-00734675.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Webster M,  Ketchum KA,  Di Francesco V,  Beasley EM;
XX
DR   WPI; 2002-499867/53.
DR   P-PSDB; AAO21899.
XX
PT   Novel peptide designated as human protease useful as target for
PT   diagnosing a disease or predisposition to the disease mediated by the

Alignment Scores:
Pred. No.:              2.01e+03        Length:         38844
Score:                  55.50           Matches:        10
Percent Similarity:     48.7%           Conservative:   9
Best Local Similarity:  25.6%           Mismatches:     11
Query Match:            34.7%           Indels:         9
DB:                     6               Gaps:           1

US-10-758-902-1 (1-30) x AAL40255 (1-38844)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr---------------------- 12
              ||||||::::::   |||:::          |||
Db      38592 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 38651

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::||||||||||   :::      ||||||
Db      38652 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 38708

RESULT 25
AAS82218/c
ID   AAS82218 standard; cDNA; 2139 BP.
XX
AC   AAS82218;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #18022.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG18031.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 1; SEQ ID NO 18022; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC   coding sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 2139 BP; 524 A; 524 C; 546 G; 545 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              65.6            Length:         2139
Score:                  55.00           Matches:        8
Percent Similarity:     70.8%           Conservative:   9
Best Local Similarity:  33.3%           Mismatches:     7
Query Match:            34.4%           Indels:         0
DB:                     5               Gaps:           0

US-10-758-902-1 (1-30) x AAS82218 (1-2139)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ::::::|||   |||::::::   |||:::|||:::||||||   :::::::::
Db       1335 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 1276

Qy         27 LysGlyThrPro 30
                ||| |||
Db       1275 TCCGGAGAGCCC 1264

RESULT 26
AAD33649/c
ID   AAD33649 standard; cDNA; 2558 BP.
XX
AC   AAD33649;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human TRICH-4 cDNA.
XX
KW   Human; transporter and ion channel; TRICH-4; transport disorder; angina;
KW   amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder;
```

```
KW   cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;
KW   depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;
KW   cell proliferated disorder; infertility; arteriosclerosis; gene therapy;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;
KW   myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;
KW   acquired immune deficiency syndrome; immunological disorder; scleroderma;
KW   endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;
KW   cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;
KW   epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;
KW   muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1980
FT                   /*tag=  a
FT                   /product= "Human TRICH-4 protein"
XX
PN   WO200212340-A2.
XX
PD   14-FEB-2002.
XX
PF   01-AUG-2001; 2001WO-US024217.
XX
PR   03-AUG-2000; 2000US-0223269P.
PR   10-AUG-2000; 2000US-0224456P.
PR   18-AUG-2000; 2000US-0226410P.
PR   25-AUG-2000; 2000US-0228140P.
PR   31-AUG-2000; 2000US-0230067P.
PR   08-SEP-2000; 2000US-0231434P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H, Thornton M, Ramkumar J, Tang YT, Azimzai Y, Baughn MR;
PI   Yang J, Yao MG, Lal P, Walia NK, Gandhi AR, Hafalia AJA, Nguyen DB;
PI   Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y, Reddy R;
PI   Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL, Greene BD;
PI   Sanjanwala MS, Raumann BE, Burford N, Ison CH, Lee EA, Ding L;
PI   Das D, Kallick DA, Khan FA, Seilhamer JJ;
XX
DR   WPI; 2002-206330/26.
DR   P-PSDB; AAE21160.
XX
PT   New human transporters and ion channels polypeptides and polynucleotides
PT   for diagnosing, preventing or treating transport, neurological, muscle,
PT   immunological and cell proliferative disorders.
XX
PS   Claim 78; Page 205; 230pp; English.
XX
CC   The invention relates to human transporter and ion channel polypeptides
CC   designated TRICH and nucleic acid molecules encoding such polypeptides.
CC   TRICH sequences are useful for diagnosis, treatment and prevention of
CC   transport, muscle, neurological, immunological and cell proliferative
CC   disorders. Transport disorders include akinesia, amyotrophic lateral
CC   sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular
CC   dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis,
CC   myocarditis, prostate cancer, cardiac disorders associated with transport
CC   e.g. polymyositis, bradyarrythmia, dermatomyositis, angina, neurological
CC   disorders associated with transport e.g. amnesia, bipolar disorder,
CC   depression, Tourette's disorder, schizophrenia, other disorders
CC   associated with transport e.g. neurofibromatosis, sickle cell anaemia,
CC   Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,
CC   goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell
CC   proliferated disorders include cancer, actinic keratosis, cirrhosis,
CC   arteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.
CC   Neurological disorders include Alzheimer's, Pick's and Parkinson's
CC   disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's
CC   disease, multiple sclerosis, dementia and other extrapyramidal disorder,
CC   motor neuron disorder, prion disease, metabolic disease of the nervous
CC   system and other developmental disorders of the central nervous system,
CC   neuromuscular disorders, metabolic, endocrine and toxic myopathies,
CC   periodic paralysis, mental disorders including mood, anxiety; and
CC   immunological disorders include acquired immune deficiency syndrome
CC   (AIDS), adult respiratory distress syndrome, Addison's disease,
CC   allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis,
CC   Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma,
CC   systemic lupus erythematosus, systemic sclerosis, ulcerative colitis,
CC   haemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal,
CC   helminthic infections and trauma; and muscle disorders include cardiac
CC   myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The
CC   TRICH polynucleotides are used in gene therapy. The present sequence is
CC   human TRICH-4 cDNA
XX
SQ   Sequence 2558 BP; 617 A; 582 C; 661 G; 697 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:                82              Length:          2558
Score:                    55.00           Matches:         8
Percent Similarity:       70.8%           Conservative:    9
Best Local Similarity:    33.3%           Mismatches:      7
Query Match:              34.4%           Indels:          0
DB:                       6               Gaps:            0

US-10-758-902-1 (1-30) x AAD33649 (1-2558)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ::::::|||   |||::::::   |||:::|||:::||||||   :::::::::
Db       1041 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 982

Qy         27 LysGlyThrPro 30
                |||   |||
Db        981 TCCGGAGAGCCC 970

RESULT 27
ADJ27234/c
ID   ADJ27234 standard; DNA; 2840 BP.
XX
AC   ADJ27234;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human TRICH-18 coding sequence, SEQ ID 66.
XX
KW   Human; TRansporters and Ion CHannels protein; TRICH; Transporter;
KW   Ion Channel; transport disorder; neurological disorder; muscle disorder;
KW   immunological disorder; cell proliferative disorder; infection;
KW   Neuroprotective; Muscular; Respiratory; Antidiabetic; Antiparkinsonian;
KW   Nootropic; Anticonvulsant; Antithyroid; Ophthalmological; Antibacterial;
KW   Antiinflammatory; Cardiant; Antianginal; Antiarrhythmic; Antiasthmatic;
KW   Endocrine; Hypotensive; Anti-HIV; Antianaemic; Antiarteriosclerotic;
KW   Dermatological; Antiarthritic; Osteopathic; Antipsoriatic; Antirheumatic;
KW   Immunosuppressive; Antiulcer; Gastrointestinal; Hepatotropic; Cytostatic;
KW   Virucide; Fungicide; Antiparasitic; Protozoacide; Antihelminthic;
KW   Gene Therapy; TRICH-18; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004013293-A2.
XX
PD   12-FEB-2004.
XX
PF   01-AUG-2003; 2003WO-US024164.
XX
PR   02-AUG-2002; 2002US-0400953P.
PR   12-AUG-2002; 2002US-0403321P.
PR   19-AUG-2002; 2002US-0404693P.
PR   29-AUG-2002; 2002US-0407062P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Richardson TW, Hafalia AJA, Khare R, Tran UK, Emerling BM;
PI   Lee SY, Chawla NK, Elliott VS, Swarnakar A, Chang H, Kable AE;
PI   Becha SD, Mason PM, Jiang X, Jackson AA, Marquis JP, Das D;
PI   Gietzen KJ, Ding L, Baughn MR, Lee EA, Thornton MB, Borowsky ML;
```

PI Harland L, Arvizu CS, Yao MG, Gandhi AR, Au-Young JK, Warren BA;
PI Lal PG, Lindquist EA;
XX
DR WPI; 2004-180430/17.
DR P-PSDB; ADJ27186.
XX
PT New human transporters and ion channels and nucleic acids encoding them,
PT useful for diagnosing, treating or preventing cystic fibrosis, Becker's
PT muscular dystrophy, Parkinson's disease, myasthenia gravis, prion disease
PT or cancers.
XX
PS Claim 5; SEQ ID NO 66; 357pp; English.
XX
CC The present invention relates to novel human TRansporters and Ion
CC CHannels proteins referred to collectively as TRICH (TRICH-1 - TRICH-48,
CC ADJ27169-ADJ27216) and their coding sequences (ADJ27217-ADJ27264). The
CC TRICH proteins and coding sequences are useful in the diagnosis,
CC treatment and prevention of transport, neurological, muscle,
CC immunological or cell proliferative disorders, e.g. akinesia, amyotrophic
CC lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's
CC muscular dystrophy, Bell's palsy, diabetes mellitus, diabetes insipidus,
CC diabetic neuropathy, Parkinson's disease, malignant hyperplasia,
CC myasthenia gravis, peripheral neuropathy, Alzheimer's disease,
CC Huntington's disease, Grave's disease, cataracts, bacterial and viral
CC meningitis, brain abscess, prion disease, Creutzfeldt-Jakob disease,
CC fatal familial insomnia, neurofibromatosis, Down syndrome,
CC cardiomyopathy, myocarditis, myotonic dystrophy, lipid myopathy, angina,
CC arrhythmias, asthma, Cushing's syndrome, hypertension, hypoglycaemia,
CC epilepsy, lactic acidosis, AIDS, anaemia, adult respiratory distress
CC syndrome, atherosclerosis, bronchitis, Crohn's disease, atopic
CC dermatitis, erythroblastosis fetalis, osteoarthritis, osteoporosis,
CC pancreatitis, psoriasis, rheumatoid arthritis, scleroderma, systemic
CC lupus erythematosus, ulcerative colitis, cirrhosis, cancers, viral,
CC bacterial, fungal, parasitic, protozoal or helminthic infections.
XX
SQ Sequence 2840 BP; 662 A; 677 C; 755 G; 746 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	93.4	Length:	2840
Score:	55.00	Matches:	8
Percent Similarity:	70.8%	Conservative:	9
Best Local Similarity:	33.3%	Mismatches:	7
Query Match:	34.4%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-1 (1-30) x ADJ27234 (1-2840)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::::::|||    |||::::::    |||:::|||:::||||||   :::::::::
Db       1330 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 1271

Qy         27 LysGlyThrPro 30
                ||| |||
Db       1270 TCCGGAGAGCCC 1259
```

RESULT 28
ADJ27233/c
ID ADJ27233 standard; DNA; 2950 BP.
XX
AC ADJ27233;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human TRICH-17 coding sequence, SEQ ID 65.
XX
KW Human; TRansporters and Ion CHannels protein; TRICH; Transporter;
KW Ion Channel; transport disorder; neurological disorder; muscle disorder;
KW immunological disorder; cell proliferative disorder; infection;
KW Neuroprotective; Muscular; Respiratory; Antidiabetic; Antiparkinsonian;
KW Nootropic; Anticonvulsant; Antithyroid; Ophthalmological; Antibacterial;
KW Antiinflammatory; Cardiant; Antianginal; Antiarrhythmic; Antiasthmatic;
KW Endocrine; Hypotensive; Anti-HIV; Antianaemic; Antiarteriosclerotic;
KW Dermatological; Antiarthritic; Osteopathic; Antipsoriatic; Antirheumatic;
KW Immunosuppressive; Antiulcer; Gastrointestinal; Hepatotropic; Cytostatic;
KW Virucide; Fungicide; Antiparasitic; Protozoacide; Antihelminthic;
KW Gene Therapy; TRICH-17; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2004013293-A2.
XX
PD 12-FEB-2004.
XX
PF 01-AUG-2003; 2003WO-US024164.
XX
PR 02-AUG-2002; 2002US-0400953P.
PR 12-AUG-2002; 2002US-0403321P.
PR 19-AUG-2002; 2002US-0404693P.
PR 29-AUG-2002; 2002US-0407062P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Richardson TW, Hafalia AJA, Khare R, Tran UK, Emerling BM;
PI Lee SY, Chawla NK, Elliott VS, Swarnakar A, Chang H, Kable AE;
PI Becha SD, Mason PM, Jiang X, Jackson AA, Marquis JP, Das D;
PI Gietzen KJ, Ding L, Baughn MR, Lee EA, Thornton MB, Borowsky ML;
PI Harland L, Arvizu CS, Yao MG, Gandhi AR, Au-Young JK, Warren BA;
PI Lal PG, Lindquist EA;
XX
DR WPI; 2004-180430/17.
DR P-PSDB; ADJ27185.
XX
PT New human transporters and ion channels and nucleic acids encoding them,
PT useful for diagnosing, treating or preventing cystic fibrosis, Becker's
PT muscular dystrophy, Parkinson's disease, myasthenia gravis, prion disease
PT or cancers.
XX
PS Claim 5; SEQ ID NO 65; 357pp; English.
XX
CC The present invention relates to novel human TRansporters and Ion
CC CHannels proteins referred to collectively as TRICH (TRICH-1 - TRICH-48,
CC ADJ27169-ADJ27216) and their coding sequences (ADJ27217-ADJ27264). The
CC TRICH proteins and coding sequences are useful in the diagnosis,
CC treatment and prevention of transport, neurological, muscle,
CC immunological or cell proliferative disorders, e.g. akinesia, amyotrophic
CC lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's
CC muscular dystrophy, Bell's palsy, diabetes mellitus, diabetes insipidus,
CC diabetic neuropathy, Parkinson's disease, malignant hyperplasia,
CC myasthenia gravis, peripheral neuropathy, Alzheimer's disease,
CC Huntington's disease, Grave's disease, cataracts, bacterial and viral
CC meningitis, brain abscess, prion disease, Creutzfeldt-Jakob disease,
CC fatal familial insomnia, neurofibromatosis, Down syndrome,
CC cardiomyopathy, myocarditis, myotonic dystrophy, lipid myopathy, angina,
CC arrhythmias, asthma, Cushing's syndrome, hypertension, hypoglycaemia,
CC epilepsy, lactic acidosis, AIDS, anaemia, adult respiratory distress
CC syndrome, atherosclerosis, bronchitis, Crohn's disease, atopic
CC dermatitis, erythroblastosis fetalis, osteoarthritis, osteoporosis,
CC pancreatitis, psoriasis, rheumatoid arthritis, scleroderma, systemic
CC lupus erythematosus, ulcerative colitis, cirrhosis, cancers, viral,
CC bacterial, fungal, parasitic, protozoal or helminthic infections.
XX
SQ Sequence 2950 BP; 689 A; 704 C; 774 G; 783 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	97.9	Length:	2950
Score:	55.00	Matches:	8
Percent Similarity:	70.8%	Conservative:	9
Best Local Similarity:	33.3%	Mismatches:	7
Query Match:	34.4%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-1 (1-30) x ADJ27233 (1-2950)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::::::|||    |||::::::    |||:::|||:::||||||   :::::::::
Db       1330 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 1271
```

```
Qy         27 LysGlyThrPro 30
              |||   |||
Db       1270 TCCGGAGAGCCC 1259

RESULT 29
AAC84981/c
ID   AAC84981 standard; cDNA; 903 BP.
XX
AC   AAC84981;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Myxoma virus immunomodulatory protein M144 encoding cDNA.
XX
KW   Leporipox virus; immunomodulatory; antiinflammatory; antirheumatic;
KW   antiarthritic; immunosuppressive; antiasthmatic; antiallergic;
KW   antipsoriatic; dermatological; neuroprotective; antidiabetic; M144;
KW   antithyroid; antianemic; antimicrobial; cytostatic; antiatherosclerotic;
KW   anti-HIV; hepatotropic; vasotropic; gene therapy; apoptosis inducer;
KW   leukocyte chemotaxis; ss.
XX
OS   Myxoma virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .903
FT                   /*tag=  a
XX
PN   WO200104318-A2.
XX
PD   18-JAN-2001.
XX
PF   12-JUL-2000; 2000WO-IB001043.
XX
PR   12-JUL-1999;   99US-0143317P.
XX
PA   (VIRO-) VIRON THERAPEUTICS INC.
XX
PI   Mcfadden G;
XX
DR   WPI; 2001-103085/11.
DR   P-PSDB; AAB61858.
XX
PT   New Leporipox virus polypeptide, useful for treating mammalian
PT   immunomodulatory disorders such as inflammation, rheumatoid arthritis,
PT   restenosis and asthma.
XX
PS   Claim 31; Fig 14; 144pp; English.
XX
CC   The invention provides Leporipox virus immunomodulatory polypeptides
CC   (AAB61845-864) and nucleic acid molecules (AAC84968-987) encoding these
CC   polypeptides. The immunomodulatory polypeptides and its modulators are
CC   useful for treating immunomodulatory disorder and for immunomodulation in
CC   mammals with conditions such as acute inflammation, rheumatoid arthritis,
CC   transplant rejection, restenosis, (bronchial) asthma, allergies, uveitis,
CC   inflammatory bowel disease, psoriasis, atopic dermatitis, pollinosis,
CC   systemic lupus erythematosus, nephrotic syndrome lupus, multiple
CC   sclerosis, myasthenia gravis, diabetes mellitus, glomerulonephritis,
CC   Hashimoto's thyroiditis, autoimmune haemolytic anemia, autoimmune
CC   thrombocytopenic purpura, malignancy and metastasis, microbial infection,
CC   autoimmune disease, cirrhosis, endotoxemia, atherosclerosis, reperfusion
CC   injury and inflammatory responses, AIDS, liver cirrhosis, ischaemic
CC   injury, neurodegeneration and myelodysplastic syndrome. Vectors
CC   comprising the encoding nucleic acids are useful for treating the above
CC   mentioned diseases by gene therapy. The present sequence represents the
CC   cDNA encoding the immunomodulatory polypeptide M144
XX
SQ   Sequence 903 BP; 252 A; 195 C; 206 G; 250 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              48.9          Length:        903
Score:                  53.00         Matches:       13
Percent Similarity:     51.4%         Conservative:  6
Best Local Similarity:  35.1%         Mismatches:    8
Query Match:            33.1%         Indels:        10
DB:                     5             Gaps:          1

US-10-758-902-1 (1-30) x AAC84981 (1-903)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp--------- 20
                |||:::||||||:::      ||||||:::   ||||||   ::::::
Db        590 GTAGCGTTTAACGTACACGTCGCGTACGACGCACCCACCAGTGTAAAGTCGGGATTGCAC 531

Qy         21 ---------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
                                       :::|||   |||   ||||||||||||
Db        530 GTAAAACGTACCCTGTTTTTATAACAGAATCGTTTAATGAAGGGAACTCCG 480

RESULT 30
AAQ89874
ID   AAQ89874 standard; cDNA; 962 BP.
XX
AC   AAQ89874;
XX
DT   21-OCT-2004  (revised)
DT   25-MAR-2003  (revised)
DT   31-JAN-1997  (first entry)
XX
DE   Bryodin-2 cDNA.
XX
KW   Ribosome inactivating protein; cell death; proliferation; tumour; cancer;
KW   virus; malaria; trypanosomiasis; inflammation; autoimmune; disease;
KW   purging; bone marrow; ss.
XX
OS   Bryonia dioica.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             28. .876
FT                   /*tag=  b
FT                   /product= "Bryodin-2"
FT   sig_peptide     28. .90
FT                   /*tag=  a
FT   mat_peptide     91. .873
FT                   /*tag=  c
XX
PN   WO9511977-A2.
XX
PD   04-MAY-1995.
XX
PF   25-OCT-1994;   94WO-US012382.
XX
PR   25-OCT-1993;   93US-00141891.
PR   20-OCT-1994;   94US-00324301.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Siegall CB,  Gawlak SL,  Marquardt H;
XX
DR   WPI; 1995-178870/23.
DR   P-PSDB; AAR74217.
XX
PT   New ribosome inactivating protein bryodin-2 and related conjugates - for
PT   killing target cells, e.g. in treatment of cancer, also related nucleic
PT   acid, vectors and transformed cells.
XX
PS   Claim 21; Page 54-55; 81pp; English.
XX
CC   The sequence encodes the ribosome inactivating protein termed bryodin-2,
CC   isolated from Bryonia dioica. Conjugates of the protein with a ligand may
CC   be used to kill target cells (i.e. those to which the ligand component
CC   binds specifically) or to inhibit proliferation of tumour cells. Typical
CC   applications include the treatment of cancer, viral infections, malaria,
CC   trypanosomiasis, inflammatory or autoimmune diseases, including in vitro
CC   purging of e.g. bone marrow. (Updated on 25-MAR-2003 to correct PN
CC   field.)
CC
```

```
CC   Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
SQ   Sequence 962 BP; 274 A; 198 C; 212 G; 278 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              52.9          Length:        962
Score:                  53.00         Matches:       10
Percent Similarity:     76.5%         Conservative:  3
Best Local Similarity:  58.8%         Mismatches:    4
Query Match:            33.1%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x AAQ89874 (1-962)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||   |||||||||:::::||||||   :::|||      |||||||||
Db        133 TACAAAACTTTTATAAGGAATCTGCGCACCAAACTCACGGTTGGAACTCCA 183

RESULT 31
ABL28589
ID   ABL28589 standard; DNA; 5366 BP.
XX
AC   ABL28589;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 37240.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 37240; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5366 BP; 1378 A; 1430 C; 1451 G; 1107 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              452           Length:        5366
Score:                  53.00         Matches:       10
Percent Similarity:     65.2%         Conservative:  5
Best Local Similarity:  43.5%         Mismatches:    8
Query Match:            33.1%         Indels:        0
DB:                     4             Gaps:          0

US-10-758-902-1 (1-30) x ABL28589 (1-5366)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::||||||   ||||||:::|||   :::   :::         ||||||      :::
Db       2292 TCGCTGGGCATGGCCTACGACTATGATTCGATTATGCACTACGCACGGAACACCTTCTCC 2351

Qy         27 LysGlyThr 29
              |||||||||
Db       2352 AAGGGCACC 2360

RESULT 32
ABL28588
ID   ABL28588 standard; DNA; 31068 BP.
XX
AC   ABL28588;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 37237.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 37237; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 31068 BP; 8424 A; 6977 C; 7023 G; 8644 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.04e+03      Length:        31068
Score:                  53.00         Matches:       10
Percent Similarity:     65.2%         Conservative:  5
Best Local Similarity:  43.5%         Mismatches:    8
Query Match:            33.1%         Indels:        0
DB:                     4             Gaps:          0

US-10-758-902-1 (1-30) x ABL28588 (1-31068)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::||||||   ||||||:::|||   :::   :::         ||||||      :::
```

```
Db      26247 TCGCTGGGCATGGCCTACGACTATGATTCGATTATGCACTACGCACGGAACACCTTCTCC 26306

Qy         27 LysGlyThr 29
              |||||||||
Db      26307 AAGGGCACC 26315

RESULT 33
ACN90027
ID   ACN90027 standard; DNA; 1040 BP.
XX
AC   ACN90027;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Breast cancer related marker, seq id 11177.
XX
KW   Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX
OS   Homo sapiens.
XX
PN   US2003099974-A1.
XX
PD   29-MAY-2003.
XX
PF   18-JUL-2002; 2002US-00198846.
XX
PR   18-JUL-2001; 2001US-0306220P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2003-787014/74.
XX
PT   Novel isolated polypeptide associated with breast cancer, useful for
PT   detecting presence of polypeptide in sample, as a marker for breast
PT   cancer.
XX
PS   Disclosure; SEQ ID NO 11177; 36pp; English.
XX
CC   The invention relates to an isolated polypeptide (I) associated with
CC   breast cancer which is encoded by a nucleic acid molecule comprising a
CC   nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC   the polypeptide of the invention. The activity of the polypeptide of the
CC   invention may be described as cytostatic. The antibody is useful for
CC   detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC   invention are useful in the detection of breast tumours. (I) is useful as
CC   a marker for breast cancer and in breast cancer therapy. Sequences given
CC   in records ACN78851-ACN92934 represent nucleic acid markers associated
CC   with breast cancer. Note: The sequence listing does not form part of the
CC   specification but may be obtained in electronic format from the USPTO web
CC   site at seqdata.uspto.gov/sequence.html?DocID=20030099974
XX
SQ   Sequence 1040 BP; 306 A; 219 C; 227 G; 288 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              86.3          Length:        1040
Score:                  52.00         Matches:       11
Percent Similarity:     62.5%         Conservative:  4
Best Local Similarity:  45.8%         Mismatches:    9
Query Match:            32.5%         Indels:        0
DB:                     11            Gaps:          0

US-10-758-902-1 (1-30) x ACN90027 (1-1040)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              |||   ||||||:::   |||:::   |||:::||||||   :::      |||   |||
Db        518 GTGTTATTTAACATTCTTGAATCTTCAGAGTGGCCAACACTTTTGTTGACTCTTCACAAT 577

Qy         24 GluLeuAlaLys 27
                 |||   |||
Db        578 AACCTATTAAAA 589
```

```
RESULT 34
ABX13666
ID   ABX13666 standard; cDNA; 1364 BP.
XX
AC   ABX13666;
XX
DT   27-OCT-2003  (revised)
DT   12-FEB-2003  (first entry)
XX
DE   Piromyces rhizinflata cellulase, cbhA, cDNA.
XX
KW   Cellulase; gene; ss; CBHA; hydrolysis; polysaccharide;
KW   beta-1,3' glycosidic linkage; beta-1,4' glycosidic linkage; biomass;
KW   cellulose; fermentation; indigestible biomass; fermentable sugar;
KW   animal feed; faecal waste; digestibility; stone-washed blue jeans.
XX
OS   Piromyces rhizinflatus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1131
FT                   /*tag=  a
FT                   /product= "CBHA"
FT                   /partial
FT                   /note= "No start codon shown"
FT   CDS             130. .1131
FT                   /*tag=  b
FT                   /product= "CBHA catalytic domain"
FT                   /partial
FT                   /note= "No start codon shown"
FT   primer_bind     complement(130. .148)
FT                   /*tag=  c
FT                   /note= "Primer binding site for ABX13667"
FT   primer_bind     1114. .1131
FT                   /*tag=  d
FT                   /note= "Primer binding site for ABX13668"
XX
PN   US6428996-B1.
XX
PD   06-AUG-2002.
XX
PF   27-OCT-1999;   99US-00428034.
XX
PR   27-OCT-1999;   99US-00428034.
XX
PA   (SINI-) ACAD SINICA.
XX
PI   Cheng K,  Liu J,  Tsai C,  Hsu Y;
XX
DR   WPI; 2003-101666/09.
DR   P-PSDB; ABG72091.
XX
PT   New Piromyces rhizinflata enzyme (cbhA) useful for hydrolyzing cellulose.
XX
PS   Claim 6; Col 3-6; 10pp; English.
XX
CC   The invention discloses an isolated Piromyces rhizinflata nucleic acid
CC   encoding a cellulase polypeptide, CBHA, that hydrolyses a polysaccharide
CC   containing a beta-1,3' or beta-1,4' glycosidic linkage. The enzyme is
CC   useful for breaking down biomass in industrial applications e.g. for
CC   hydrolysing cellulose for use in alcoholic fermentation (for converting
CC   indigestible biomass into fermentable sugars), animal feeds (for
CC   decreasing the production of faecal waste by increasing the digestibility
CC   of the feed) and for producing stone-washed blue jeans. The sequence
CC   presented is the P. rhizinflata cellulase, cbhA, cDNA. (Updated on 27-OCT
CC   -2003 to standardise OS field)
XX
SQ   Sequence 1364 BP; 436 A; 237 C; 228 G; 463 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              121           Length:        1364
Score:                  52.00         Matches:       10
Percent Similarity:     61.5%         Conservative:  6
Best Local Similarity:  38.5%         Mismatches:    10
```

```
Query Match:            32.5%          Indels:        0
DB:                     8              Gaps:          0

US-10-758-902-1 (1-30) x ABX13666 (1-1364)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::|||   |||   |||   |||      |||   ||||||:::::::::   :::
Db        148 AACTTTTTCTTAAATGAAATTTATGCTAATCCAAAATTCATTGAAGAAGTTGAAGATTCC 207

Qy         25 LeuAlaLysGlyThrPro 30
              :::   |||   ||||||
Db        208 ATTGAAAAATTAACTCCT 225

RESULT 35
ACL66796
ID   ACL66796 standard; DNA; 1380 BP.
XX
AC   ACL66796;
XX
DT   02-JUN-2005  (first entry)
XX
DE   M. xanthus gene sequence, seq id 3259.
XX
KW   Transgenic plant; DNA replication; gene regulation; gene expression;
KW   gene; ds.
XX
OS   Myxococcus xanthus.
XX
PN   US6833447-B1.
XX
PD   21-DEC-2004.
XX
PF   10-JUL-2001; 2001US-00902540.
XX
PR   10-JUL-2000; 2000US-0217883P.
XX
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI   Goldman BS,  Hinkle GJ,  Slater SC,  Wiegand RC;
XX
DR   WPI; 2005-028716/03.
XX
PT   New substantially purified Myxococcus xanthus nucleic acid molecule
PT   encoding a nitrite reductase, useful for determining gene expression,
PT   identifying mutations in a gene of interest, and for constructing
PT   mutations in a gene of interest.
XX
PS   Example 2; SEQ ID NO 3259; 25pp; English.
XX
CC   The invention relates to a substantially purified nucleic acid molecule
CC   encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC   recombinant DNA construct for expression of a nitrite reductase gene in a
CC   plant cell, and a plant cell comprising the recombinant DNA construct.
CC   The nucleic acid is useful for determining gene expression, identifying
CC   mutations in a gene of interest, and for constructing mutations in a gene
CC   of interest. Sequences given in records for SEQ IDs 1850-9691 represent a
CC   set of about 7842 genes or partial genes from the genome of the bacterium
CC   Mxyococcus xanthus. Note: The sequence data for this patent did not form
CC   part of the printed specification, but was obtained in electronic format
CC   directly from USPTO
XX
SQ   Sequence 1380 BP; 231 A; 468 C; 501 G; 180 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              123            Length:        1380
Score:                  52.00          Matches:       10
Percent Similarity:     71.4%          Conservative:  5
Best Local Similarity:  47.6%          Mismatches:    6
Query Match:            32.5%          Indels:        0
DB:                     14             Gaps:          0

US-10-758-902-1 (1-30) x ACL66796 (1-1380)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              |||   |||   ||||||:::|||      :::::::::|||||||||   |||   :::
Db       1006 CTCTTCGAGGGCTATGAGTGGCCGGGCAACGTGCGCGAGCTGCGCAACGTGCTGGAGCGC 1065

Qy         28 Gly 28
              |||
Db       1066 GGC 1068

RESULT 36
ADW07610/c
ID   ADW07610 standard; DNA; 1467 BP.
XX
AC   ADW07610;
XX
DT   10-MAR-2005  (first entry)
XX
DE   GTase cDNA sequence #107.
XX
KW   Protein purification; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; virucide; antibacterial;
KW   fungicide; antiparasitic; cytostatic; GTase; ss.
XX
OS   Unidentified.
XX
PN   WO2004113540-A1.
XX
PD   29-DEC-2004.
XX
PF   09-JUN-2004; 2004WO-GB002432.
XX
PR   18-JUN-2003; 2003GB-00014102.
PR   03-FEB-2004; 2004GB-00002293.
XX
PA   (UYYO-) UNIV YORK.
XX
PI   Eastmond P;
XX
DR   WPI; 2005-048833/05.
XX
PT   New nucleic acid molecule that encodes a chimeric polypeptide comprises a
PT   first part and a second part that encodes a heterologous polypeptide,
PT   useful for treating viral, bacterial, fungal, or parasitic infections, or
PT   cancer.
XX
PS   Disclosure; Page 79-80; 95pp; English.
XX
CC   The invention relates to a nucleic acid molecule that encodes a chimeric
CC   polypeptide comprising a first part and a second part that encodes a
CC   heterologous polypeptide. The invention also relates to a chimeric
CC   polypeptide encoded by the nucleic acid, a vector comprising the nucleic
CC   acid, a cell transfected or transformed with the nucleic acid or the
CC   vector, a method of producing the chimeric polypeptide, a plant
CC   comprising the cell, a seed comprising the cell, a vessel comprising the
CC   cell and/or the polypeptide, a vaccine preparation comprising the cell, a
CC   fraction of the cell or the plant, a method of immunizing an animal to at
CC   least the second part of the chimeric polypeptide, an antibody obtainable
CC   by the method, a method for preparing a hybridoma cell-line producing
CC   monoclonal antibodies and a method for preparing the vaccine preparation.
CC   The method of producing the chimeric polypeptide comprises providing cell
CC   and growth conditions conducive to the production of a chimeric
CC   polypeptide and optionally purifying the chimeric polypeptide from the
CC   cell or growth media. The method of immunizing an animal to at least the
CC   second part of the chimeric polypeptide comprises administering an amount
CC   of the chimeric polypeptide or preparation to stimulate an immune
CC   response to the second part. The method of preparing a hybridoma cell-
CC   line producing monoclonal antibodies comprises immunizing an
CC   immunocompetent mammal with a chimeric polypeptide or preparation, fusing
CC   lymphocytes of the immunized immunocompetent mammal with myeloma cells to
CC   form hybridoma cells, screening monoclonal antibodies produced by the
CC   hybridoma cells for binding activity to the polypeptide, culturing the
CC   hybridoma cells to proliferate and/or to secrete the monoclonal antibody
CC   and recovering the monoclonal antibody from the culture supernatant. The
CC   method of preparing the vaccine preparation comprises forming a cell
```

```
CC   extract from a plant cell culture or plant and separating the extract
CC   into an oil body rich fraction. The extract is incubated with a protease
CC   that cleaves the second part from the first part. The nucleic acid,
CC   polypeptide, antibody, and vaccine are useful for treating viral,
CC   bacterial, fungal and parasitic infections and cancer. This sequence
CC   represents GTase cDNA used in the scope of the invention.
XX
SQ   Sequence 1467 BP; 402 A; 261 C; 392 G; 412 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              133          Length:        1467
Score:                  52.00        Matches:       9
Percent Similarity:     92.9%        Conservative:  4
Best Local Similarity:  64.3%        Mismatches:    1
Query Match:            32.5%        Indels:        0
DB:                     14           Gaps:          0

US-10-758-902-1 (1-30) x ADW07610 (1-1467)

Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::|||||||||||||:::|||::::::||||||
Db        369 CCCTTCTTCCTTCAAGATCTTCGTCATGAAGTCTCGAAAGGG 328

RESULT 37
ADX50786
ID   ADX50786 standard; cDNA; 1689 BP.
XX
AC   ADX50786;
XX
DT   21-APR-2005  (first entry)
XX
DE   Plant full length insert polynucleotide seqid 25526.
XX
KW   plant protectant; plant growth regulant; gene therapy; plant;
KW   recombinant DNA construct; physical array; plant breeding marker;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW   extreme osmotic condition; pathogen tolerance; pest tolerance;
KW   growth rate; cell cycle pathway; disease resistance;
KW   galactomannan production; lignin production; plant growth regulator;
KW   yield; plant growth; plant development; seed oil; protein yield;
KW   protein content; gene; ss.
XX
OS   Unidentified.
XX
PN   US2004034888-A1.
XX
PD   19-FEB-2004.
XX
PF   28-APR-2003; 2003US-00425114.
XX
PR   06-MAY-1999;   99US-00304517.
PR   05-NOV-2001; 2001US-00985678.
XX
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
XX
PI   Liu J,  Zhou Y,  Kovalic DK,  Screen SE,  Tabaska JE,  Cao Y;
XX
DR   WPI; 2004-180133/17.
XX
PT   New recombinant DNA construct, useful for improving plant tolerance to
PT   cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT   pests, for conferring increased resistance to plant disease, or for
PT   improving yield.
XX
PS   Claim 1; SEQ ID NO 25526; 15pp; English.
XX
CC   The invention describes a recombinant DNA construct comprising a
CC   polynucleotide consisting of a sequence encoding an amino acid sequence
CC   available in electronic form from the US patent office at
CC   ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC   of the invention are also useful in physical arrays of molecules and as
CC   plant breeding markers. The recombinant DNA construct is useful for
CC   improving plant tolerance to cold, heat, drought, herbicides, extreme
CC   osmotic conditions, pathogens or pests, for manipulating growth rate in
CC   plant cells by modification of the cell cycle pathway, for conferring
CC   increased resistance to plant disease, for producing galactomannan,
CC   lignin or plant growth regulators, for increasing the rate of homologous
CC   recombination in plants, for improving yield by modification of
CC   photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC   or by providing improved plant growth and development under at least one
CC   stress condition or for modifying seed oil or protein yield and/or
CC   content. This sequence represents a plant full length insert
CC   polynucleotide that can be used in the recombinant DNA construct of the
CC   invention.
XX
SQ   Sequence 1689 BP; 419 A; 383 C; 440 G; 447 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              158          Length:        1689
Score:                  52.00        Matches:       10
Percent Similarity:     66.7%        Conservative:  4
Best Local Similarity:  47.6%        Mismatches:    7
Query Match:            32.5%        Indels:        0
DB:                     13           Gaps:          0

US-10-758-902-1 (1-30) x ADX50786 (1-1689)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||   |||   :::||||||             :::|||:::|||
Db       1287 GGCGAAGCATATGAACCGCCTTGTTACATACAACCTTTTGAAAAGGGAGTGGCAGAAGGT 1346

Qy         29 Thr 29
              :::
Db       1347 TCC 1349

RESULT 38
ADX34957
ID   ADX34957 standard; cDNA; 1692 BP.
XX
AC   ADX34957;
XX
DT   21-APR-2005  (first entry)
XX
DE   Plant full length insert polynucleotide seqid 17777.
XX
KW   plant protectant; plant growth regulant; gene therapy; plant;
KW   recombinant DNA construct; physical array; plant breeding marker;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW   extreme osmotic condition; pathogen tolerance; pest tolerance;
KW   growth rate; cell cycle pathway; disease resistance;
KW   galactomannan production; lignin production; plant growth regulator;
KW   yield; plant growth; plant development; seed oil; protein yield;
KW   protein content; gene; ss.
XX
OS   Unidentified.
XX
PN   US2004034888-A1.
XX
PD   19-FEB-2004.
XX
PF   28-APR-2003; 2003US-00425114.
XX
PR   06-MAY-1999;   99US-00304517.
PR   05-NOV-2001; 2001US-00985678.
XX
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
```

```
XX
PI   Liu J,  Zhou Y,  Kovalic DK,  Screen SE,  Tabaska JE,  Cao Y;
XX
DR   WPI; 2004-180133/17.
XX
PT   New recombinant DNA construct, useful for improving plant tolerance to
PT   cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT   pests, for conferring increased resistance to plant disease, or for
PT   improving yield.
XX
PS   Claim 1; SEQ ID NO 17777; 15pp; English.
XX
CC   The invention describes a recombinant DNA construct comprising a
CC   polynucleotide consisting of a sequence encoding an amino acid sequence
CC   available in electronic form from the US patent office at
CC   ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC   of the invention are also useful in physical arrays of molecules and as
CC   plant breeding markers. The recombinant DNA construct is useful for
CC   improving plant tolerance to cold, heat, drought, herbicides, extreme
CC   osmotic conditions, pathogens or pests, for manipulating growth rate in
CC   plant cells by modification of the cell cycle pathway, for conferring
CC   increased resistance to plant disease, for producing galactomannan,
CC   lignin or plant growth regulators, for increasing the rate of homologous
CC   recombination in plants, for improving yield by modification of
CC   photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC   or by providing improved plant growth and development under at least one
CC   stress condition or for modifying seed oil or protein yield and/or
CC   content. This sequence represents a plant full length insert
CC   polynucleotide that can be used in the recombinant DNA construct of the
CC   invention.
XX
SQ   Sequence 1692 BP; 421 A; 382 C; 439 G; 450 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              158          Length:         1692
Score:                  52.00        Matches:        10
Percent Similarity:     66.7%        Conservative:   4
Best Local Similarity:  47.6%        Mismatches:     7
Query Match:            32.5%        Indels:         0
DB:                     13           Gaps:           0

US-10-758-902-1 (1-30) x ADX34957 (1-1692)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||||||||||||||   |||   :::||||||           :::|||:::|||
Db       1284 GGCGAAGCATATGAACCGCCTTGTTACATACAACCTTTTGAAAAGGGAGTGGCAGAAGGT 1343

Qy         29 Thr 29
              :::
Db       1344 TCC 1346

RESULT 39
ACL64687
ID   ACL64687 standard; DNA; 19954 BP.
XX
AC   ACL64687;
XX
DT   02-JUN-2005  (first entry)
XX
DE   M. xanthus DNA fragment, seq id 1150.
XX
KW   Transgenic plant; DNA replication; gene regulation; gene expression; ds.
XX
OS   Myxococcus xanthus.
XX
PN   US6833447-B1.
XX
PD   21-DEC-2004.
XX
PF   10-JUL-2001; 2001US-00902540.
XX
PR   10-JUL-2000; 2000US-0217883P.
XX
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI   Goldman BS,  Hinkle GJ,  Slater SC,  Wiegand RC;
XX
DR   WPI; 2005-028716/03.
XX
PT   New substantially purified Myxococcus xanthus nucleic acid molecule
PT   encoding a nitrite reductase, useful for determining gene expression,
PT   identifying mutations in a gene of interest, and for constructing
PT   mutations in a gene of interest.
XX
PS   Example 1; SEQ ID NO 1150; 25pp; English.
XX
CC   The invention relates to a substantially purified nucleic acid molecule
CC   encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC   recombinant DNA construct for expression of a nitrite reductase gene in a
CC   plant cell, and a plant cell comprising the recombinant DNA construct.
CC   The nucleic acid is useful for determining gene expression, identifying
CC   mutations in a gene of interest, and for constructing mutations in a gene
CC   of interest. Sequences given in records for SEQ IDs 1-1849 represent a
CC   set of 1849 contig and singleton sequences comprising coding sequences,
CC   DNA replication elements, promoters and other regulatory elements from
CC   the genome of the bacterium Mxyococcus xanthus. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO
XX
SQ   Sequence 19954 BP; 3198 A; 7145 C; 6570 G; 3041 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.44e+03     Length:         19954
Score:                  52.00        Matches:        10
Percent Similarity:     71.4%        Conservative:   5
Best Local Similarity:  47.6%        Mismatches:     6
Query Match:            32.5%        Indels:         0
DB:                     14           Gaps:           0

US-10-758-902-1 (1-30) x ACL64687 (1-19954)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              |||   |||   ||||||:::|||      :::::::::||||||||||   |||   :::
Db      12372 CTCTTCGAGGGCTATGAGTGGCCGGGCAACGTGCGCGAGCTGCGCAACGTGCTGGAGCGC 12431

Qy         28 Gly 28
              |||
Db      12432 GGC 12434

RESULT 40
ADZ45062_06
Continuation (7 of 10) of ADZ45062 from base 600001 (Human cholecystokinin type-A recep
WP Sequence split into 10 fragments  LOCUS ADZ45062 Accession Adz45062
WP     Fragment Name      Begin     End
WP     ADZ45062_00            1     110000
WP     ADZ45062_01       100001     210000
WP     ADZ45062_02       200001     310000
WP     ADZ45062_03       300001     410000
WP     ADZ45062_04       400001     510000
WP     ADZ45062_05       500001     610000
WP     ADZ45062_06       600001     710000
WP     ADZ45062_07       700001     810000
WP     ADZ45062_08       800001     910000
WP     ADZ45062_09       900001     998825

Alignment Scores:
Pred. No.:              2.89e+04     Length:         110000
Score:                  52.00        Matches:        8
Percent Similarity:     72.2%        Conservative:   5
Best Local Similarity:  44.4%        Mismatches:     5
Query Match:            32.5%        Indels:         0
DB:                     14           Gaps:           0

US-10-758-902-1 (1-30) x ADZ45062_06 (1-110000)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
```

```
            |||:::|||:::   ::::::      |||   |||||||||   ||||||:::
Db      78151 TATTCAACTATTCTTTATTCATTCAGTGAAAATTATGAATATAAAACATTTCTT 78204
```

Search completed: February 20, 2006, 07:54:46
Job time : 164.989 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:19:21 ; Search time 45.5866 Seconds
(without alignments)
1169.792 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160806_3773/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss08 -USER=US10758902_@CGN_1_1_237_@runat_17022006_160806_3773 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	111	69.4	65	3	US-09-445-160B-5	Sequence 5, Appli
2	72	45.0	363	3	US-09-445-160B-8	Sequence 8, Appli
3	61	38.1	1195	2	US-08-373-858-1	Sequence 1, Appli
4	61	38.1	1195	2	US-08-342-786B-1	Sequence 1, Appli
5	61	38.1	1379	2	US-08-500-611-1	Sequence 1, Appli
6	61	38.1	1379	2	US-08-500-694-1	Sequence 1, Appli
7	61	38.1	1379	3	US-07-865-169-1	Sequence 1, Appli
8	61	38.1	1379	3	US-09-005-273-1	Sequence 1, Appli
9	61	38.1	1379	3	US-08-501-253A-1	Sequence 1, Appli
10	61	38.1	1379	6	PCT-US96-11546-1	Sequence 1, Appli
11	57.5	35.9	678	3	US-09-107-532A-3648	Sequence 3648, Ap
12	56	35.0	1379	3	US-07-865-169-2	Sequence 2, Appli
13	56	35.0	1379	3	US-09-005-273-3	Sequence 3, Appli
14	55.5	34.7	38844	3	US-09-734-675-3	Sequence 3, Appli
15	55.5	34.7	38844	3	US-10-060-333-3	Sequence 3, Appli
c 16	53.5	33.4	601	3	US-09-949-016-62787	Sequence 62787, A
c 17	53.5	33.4	601	3	US-09-949-016-62788	Sequence 62788, A
18	53.5	33.4	103792	3	US-09-949-016-13553	Sequence 13553, A
19	53.5	33.4	103993	3	US-09-949-016-12317	Sequence 12317, A
20	53	33.1	962	2	US-08-324-301-14	Sequence 14, Appl
21	52	32.5	999	3	US-09-428-034-3	Sequence 3, Appli
22	52	32.5	1364	3	US-09-428-034-1	Sequence 1, Appli
23	52	32.5	1380	3	US-09-902-540-3259	Sequence 3259, Ap
24	52	32.5	19954	3	US-09-902-540-1150	Sequence 1150, Ap
25	52	32.5	51822	3	US-09-949-016-15233	Sequence 15233, A
26	51.5	32.2	717	3	US-09-902-540-8868	Sequence 8868, Ap
27	51.5	32.2	12028	3	US-09-902-540-1071	Sequence 1071, Ap
28	51	31.9	3702	3	US-09-134-000C-1566	Sequence 1566, Ap
29	51	31.9	4249	3	US-09-071-035-403	Sequence 403, App
30	51	31.9	4249	3	US-10-206-576-403	Sequence 403, App
31	51	31.9	4359	3	US-09-071-035-401	Sequence 401, App
32	51	31.9	4359	3	US-10-206-576-401	Sequence 401, App
33	51	31.9	13222	3	US-09-736-116-60	Sequence 60, Appl
34	50	31.2	670	3	US-09-306-446C-15	Sequence 15, Appl
35	50	31.2	5108	3	US-09-306-446C-8	Sequence 8, Appli
36	50	31.2	133559	3	US-09-949-016-15845	Sequence 15845, A
37	49.5	30.9	4953	3	US-09-602-787A-13	Sequence 13, Appl
38	49.5	30.9	4953	3	US-09-602-787A-55	Sequence 55, Appl
c 39	49.5	30.9	6053	3	US-09-573-080A-22	Sequence 22, Appl
40	49.5	30.9	6567	3	US-09-328-352-3637	Sequence 3637, Ap
41	49	30.6	949	3	US-09-221-017B-615	Sequence 615, App
42	49	30.6	6960	2	US-08-841-349-3	Sequence 3, Appli
43	49	30.6	6960	3	US-09-431-184A-3	Sequence 3, Appli
44	49	30.6	8176	2	US-08-841-349-5	Sequence 5, Appli
45	49	30.6	8176	3	US-09-431-184A-5	Sequence 5, Appli
46	49	30.6	134890	3	US-09-949-016-15602	Sequence 15602, A
c 47	49	30.6	174493	3	US-09-804-471A-3	Sequence 3, Appli
c 48	49	30.6	174493	3	US-10-238-709-3	Sequence 3, Appli
c 49	49	30.6	174493	3	US-10-724-594-3	Sequence 3, Appli
c 50	48.5	30.3	80706	3	US-09-949-016-15347	Sequence 15347, A
51	48	30.0	162	3	US-09-513-999C-30353	Sequence 30353, A
52	48	30.0	405	3	US-09-401-064-194	Sequence 194, App
53	48	30.0	887	3	US-09-949-016-5729	Sequence 5729, Ap
54	48	30.0	887	3	US-09-949-016-5730	Sequence 5730, Ap
55	48	30.0	887	3	US-09-949-016-5731	Sequence 5731, Ap
56	48	30.0	1083	3	US-09-549-831-12	Sequence 12, Appl
57	48	30.0	1119	3	US-08-911-321-2	Sequence 2, Appli
58	48	30.0	1125	2	US-08-105-483-290	Sequence 290, App
59	48	30.0	1125	2	US-08-709-209-290	Sequence 290, App
60	48	30.0	1125	2	US-08-458-101-290	Sequence 290, App
61	48	30.0	1195	3	US-09-549-831-9	Sequence 9, Appli
62	48	30.0	1491	3	US-09-902-540-3335	Sequence 3335, Ap
c 63	48	30.0	1659	3	US-09-252-991A-9018	Sequence 9018, Ap
64	48	30.0	2139	3	US-09-614-221A-341	Sequence 341, App
65	48	30.0	2330	6	PCT-US95-13975-71	Sequence 71, Appl
c 66	48	30.0	3365	3	US-09-221-017B-318	Sequence 318, App
67	48	30.0	3687	3	US-09-891-641-1	Sequence 1, Appli
68	48	30.0	6176	3	US-08-911-321-6	Sequence 6, Appli
c 69	48	30.0	7374	3	US-09-252-991A-9100	Sequence 9100, Ap
70	48	30.0	16387	3	US-09-902-540-1156	Sequence 1156, Ap
71	48	30.0	92387	3	US-09-949-016-14563	Sequence 14563, A
72	48	30.0	151295	3	US-09-949-016-14568	Sequence 14568, A
73	48	30.0	151295	3	US-09-949-016-14569	Sequence 14569, A
74	48	30.0	151295	3	US-09-949-016-14570	Sequence 14570, A
75	48	30.0	151295	3	US-09-949-016-14571	Sequence 14571, A
76	48	30.0	151295	3	US-09-949-016-14572	Sequence 14572, A
77	48	30.0	269223	3	US-09-596-002-41	Sequence 41, Appl
78	48	30.0	319608	3	US-09-539-333D-1	Sequence 1, Appli
79	48	30.0	319608	3	US-09-679-409-1	Sequence 1, Appli
80	48	30.0	393753	3	US-09-949-016-14573	Sequence 14573, A
81	48	30.0	393753	3	US-09-949-016-14574	Sequence 14574, A
c 82	48	30.0	670689	3	US-09-949-016-12505	Sequence 12505, A

c	83	48	30.0	670690	3	US-09-949-016-14207 Sequence 14207, A
	84	48	30.0	678533	3	US-09-949-016-14577 Sequence 14577, A
	85	48	30.0	678533	3	US-09-949-016-14578 Sequence 14578, A
	86	48	30.0	818128	3	US-09-949-016-14546 Sequence 14546, A
	87	48	30.0	818128	3	US-09-949-016-14547 Sequence 14547, A
	88	48	30.0	818128	3	US-09-949-016-14548 Sequence 14548, A
	89	48	30.0	818128	3	US-09-949-016-14549 Sequence 14549, A
	90	48	30.0	818128	3	US-09-949-016-14550 Sequence 14550, A
	91	48	30.0	818128	3	US-09-949-016-14551 Sequence 14551, A
	92	48	30.0	818128	3	US-09-949-016-14552 Sequence 14552, A
	93	48	30.0	818128	3	US-09-949-016-14553 Sequence 14553, A
	94	48	30.0	818128	3	US-09-949-016-14554 Sequence 14554, A
	95	48	30.0	818128	3	US-09-949-016-14555 Sequence 14555, A
	96	48	30.0	818128	3	US-09-949-016-14556 Sequence 14556, A
	97	48	30.0	818128	3	US-09-949-016-14557 Sequence 14557, A
	98	48	30.0	818128	3	US-09-949-016-14558 Sequence 14558, A
	99	48	30.0	818128	3	US-09-949-016-14559 Sequence 14559, A
	100	48	30.0	818128	3	US-09-949-016-14560 Sequence 14560, A

ALIGNMENTS

```
RESULT 1
US-09-445-160B-5
; Sequence 5, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 5
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;  PUBLICATION INFORMATION:
US-09-445-160B-5

Alignment Scores:
Pred. No.:              1.72e-11        Length:         65
Score:                  111.00          Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            69.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-445-160B-5 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 2
US-09-445-160B-8
; Sequence 8, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;  PUBLICATION INFORMATION:
US-09-445-160B-8

Alignment Scores:
Pred. No.:              0.00112         Length:         363
Score:                  72.00           Matches:        14
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            45.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-445-160B-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 3
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Man-Keun
;    APPLICANT:  Lee, Kwan-Ho
;    APPLICANT:  Na, Byeong-Kook
;    APPLICANT:  Jeong, Han-Seung
;    APPLICANT:  Choi, Kyu-Whan
;    APPLICANT:  Moon, Young-Ho
;    APPLICANT:  Jeon, Hong-Seob
;    TITLE OF INVENTION:  Expression Vector for Phytolacca
;    TITLE OF INVENTION:  Antiviral Protein and Process for Preparing Transgenic
;    TITLE OF INVENTION:  Plant Transformed Thereof.
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  US
;      ZIP:  10022-7513
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,858
;      FILING DATE:  18-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Peter
;      REGISTRATION NUMBER:  25,351
;      REFERENCE/DOCKET NUMBER:  0136/17986-US1
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7770
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Phytolacca americana
;      TISSUE TYPE:  Leaf
US-08-373-858-1

Alignment Scores:
Pred. No.:              0.441          Length:         1195
Score:                  61.00          Matches:        12
Percent Similarity:     68.0%          Conservative:   5
Best Local Similarity:  48.0%          Mismatches:     6
Query Match:            38.1%          Indels:         2
DB:                     2              Gaps:           1

US-10-758-902-1 (1-30) x US-08-373-858-1 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              |||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 4
US-08-342-786B-1
; Sequence 1, Application US/08342786B
; Patent No. 5648234
;  GENERAL INFORMATION:
;    APPLICANT:  Moon, Young-Ho
;    APPLICANT:  Jeon, Hong-Seob
;    APPLICANT:  Choi, Kyu-Whan
;    APPLICANT:  Lee, Kwan-Ho
;    APPLICANT:  Kim, Man-Keun
;    TITLE OF INVENTION:  A No. 5648234el Expression Vector for Phytolacca
;    TITLE OF INVENTION:  Antiviral Protein
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby
;      STREET:  805 Third Ave.
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/342,786B
;      FILING DATE:  21-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/147,024
;      FILING DATE:  01-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, S. Peter
;      REGISTRATION NUMBER:  25,351
;      REFERENCE/DOCKET NUMBER:  0136/08862-US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)527-7700
;      TELEFAX:  (212)753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Phytolacca americana L.
;    IMMEDIATE SOURCE:
;      CLONE:  PAP
US-08-342-786B-1

Alignment Scores:
Pred. No.:              0.441          Length:         1195
Score:                  61.00          Matches:        12
Percent Similarity:     68.0%          Conservative:   5
Best Local Similarity:  48.0%          Mismatches:     6
Query Match:            38.1%          Indels:         2
DB:                     2              Gaps:           1

US-10-758-902-1 (1-30) x US-08-342-786B-1 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              |||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 5
US-08-500-611-1
; Sequence 1, Application US/08500611
; Patent No. 5756322
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  Pokeweed Antiviral Protein Mutants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/500,611
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.0-034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;      TELEX:  139-125
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
```

```
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(233, "a")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(349, "g")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(435, "c")
US-08-500-611-1

Alignment Scores:
Pred. No.:              0.529          Length:        1379
Score:                  61.00          Matches:       12
Percent Similarity:     68.0%          Conservative:  5
Best Local Similarity:  48.0%          Mismatches:    6
Query Match:            38.1%          Indels:        2
DB:                     2              Gaps:          1

US-10-758-902-1 (1-30) x US-08-500-611-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 6
US-08-500-694-1
; Sequence 1, Application US/08500694
; Patent No. 5880329
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  DNAs Encoding Pokeweed Antiviral Protein
;    TITLE OF INVENTION:  Mutants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/500,694
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.0-039
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;      TELEX:  139-125
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(233, "a")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(349, "g")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(435, "c")
US-08-500-694-1

Alignment Scores:
Pred. No.:              0.529          Length:        1379
Score:                  61.00          Matches:       12
Percent Similarity:     68.0%          Conservative:  5
Best Local Similarity:  48.0%          Mismatches:    6
Query Match:            38.1%          Indels:        2
DB:                     2              Gaps:          1

US-10-758-902-1 (1-30) x US-08-500-694-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 7
US-07-865-169-1
; Sequence 1, Application US/07865169
; Patent No. 6015940
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    APPLICANT:  Lodge, Jennifer K.
;    APPLICANT:  Kaniewski, Wojciech K.
;    TITLE OF INVENTION:  Virus Resistant Potato Plants
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis R. Hoerner, Jr., Monsanto Co.  BB4F
;      STREET:  700 Chesterfield Parkway No. 6015940th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/865,169
;      FILING DATE:  19920407
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoerner Jr., Dennis R.
;      REGISTRATION NUMBER:  30,914
;      REFERENCE/DOCKET NUMBER:  38-21(10547)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6099
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-865-169-1

Alignment Scores:
Pred. No.:              0.529          Length:        1379
```

```
Score:                 61.00          Matches:       12
Percent Similarity:    68.0%          Conservative:  5
Best Local Similarity: 48.0%          Mismatches:    6
Query Match:           38.1%          Indels:        2
DB:                    3              Gaps:          1

US-10-758-902-1 (1-30) x US-07-865-169-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 8
US-09-005-273-1
; Sequence 1, Application US/09005273
; Patent No. 6137030
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
;    TITLE OF INVENTION:  AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ &
;      ADDRESSEE:  MENTILIK
;      STREET:  600 South, Avenue West
;      CITY:  Westfield
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07090
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/005,273
;      FILING DATE:  09-JAN-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,611
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,694
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11546
;      FILING DATE:  11-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REGISTRATION NUMBER:  33,071
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.3-034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  225..290
US-09-005-273-1

Alignment Scores:
Pred. No.:             0.529          Length:        1379
Score:                 61.00          Matches:       12
Percent Similarity:    68.0%          Conservative:  5
Best Local Similarity: 48.0%          Mismatches:    6
Query Match:           38.1%          Indels:        2
DB:                    3              Gaps:          1

US-10-758-902-1 (1-30) x US-09-005-273-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 9
US-08-501-253A-1
; Sequence 1, Application US/08501253A
; Patent No. 6146628
;  GENERAL INFORMATION:
;    APPLICANT:  Uckun, Fatih
;    APPLICANT:  Tumer, Nilgun
;    TITLE OF INVENTION:  Biotherapeutic Agents Comprising
;    TITLE OF INVENTION:  Recombinant PAp and PAP Mutants
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  90 South 7th Street, 3100 No. 6146628west Center
;      CITY:  Minneapolis
;      STATE:  MM
;      COUNTRY:  US
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/501,253A
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M.
;      REGISTRATION NUMBER:  33,924
;      REFERENCE/DOCKET NUMBER:  600.323US01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
US-08-501-253A-1

Alignment Scores:
Pred. No.:             0.529          Length:        1379
Score:                 61.00          Matches:       12
Percent Similarity:    68.0%          Conservative:  5
Best Local Similarity: 48.0%          Mismatches:    6
Query Match:           38.1%          Indels:        2
DB:                    3              Gaps:          1

US-10-758-902-1 (1-30) x US-08-501-253A-1 (1-1379)
```

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 10
PCT-US96-11546-1
; Sequence 1, Application PC/TUS9611546
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  DNAs Encoding Pokeweed Antiviral Protein
;    TITLE OF INVENTION:  Mutants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11546
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,694
;      FILING DATE:  11-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.0-039
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;      TELEX:  139-125
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(233, "a")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(349, "g")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(435, "c")
PCT-US96-11546-1

Alignment Scores:
Pred. No.:          0.529          Length:        1379
Score:              61.00          Matches:       12
Percent Similarity: 68.0%          Conservative:  5
Best Local Similarity: 48.0%       Mismatches:    6
Query Match:        38.1%          Indels:        2
DB:                 6              Gaps:          1

US-10-758-902-1 (1-30) x PCT-US96-11546-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 11
US-09-107-532A-3648
; Sequence 3648, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3648:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 678 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...678
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3648:
US-09-107-532A-3648

Alignment Scores:
Pred. No.:          0.88           Length:        678
Score:              57.50          Matches:       11
Percent Similarity: 62.9%          Conservative:  11
Best Local Similarity: 31.4%       Mismatches:    8
Query Match:        35.9%          Indels:        5
DB:                 3              Gaps:          1

US-10-758-902-1 (1-30) x US-09-107-532A-3648 (1-678)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::      |||   :::|||||||||   |||::::::      |||:::::::|||
Db        112 TTCTCAAAAACTTCTATGGATTTGGGAGAAAGATATGATTTTAAGGGGTTTATGGAAGAT 171
```

```
Qy         21 LeuArgAsnGluLeuAla----------LysGlyThrPro 30
                 :::|||::::::              :::||||||||||
Db        172 AAAATGGACGAGGTATCAAGTAGGGAAATTCCAGAAGGCACACCT 216

RESULT 12
US-07-865-169-2
; Sequence 2, Application US/07865169
; Patent No. 6015940
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    APPLICANT:  Lodge, Jennifer K.
;    APPLICANT:  Kaniewski, Wojciech K.
;    TITLE OF INVENTION:  Virus Resistant Potato Plants
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis R. Hoerner, Jr., Monsanto Co.  BB4F
;      STREET:  700 Chesterfield Parkway No. 6015940th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/865,169
;      FILING DATE:  19920407
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoerner Jr., Dennis R.
;      REGISTRATION NUMBER:  30,914
;      REFERENCE/DOCKET NUMBER:  38-21(10547)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6099
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-865-169-2

Alignment Scores:
Pred. No.:                4.01          Length:          1379
Score:                    56.00         Matches:         12
Percent Similarity:       64.0%         Conservative:    4
Best Local Similarity:    48.0%         Mismatches:      7
Query Match:              35.0%         Indels:          2
DB:                       3             Gaps:            1

US-10-758-902-1 (1-30) x US-07-865-169-2 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCGGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 13
US-09-005-273-3
; Sequence 3, Application US/09005273
; Patent No. 6137030
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
;    TITLE OF INVENTION:  AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ &
;      ADDRESSEE:  MENTILIK
;      STREET:  600 South, Avenue West
;      CITY:  Westfield
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07090
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/005,273
;      FILING DATE:  09-JAN-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,611
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,694
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11546
;      FILING DATE:  11-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REGISTRATION NUMBER:  33,071
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.3-034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  225..290
US-09-005-273-3

Alignment Scores:
Pred. No.:                4.01          Length:          1379
Score:                    56.00         Matches:         12
Percent Similarity:       64.0%         Conservative:    4
Best Local Similarity:    48.0%         Mismatches:      7
Query Match:              35.0%         Indels:          2
DB:                       3             Gaps:            1

US-10-758-902-1 (1-30) x US-09-005-273-3 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCGGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 14
US-09-734-675-3
; Sequence 3, Application US/09734675
; Patent No. 6365391
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
```

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000862
; CURRENT APPLICATION NUMBER: US/09/734,675
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 38844
; TYPE: DNA
; ORGANISM: Human
US-09-734-675-3

Alignment Scores:

Pred. No.:	353	Length:	38844
Score:	55.50	Matches:	10
Percent Similarity:	48.7%	Conservative:	9
Best Local Similarity:	25.6%	Mismatches:	11
Query Match:	34.7%	Indels:	9
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-734-675-3 (1-38844)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr----------------------- 12
              ||||||:::::::   |||:::            |||
Db      38592 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 38651

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                :::::|||   ::::::      :::|||||||||   :::      ||||||
Db      38652 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 38708
```

RESULT 15
US-10-060-333-3
; Sequence 3, Application US/10060333
; Patent No. 6927054
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000862DIV
; CURRENT APPLICATION NUMBER: US/10/060,333
; CURRENT FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 38844
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-060-333-3

Alignment Scores:

Pred. No.:	353	Length:	38844
Score:	55.50	Matches:	10
Percent Similarity:	48.7%	Conservative:	9
Best Local Similarity:	25.6%	Mismatches:	11
Query Match:	34.7%	Indels:	9
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-10-060-333-3 (1-38844)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr----------------------- 12
              ||||||:::::::   |||:::            |||
Db      38592 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 38651

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                :::::|||   ::::::      :::|||||||||   :::      ||||||
Db      38652 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 38708
```

RESULT 16
US-09-949-016-62787/c
; Sequence 62787, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62787
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-62787

Alignment Scores:

Pred. No.:	3.81	Length:	601
Score:	53.50	Matches:	14
Percent Similarity:	46.2%	Conservative:	4
Best Local Similarity:	35.9%	Mismatches:	8
Query Match:	33.4%	Indels:	13
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-949-016-62787 (1-601)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGly------------------------------- 9
              |||       ::::::||||||||||||
Db        425 TATTTCTTTATTACATTTAATCTTGGCAGACCATCTCTGATCTTTGAACTATGAATGAAT 366

Qy         10 ------GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
                    :::          ||||||   ||||||       ||||||||||:::||||||
Db        365 CAGACCAAGTTTCTTCATTATCCTTTTTTCATCTCTTTTCTGCGTAATCAACTAGCT 309
```

RESULT 17
US-09-949-016-62788/c
; Sequence 62788, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62788
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-62788

Alignment Scores:

Pred. No.:	3.81	Length:	601
Score:	53.50	Matches:	14
Percent Similarity:	46.2%	Conservative:	4
Best Local Similarity:	35.9%	Mismatches:	8
Query Match:	33.4%	Indels:	13
DB:	3	Gaps:	1

```
US-10-758-902-1 (1-30) x US-09-949-016-62788 (1-601)

Qy          1 TyrAsnThrValSerPheAsnLeuGly------------------------------- 9
              |||      ::::::||||||||||||
Db        454 TATTTCTTTATTACATTTAATCTTGGCAGACCATCTCTGATCTTTGAACTATGAATGAAT 395

Qy         10 ------GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
                  :::          ||||||   ||||||      |||||||||:::||||||
Db        394 CAGACCAAGTTTCTTCATTATCCTTTTTTCATCTCTTTTCTGCGTAATCAACTAGCT 338

RESULT 18
US-09-949-016-13553
; Sequence 13553, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13553
;   LENGTH: 103792
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(103792)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13553

Alignment Scores:
Pred. No.:              2.79e+03        Length:         103792
Score:                  53.50           Matches:        14
Percent Similarity:     46.2%           Conservative:   4
Best Local Similarity:  35.9%           Mismatches:     8
Query Match:            33.4%           Indels:         13
DB:                     3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-949-016-13553 (1-103792)

Qy          1 TyrAsnThrValSerPheAsnLeuGly------------------------------- 9
              |||      ::::::||||||||||||
Db      12558 TATTTCTTTATTACATTTAATCTTGGCAGACCATCTCTGATCTTTGAACTATGAATGAAT 12617

Qy         10 ------GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
                  :::          ||||||   ||||||      |||||||||:::||||||
Db      12618 CAGACCAAGTTTCTTCATTATCCTTTTTTCATCTCTTTTCTGCGTAATCAACTAGCT 12674

RESULT 19
US-09-949-016-12317
; Sequence 12317, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12317
;   LENGTH: 103993
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(103993)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12317

Alignment Scores:
Pred. No.:              2.8e+03         Length:         103993
Score:                  53.50           Matches:        14
Percent Similarity:     46.2%           Conservative:   4
Best Local Similarity:  35.9%           Mismatches:     8
Query Match:            33.4%           Indels:         13
DB:                     3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-949-016-12317 (1-103993)

Qy          1 TyrAsnThrValSerPheAsnLeuGly------------------------------- 9
              |||      ::::::||||||||||||
Db      12558 TATTTCTTTATTACATTTAATCTTGGCAGACCATCTCTGATCTTTGAACTATGAATGAAT 12617

Qy         10 ------GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
                  :::          ||||||   ||||||      |||||||||:::||||||
Db      12618 CAGACCAAGTTTCTTCATTATCCTTTTTTCATCTCTTTTCTGCGTAATCAACTAGCT 12674

RESULT 20
US-08-324-301-14
; Sequence 14, Application US/08324301
; Patent No. 5597569
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    APPLICANT:  Gawlak, Susan L.
;    APPLICANT:  Marquardt, Hans
;    TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;    TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONICA DIOICA
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,301
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/141,891
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0109A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-728-4800
;      TELEFAX:  206-727-3601
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  962 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
;      TISSUE TYPE:  leaf
US-08-324-301-14

Alignment Scores:
Pred. No.:              8.51          Length:        962
Score:                  53.00         Matches:       10
Percent Similarity:     76.5%         Conservative:  3
Best Local Similarity:  58.8%         Mismatches:    4
Query Match:            33.1%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x US-08-324-301-14 (1-962)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||   |||||||||:::::|||||   :::|||      |||||||||
Db        133 TACAAAACTTTTATAAGGAATCTGCGCACCAAACTCACGGTTGGAACTCCA 183

RESULT 21
US-09-428-034-3
; Sequence 3, Application US/09428034
; Patent No. 6428996
; GENERAL INFORMATION:
;  APPLICANT:  Cheng, Kuo-Joan
;  APPLICANT:  Liu, Jin-Hao
;  APPLICANT:  Tsai, Cheng-Fang
;  APPLICANT:  Hsu, Yih-Chin
;  TITLE OF INVENTION:  CELLULASE ENZYMES
;  FILE REFERENCE:  08919/036001
;  CURRENT APPLICATION NUMBER: US/09/428,034
;  CURRENT FILING DATE:  1999-10-27
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 999
;   TYPE: DNA
;   ORGANISM: Piromyces rhizinflata
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(996)
US-09-428-034-3

Alignment Scores:
Pred. No.:              13.4          Length:        999
Score:                  52.00         Matches:       10
Percent Similarity:     61.5%         Conservative:  6
Best Local Similarity:  38.5%         Mismatches:    10
Query Match:            32.5%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-09-428-034-3 (1-999)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::|||   |||   |||   |||       |||   |||||:::::::::   :::
Db         19 AACTTTTTCTTAAATGAAATTTATGCTAATCCAAAATTCATTGAAGAAGTTGAAGATTCC 78

Qy         25 LeuAlaLysGlyThrPro 30
              :::   |||   ||||||
Db         79 ATTGAAAAATTAACTCCT 96

RESULT 22
US-09-428-034-1
; Sequence 1, Application US/09428034
; Patent No. 6428996
; GENERAL INFORMATION:
;  APPLICANT:  Cheng, Kuo-Joan
;  APPLICANT:  Liu, Jin-Hao
;  APPLICANT:  Tsai, Cheng-Fang
;  APPLICANT:  Hsu, Yih-Chin
;  TITLE OF INVENTION:  CELLULASE ENZYMES
;  FILE REFERENCE:  08919/036001
;  CURRENT APPLICATION NUMBER: US/09/428,034
;  CURRENT FILING DATE:  1999-10-27
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1364
;   TYPE: DNA
;   ORGANISM: Piromyces rhizinflata
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1128)
US-09-428-034-1

Alignment Scores:
Pred. No.:              20            Length:        1364
Score:                  52.00         Matches:       10
Percent Similarity:     61.5%         Conservative:  6
Best Local Similarity:  38.5%         Mismatches:    10
Query Match:            32.5%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-09-428-034-1 (1-1364)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::|||   |||   |||   |||       |||   |||||:::::::::   :::
Db        148 AACTTTTTCTTAAATGAAATTTATGCTAATCCAAAATTCATTGAAGAAGTTGAAGATTCC 207

Qy         25 LeuAlaLysGlyThrPro 30
              :::   |||   ||||||
Db        208 ATTGAAAAATTAACTCCT 225

RESULT 23
US-09-902-540-3259
; Sequence 3259, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3259
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-3259

Alignment Scores:
Pred. No.:              20.3          Length:        1380
Score:                  52.00         Matches:       10
Percent Similarity:     71.4%         Conservative:  5
Best Local Similarity:  47.6%         Mismatches:    6
Query Match:            32.5%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-09-902-540-3259 (1-1380)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              |||   |||   ||||||:::|||       :::::::::|||||||||   |||   :::
Db       1006 CTCTTCGAGGGCTATGAGTGGCCGGGCAACGTGCGCGAGCTGCGCAACGTGCTGGAGCGC 1065

Qy         28 Gly 28
              |||
Db       1066 GGC 1068
```

```
RESULT 24
US-09-902-540-1150
; Sequence 1150, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1150
;   LENGTH: 19954
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-1150

Alignment Scores:
Pred. No.:              620          Length:         19954
Score:                  52.00        Matches:        10
Percent Similarity:     71.4%        Conservative:   5
Best Local Similarity:  47.6%        Mismatches:     6
Query Match:            32.5%        Indels:         0
DB:                     3            Gaps:           0

US-10-758-902-1 (1-30) x US-09-902-540-1150 (1-19954)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              |||   |||   ||||||:::|||      :::::::::|||||||||   |||   :::
Db      12372 CTCTTCGAGGGCTATGAGTGGCCGGGCAACGTGCGCGAGCTGCGCAACGTGCTGGAGCGC 12431

Qy         28 Gly 28
              |||
Db      12432 GGC 12434

RESULT 25
US-09-949-016-15233
; Sequence 15233, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15233
;   LENGTH: 51822
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(51822)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15233

Alignment Scores:
Pred. No.:              2.1e+03      Length:         51822
Score:                  52.00        Matches:        11
Percent Similarity:     70.4%        Conservative:   8
Best Local Similarity:  40.7%        Mismatches:     7
Query Match:            32.5%        Indels:         1
DB:                     3            Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-15233 (1-51822)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGlu-TyrProThrPheIleGlnAspLeuArgAsnGl 24
              |||   |||:::||||||:::   ||| :::|||   |||::::::      ||||||::
Db      19503 TCCAAAAACATGGGTGAAAGTTCAGAATCACCCCCTTTTTGTGAAGACTTTCCGTAATGA 19562

Qy         24 uLeuAlaLysGlyThrPro 30
              :|||   :::   :::|||
Db      19563 TCTTCCCAGAAAGTCCCCC 19581

RESULT 26
US-09-902-540-8868
; Sequence 8868, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8868
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-8868

Alignment Scores:
Pred. No.:              10.7         Length:         717
Score:                  51.50        Matches:        14
Percent Similarity:     56.2%        Conservative:   4
Best Local Similarity:  43.8%        Mismatches:     11
Query Match:            32.2%        Indels:         3
DB:                     3            Gaps:           2

US-10-758-902-1 (1-30) x US-09-902-540-8868 (1-717)

Qy          1 TyrAsnThrVal------SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              |||   |||:::      ||||||      ||||||            ||||||   :::
Db        178 TACAAGACACTCGGCGGCTCATTCACC---GGTGAGCTCGTCGTGGACCCGACTCATCTG 234

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              :::|||:::|||      ||||||   |||   |||
Db        235 CGGGACATGCGCCGTCGGCTCGCGGCTGGAGAGCCA 270

RESULT 27
US-09-902-540-1071
; Sequence 1071, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1071
;   LENGTH: 12028
```

```
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-1071

Alignment Scores:
Pred. No.:              397           Length:        12028
Score:                  51.50         Matches:       14
Percent Similarity:     56.2%         Conservative:  4
Best Local Similarity:  43.8%         Mismatches:    11
Query Match:            32.2%         Indels:        3
DB:                     3             Gaps:          2

US-10-758-902-1 (1-30) x US-09-902-540-1071 (1-12028)

Qy          1 TyrAsnThrVal------SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              |||   |||:::      ||||||      ||||||           ||||||   :::
Db        564 TACAAGACACTCGGCGGCTCATTCACC---GGTGAGCTCGTCGTGGACCCGACTCATCTG 620

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              :::|||:::|||      ||||||   |||   |||
Db        621 CGGGACATGCGCCGTCGGCTCGCGGCTGGAGAGCCA 656

RESULT 28
US-09-134-000C-1566
; Sequence 1566, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1566
;   LENGTH: 3702
;   TYPE: DNA
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-1566

Alignment Scores:
Pred. No.:              107           Length:        3702
Score:                  51.00         Matches:       10
Percent Similarity:     57.7%         Conservative:  5
Best Local Similarity:  38.5%         Mismatches:    11
Query Match:            31.9%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-09-134-000C-1566 (1-3702)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||   |||   |||:::   |||         |||         :::
Db       2710 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2769

Qy         21 LeuArgAsnGluLeuAla 26
                 |||::::::::::
Db       2770 ACATTGAACCAGATGTCT 2787

RESULT 29
US-09-071-035-403
; Sequence 403, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  403:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4249 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-071-035-403

Alignment Scores:
Pred. No.:              128           Length:        4249
Score:                  51.00         Matches:       10
Percent Similarity:     57.7%         Conservative:  5
Best Local Similarity:  38.5%         Mismatches:    11
Query Match:            31.9%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-09-071-035-403 (1-4249)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||   |||   |||:::   |||         |||         :::
Db       2618 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2677

Qy         21 LeuArgAsnGluLeuAla 26
                 |||::::::::::
Db       2678 ACATTGAACCAGATGTCT 2695

RESULT 30
US-10-206-576-403
; Sequence 403, Application US/10206576
; Patent No. 6913907
;   GENERAL INFORMATION:
;        APPLICANT: Choi et al.
;        TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;        NUMBER OF SEQUENCES: 497
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: Dell Latitude
;             OPERATING SYSTEM: Windows 98
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/206,576
;             FILING DATE: 29-Jul-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
```

```
;             APPLICATION NUMBER: US 09/071,035
;             FILING DATE: 1998-05-04
;             APPLICATION NUMBER: US 60/046,655
;             FILING DATE: 1997-05-16
;             APPLICATION NUMBER: US 60/044,031
;             FILING DATE: 1997-05-06
;             APPLICATION NUMBER: US 60/066,009
;             FILING DATE: 1997-11-14
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hyman, Mark J.
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB369P1D1
;   INFORMATION FOR SEQ ID NO: 403:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4249 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 403:
US-10-206-576-403

Alignment Scores:
Pred. No.:              128           Length:        4249
Score:                  51.00         Matches:       10
Percent Similarity:     57.7%         Conservative:  5
Best Local Similarity:  38.5%         Mismatches:    11
Query Match:            31.9%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-10-206-576-403 (1-4249)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||   |||   |||:::   |||         |||          :::
Db       2618 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2677

Qy         21 LeuArgAsnGluLeuAla 26
                |||:::::::::
Db       2678 ACATTGAACCAGATGTCT 2695

RESULT 31
US-09-071-035-401
; Sequence 401, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  401:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4359 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-071-035-401

Alignment Scores:
Pred. No.:              132           Length:        4359
Score:                  51.00         Matches:       10
Percent Similarity:     57.7%         Conservative:  5
Best Local Similarity:  38.5%         Mismatches:    11
Query Match:            31.9%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-09-071-035-401 (1-4359)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||   |||   |||:::   |||         |||          :::
Db       2713 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2772

Qy         21 LeuArgAsnGluLeuAla 26
                |||:::::::::
Db       2773 ACATTGAACCAGATGTCT 2790

RESULT 32
US-10-206-576-401
; Sequence 401, Application US/10206576
; Patent No. 6913907
;  GENERAL INFORMATION:
;       APPLICANT: Choi et al.
;       TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;       NUMBER OF SEQUENCES: 497
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Human Genome Sciences, Inc.
;            STREET: 9410 Key West Avenue
;            CITY: Rockville
;            STATE: Maryland
;            COUNTRY: USA
;            ZIP: 20850
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: Dell Latitude
;            OPERATING SYSTEM: Windows 98
;            SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/206,576
;            FILING DATE: 29-Jul-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 09/071,035
;            FILING DATE: 1998-05-04
;            APPLICATION NUMBER: US 60/046,655
;            FILING DATE: 1997-05-16
;            APPLICATION NUMBER: US 60/044,031
;            FILING DATE: 1997-05-06
;            APPLICATION NUMBER: US 60/066,009
;            FILING DATE: 1997-11-14
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hyman, Mark J.
;            REGISTRATION NUMBER: 46,789
;            REFERENCE/DOCKET NUMBER: PB369P1D1
;   INFORMATION FOR SEQ ID NO: 401:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 4359 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 401:
US-10-206-576-401

Alignment Scores:
```

```
Pred. No.:              132             Length:         4359
Score:                  51.00           Matches:        10
Percent Similarity:     57.7%           Conservative:   5
Best Local Similarity:  38.5%           Mismatches:     11
Query Match:            31.9%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-10-206-576-401 (1-4359)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||   |||   |||:::   |||          |||         :::
Db       2713 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2772

Qy         21 LeuArgAsnGluLeuAla 26
                  |||:::::::::
Db       2773 ACATTGAACCAGATGTCT 2790

RESULT 33
US-09-736-116-60
; Sequence 60, Application US/09736116
; Patent No. 6727085
; GENERAL INFORMATION:
;  APPLICANT: Sejersgard, Tina
;  APPLICANT:  Mikkelsen, Frank
;  TITLE OF INVENTION: Subtilase variants having an improved wash peformance on egg stai
;  FILE REFERENCE: 6108.410
;  CURRENT APPLICATION NUMBER: US/09/736,116
;  CURRENT FILING DATE:  2001-05-24
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 60
;   LENGTH: 13222
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-736-116-60

Alignment Scores:
Pred. No.:              548             Length:         13222
Score:                  51.00           Matches:        12
Percent Similarity:     44.4%           Conservative:   4
Best Local Similarity:  33.3%           Mismatches:     14
Query Match:            31.9%           Indels:         6
DB:                     3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-736-116-60 (1-13222)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||          ||||||||||          :::   |||   ::::::
Db       9100 CATAATAACTATAAATTCAATTTGGGTCATTTACTTCAGGTACCTTATTATCTTTCTCTT 9159

Qy         21 LeuArg-----------------AsnGluLeuAlaLysGlyThrPro 30
                 |||                 |||   |||   ||||||   |||
Db       9160 TTTCGTAAAAGTCCATATCCACAAAACCCTTTGTTAAAGGGCGAACCA 9207

RESULT 34
US-09-306-446C-15
; Sequence 15, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
;  APPLICANT: KIM, Dong Soo
;  APPLICANT:  KIM, Chul Geun
;  APPLICANT:  NAM, Yoon Kwon
;  APPLICANT:  NOH, Jae Koo
;  APPLICANT:  CHO, Kyou Nam
;  TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
;  FILE REFERENCE: P06344US0/BAS
;  CURRENT APPLICATION NUMBER: US/09/306,446C
;  CURRENT FILING DATE:  1999-05-06
;  PRIOR APPLICATION NUMBER: KR 98/20255
;  PRIOR FILING DATE: 1998-06-01
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 670
;   TYPE: DNA
;   ORGANISM: Misgurnus mizolepus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (15)..(644)
US-09-306-446C-15

Alignment Scores:
Pred. No.:              18              Length:         670
Score:                  50.00           Matches:        12
Percent Similarity:     55.2%           Conservative:   4
Best Local Similarity:  41.4%           Mismatches:     11
Query Match:            31.2%           Indels:         2
DB:                     3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-306-446C-15 (1-670)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrPro------ThrPheIleGlnAspLeu 21
              :::||||||   |||   |||:::::::|||||||||      |||         :::
Db        300 ATCTCCTTCCGCCTCATTGAGTCTTGGGAGTATCCCAGCCAGACCCTTAGTGGAACCATC 359

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
                 |||   |||       |||   |||
Db        360 TCAAACAGCCTGACCATCGGCAACCCC 386

RESULT 35
US-09-306-446C-8
; Sequence 8, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
;  APPLICANT: KIM, Dong Soo
;  APPLICANT:  KIM, Chul Geun
;  APPLICANT:  NAM, Yoon Kwon
;  APPLICANT:  NOH, Jae Koo
;  APPLICANT:  CHO, Kyou Nam
;  TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
;  FILE REFERENCE: P06344US0/BAS
;  CURRENT APPLICATION NUMBER: US/09/306,446C
;  CURRENT FILING DATE:  1999-05-06
;  PRIOR APPLICATION NUMBER: KR 98/20255
;  PRIOR FILING DATE: 1998-06-01
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 5108
;   TYPE: DNA
;   ORGANISM: Misgurnus mizolepus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2910)..(2921)
;   NAME/KEY: CDS
;   LOCATION: (3185)..(3322)
;   NAME/KEY: CDS
;   LOCATION: (3485)..(3601)
;   NAME/KEY: CDS
;   LOCATION: (3762)..(3923)
;   NAME/KEY: CDS
;   LOCATION: (4203)..(4403)
US-09-306-446C-8

Alignment Scores:
Pred. No.:              243             Length:         5108
Score:                  50.00           Matches:        12
Percent Similarity:     55.2%           Conservative:   4
Best Local Similarity:  41.4%           Mismatches:     11
Query Match:            31.2%           Indels:         2
DB:                     3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-306-446C-8 (1-5108)
```

```
Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrPro------ThrPheIleGlnAspLeu 21
              :::||||||   |||   |||::::::||||||||||      |||          :::
Db       3780 ATCTCCTTCCGCCTCATTGAGTCTTGGGAGTATCCCAGCCAGACCCTTAGTGGAACCATC 3839

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
                |||   |||       |||   |||
Db       3840 TCAAACAGCCTGACCATCGGCAACCCC 3866

RESULT 36
US-09-949-016-15845
; Sequence 15845, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15845
;   LENGTH: 133559
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(133559)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15845

Alignment Scores:
Pred. No.:                1.59e+04        Length:         133559
Score:                    50.00           Matches:        9
Percent Similarity:       75.0%           Conservative:   6
Best Local Similarity:    45.0%           Mismatches:     5
Query Match:              31.2%           Indels:         0
DB:                       3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-15845 (1-133559)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   :::   |||   |||||||||||||||   :::   |||:::::::::|||
Db     131657 TTTAATTGTTTAGATTTCTGCCTTGGTGAGGCATATCTTCATTAGACTTATCTAAAGGAC 131716

RESULT 37
US-09-602-787A-13
; Sequence 13, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr"ger, Burkhard
;  APPLICANT:  Sch"der, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CP
;  CURRENT APPLICATION NUMBER: US/09/602,787A
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932182.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932190.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932191.4
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932209.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932212.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932227.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932228.7
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932229.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932230.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932927.3
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933005.0
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933006.9
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19940764.9
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940765.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940766.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940830.0
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940831.9
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940832.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940833.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19941378.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941379.7
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941395.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19942077.7
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942078.5
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942079.3
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942088.2
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 13
;   LENGTH: 4953
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(4930)
;   OTHER INFORMATION: RXA02582
```

US-09-602-787A-13

Alignment Scores:

Pred. No.:	286	Length:	4953
Score:	49.50	Matches:	11
Percent Similarity:	65.0%	Conservative:	2
Best Local Similarity:	55.0%	Mismatches:	6
Query Match:	30.9%	Indels:	1
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-602-787A-13 (1-4953)

```
Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||   |||:::   |||         |||   :::|||   |||
Db        311 GCTTATGAGTACCCAACG---ATCCGTAGTTTGGCGCAGCGCCTTGTTGAGGGCGAGCCT 367
```

RESULT 38
US-09-602-787A-55
; Sequence 55, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kr"ger, Burkhard
; APPLICANT: Sch"der, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 55
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(4930)
; OTHER INFORMATION: RXA02582

US-09-602-787A-55

Alignment Scores:

Pred. No.:	286	Length:	4953
Score:	49.50	Matches:	11
Percent Similarity:	65.0%	Conservative:	2
Best Local Similarity:	55.0%	Mismatches:	6
Query Match:	30.9%	Indels:	1
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-602-787A-55 (1-4953)

```
Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||   |||:::   |||         |||   :::|||   |||
Db        311 GCTTATGAGTACCCAACG---ATCCGTAGTTTGGCGCAGCGCCTTGTTGAGGGCGAGCCT 367
```

RESULT 39
US-09-573-080A-22/c
; Sequence 22, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATI
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 6053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region

```
;   LOCATION: (1)..(6053)
;   OTHER INFORMATION: herv18
;  PUBLICATION INFORMATION:
;  PUBLICATION INFORMATION:
;   AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
;   TITLE: Prototypic sequences for human repetitive DNA
;   JOURNAL: Journal of Molecular Evolution
;   VOLUME: 35
;   ISSUE: 4
;   PAGES: 286-291
;   DATE: 1992-10-__
;   DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
;   DATABASE ENTRY DATE: ____-__-__
;   DATABASE ENTRY DATE: 1996-01-26
US-09-573-080A-22

Alignment Scores:
Pred. No.:              370          Length:        6053
Score:                  49.50        Matches:       13
Percent Similarity:     65.5%        Conservative:  6
Best Local Similarity:  44.8%        Mismatches:    9
Query Match:            30.9%        Indels:        2
DB:                     3            Gaps:          1

US-10-758-902-1 (1-30) x US-09-573-080A-22 (1-6053)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::   |||         |||   |||:::   :::|||   |||||||||||||
Db       4357 AACAGTGCCTCCACTGGGGCTGGGCC-GCCTTTCCGTGGCCA---TTCATTCAAGATTTG 4302

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
                :::::::::      |||||||||
Db       4301 GAGCACCAGGTCCAGCCTGGAACTCCA 4275

RESULT 40
US-09-328-352-3637
; Sequence 3637, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3637
;   LENGTH: 6567
;   TYPE: DNA
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-3637

Alignment Scores:
Pred. No.:              411          Length:        6567
Score:                  49.50        Matches:       11
Percent Similarity:     69.6%        Conservative:  5
Best Local Similarity:  47.8%        Mismatches:    6
Query Match:            30.9%        Indels:        1
DB:                     3            Gaps:          1

US-10-758-902-1 (1-30) x US-09-328-352-3637 (1-6567)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   :::   ||||||   |||         ||||||:::::|||   |||:::
Db        370 AGTTTGAATAAACCGTATGAA---CCTGTTTCATACCAAGACATACAAAATGTTTTGTCT 426

Qy         27 LysGlyThr 29
              |||||||||
Db        427 AAAGGTACG 435


Search completed: February 20, 2006, 00:54:14
Job time : 58.5866 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:21:03 ; Search time 225.084 Seconds
(without alignments)
1102.173 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160808_3828/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03p
-USER=US10758902_@CGN_1_1_2064_@runat_17022006_160808_3828 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	100.0	2404	10	US-11-084-080-15	Sequence 15, Appl
2	160	100.0	2404	10	US-11-084-080-19	Sequence 19, Appl
3	160	100.0	2404	10	US-11-084-080-21	Sequence 21, Appl
4	160	100.0	2404	10	US-11-084-080-23	Sequence 23, Appl
5	160	100.0	2431	10	US-11-084-080-27	Sequence 27, Appl
6	111	69.4	65	8	US-10-758-902-5	Sequence 5, Appli
7	72	45.0	363	8	US-10-758-902-8	Sequence 8, Appli
8	61	38.1	1376	8	US-10-467-009-1	Sequence 1, Appli
9	61	38.1	1379	3	US-09-978-274A-30	Sequence 30, Appl
10	61	38.1	1379	10	US-11-106-187-1	Sequence 1, Appli
c 11	60.5	37.8	596	5	US-10-027-632-230755	Sequence 230755,
c 12	60.5	37.8	596	5	US-10-027-632-230756	Sequence 230756,
c 13	60.5	37.8	596	5	US-10-027-632-230757	Sequence 230757,
c 14	60.5	37.8	596	6	US-10-027-632-230755	Sequence 230755,
c 15	60.5	37.8	596	6	US-10-027-632-230756	Sequence 230756,
c 16	60.5	37.8	596	6	US-10-027-632-230757	Sequence 230757,
17	59	36.9	526	7	US-10-424-599-70917	Sequence 70917, A
18	57	35.6	1452	7	US-10-437-963-43964	Sequence 43964, A
19	56	35.0	465	3	US-09-978-274A-5	Sequence 5, Appli
20	56	35.0	655	7	US-10-767-701-6363	Sequence 6363, Ap
21	56	35.0	791	8	US-10-425-115-166418	Sequence 166418,
22	56	35.0	792	3	US-09-978-274A-3	Sequence 3, Appli
23	56	35.0	945	3	US-09-978-274A-1	Sequence 1, Appli
24	56	35.0	945	6	US-10-128-713A-15	Sequence 15, Appl
25	56	35.0	1020	8	US-10-425-115-166417	Sequence 166417,
26	56	35.0	1092	3	US-09-978-274A-19	Sequence 19, Appl
27	56	35.0	1368	3	US-09-978-274A-31	Sequence 31, Appl
28	56	35.0	2197	7	US-10-425-114-31620	Sequence 31620, A
29	56	35.0	2380	8	US-10-425-115-166421	Sequence 166421,
30	55.5	34.7	38844	5	US-10-060-333-3	Sequence 3, Appli
31	55.5	34.7	38844	10	US-11-074-697-3	Sequence 3, Appli
c 32	55	34.4	2139	9	US-10-450-763-18022	Sequence 18022, A
c 33	55	34.4	2558	8	US-10-343-903-34	Sequence 34, Appl
34	54.5	34.1	1142	7	US-10-424-599-131861	Sequence 131861,
c 35	54	33.8	333	8	US-10-425-115-72394	Sequence 72394, A
36	54	33.8	546	4	US-09-925-065A-373047	Sequence 373047,
37	54	33.8	569	4	US-09-925-065A-748607	Sequence 748607,
38	54	33.8	569	4	US-09-925-065A-748608	Sequence 748608,
39	54	33.8	569	4	US-09-925-065A-748609	Sequence 748609,
40	54	33.8	570	4	US-09-925-065A-799267	Sequence 799267,
41	54	33.8	570	4	US-09-925-065A-799268	Sequence 799268,
42	54	33.8	570	4	US-09-925-065A-799269	Sequence 799269,
43	54	33.8	592	4	US-09-925-065A-891048	Sequence 891048,
44	54	33.8	593	4	US-09-925-065A-871708	Sequence 871708,
c 45	54	33.8	651	8	US-10-425-115-74403	Sequence 74403, A
46	54	33.8	1683	7	US-10-424-599-72856	Sequence 72856, A
c 47	53	33.1	903	5	US-10-010-901-14	Sequence 14, Appl
48	53	33.1	5366	10	US-11-097-143-40124	Sequence 40124, A
49	53	33.1	31068	10	US-11-097-143-40123	Sequence 40123, A
50	52.5	32.8	710	7	US-10-424-599-26095	Sequence 26095, A
c 51	52	32.5	593	4	US-09-925-065A-382110	Sequence 382110,
52	52	32.5	1040	5	US-10-198-846-11177	Sequence 11177, A
53	52	32.5	1689	7	US-10-425-114-25526	Sequence 25526, A
54	52	32.5	1692	7	US-10-425-114-17777	Sequence 17777, A
55	52	32.5	2622	8	US-10-425-115-68440	Sequence 68440, A
56	51.5	32.2	258	6	US-10-029-386-16475	Sequence 16475, A
57	51.5	32.2	543	6	US-10-029-386-2775	Sequence 2775, Ap
c 58	51.5	32.2	549	6	US-10-149-930-2	Sequence 2, Appli
c 59	51.5	32.2	1398	3	US-09-893-321-1	Sequence 1, Appli
c 60	51.5	32.2	1446	7	US-10-380-727-48	Sequence 48, Appl
c 61	51.5	32.2	1455	7	US-10-092-900A-7	Sequence 7, Appli
c 62	51.5	32.2	1457	7	US-10-092-900A-3	Sequence 3, Appli
c 63	51.5	32.2	1568	3	US-09-893-321-5	Sequence 5, Appli
c 64	51.5	32.2	1672	9	US-10-482-834A-99	Sequence 99, Appl
c 65	51.5	32.2	1672	9	US-10-482-834A-100	Sequence 100, App
66	51.5	32.2	2355	7	US-10-437-963-34100	Sequence 34100, A
c 67	51.5	32.2	2819	3	US-09-818-657-1	Sequence 1, Appli
c 68	51.5	32.2	2819	10	US-11-136-623-1	Sequence 1, Appli
c 69	51.5	32.2	82938	3	US-09-818-657-3	Sequence 3, Appli
c 70	51.5	32.2	82938	10	US-11-136-623-3	Sequence 3, Appli
71	51	31.9	460	7	US-10-767-701-18898	Sequence 18898, A
72	51	31.9	505	4	US-09-925-065A-826328	Sequence 826328,
73	51	31.9	505	4	US-09-925-065A-826329	Sequence 826329,
74	51	31.9	511	4	US-09-925-065A-852041	Sequence 852041,
75	51	31.9	511	4	US-09-925-065A-852042	Sequence 852042,
c 76	51	31.9	513	4	US-09-925-065A-828656	Sequence 828656,
c 77	51	31.9	513	4	US-09-925-065A-828657	Sequence 828657,
c 78	51	31.9	536	4	US-09-925-065A-272151	Sequence 272151,
79	51	31.9	542	6	US-10-029-386-6386	Sequence 6386, Ap
c 80	51	31.9	628	4	US-09-925-065A-97405	Sequence 97405, A

81	51	31.9	1855	7	US-10-767-701-12730	Sequence 12730, A
c 82	51	31.9	1981	3	US-09-864-761-4745	Sequence 4745, Ap
83	51	31.9	4249	3	US-09-071-035-403	Sequence 403, App
84	51	31.9	4249	5	US-10-206-576-403	Sequence 403, App
85	51	31.9	4249	8	US-10-912-362-403	Sequence 403, App
86	51	31.9	4359	3	US-09-071-035-401	Sequence 401, App
87	51	31.9	4359	5	US-10-206-576-401	Sequence 401, App
88	51	31.9	4359	8	US-10-912-362-401	Sequence 401, App
89	51	31.9	6449	3	US-09-938-842A-69	Sequence 69, Appl
90	51	31.9	6449	3	US-09-938-842A-69	Sequence 69, Appl
91	51	31.9	12445	3	US-09-070-927A-242	Sequence 242, App
92	51	31.9	13222	3	US-09-736-116-60	Sequence 60, Appl
c 93	51	31.9	14785	7	US-10-741-601-5714	Sequence 5714, Ap
c 94	51	31.9	14785	8	US-10-741-600-17819	Sequence 17819, A
c 95	51	31.9	110459	10	US-11-013-314-47	Sequence 47, Appl
c 96	51	31.9	118356	8	US-10-741-600-17643	Sequence 17643, A
97	50.5	31.6	3636	8	US-10-474-792-37	Sequence 37, Appl
98	50.5	31.6	42360	7	US-10-367-094-148	Sequence 148, App
c 99	50	31.2	503	4	US-09-925-065A-454821	Sequence 454821,
100	50	31.2	522	4	US-09-925-065A-449581	Sequence 449581,

ALIGNMENTS

```
RESULT 1
US-11-084-080-15
; Sequence 15, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-15

Alignment Scores:
Pred. No.:                6.66e-18        Length:         2404
Score:                    160.00          Matches:        30
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       10              Gaps:           0

US-10-758-902-1 (1-30) x US-11-084-080-15 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 884

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        885 TTGCGCAATGAATTGGCTAAGGGCACACCA 914
```

```
RESULT 2
US-11-084-080-19
; Sequence 19, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Alignment Scores:
Pred. No.:                6.66e-18        Length:         2404
Score:                    160.00          Matches:        30
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       10              Gaps:           0

US-10-758-902-1 (1-30) x US-11-084-080-19 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1643 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1702

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db       1703 TTGCGCAATGAATTGGCTAAGGGCACACCA 1732
```

```
RESULT 3
US-11-084-080-21
; Sequence 21, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
```

```
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-21

Alignment Scores:
Pred. No.:              6.66e-18        Length:         2404
Score:                  160.00          Matches:        30
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-1 (1-30) x US-11-084-080-21 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 191

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        192 TTGCGCAATGAATTGGCTAAGGGCACACCA 221

RESULT 4
US-11-084-080-23
; Sequence 23, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Alignment Scores:
Pred. No.:              6.66e-18        Length:         2404
Score:                  160.00          Matches:        30
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-1 (1-30) x US-11-084-080-23 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        950 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1009

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db       1010 TTGCGCAATGAATTGGCTAAGGGCACACCA 1039

RESULT 5
US-11-084-080-27
; Sequence 27, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 2431
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-011
US-11-084-080-27

Alignment Scores:
Pred. No.:              6.76e-18        Length:         2431
Score:                  160.00          Matches:        30
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-1 (1-30) x US-11-084-080-27 (1-2431)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 911

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        912 TTGCGCAATGAATTGGCTAAGGGCACACCA 941

RESULT 6
US-10-758-902-5
; Sequence 5, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-5

Alignment Scores:
Pred. No.:              4.23e-11        Length:         65
Score:                  111.00          Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            69.4%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-10-758-902-5 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 7
US-10-758-902-8
; Sequence 8, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)...(361)
US-10-758-902-8

Alignment Scores:
Pred. No.:              0.00505         Length:         363
Score:                  72.00           Matches:        14
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            45.0%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-10-758-902-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 8
US-10-467-009-1
; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
;  APPLICANT: RUTGERS, THE STATE UNIVERSITY
;  TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
;  FILE REFERENCE: OCIRS 3.4-076
;  CURRENT APPLICATION NUMBER: US/10/467,009
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: 60/266,396
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1376
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (225)..(1160)
US-10-467-009-1

Alignment Scores:
Pred. No.:              2.97            Length:         1376
Score:                  61.00           Matches:        12
Percent Similarity:     68.0%           Conservative:   5
Best Local Similarity:  48.0%           Mismatches:     6
Query Match:            38.1%           Indels:         2
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-10-467-009-1 (1-1376)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              |||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 9
US-09-978-274A-30
; Sequence 30, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 1379
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-30

Alignment Scores:
Pred. No.:              2.98            Length:         1379
Score:                  61.00           Matches:        12
Percent Similarity:     68.0%           Conservative:   5
Best Local Similarity:  48.0%           Mismatches:     6
Query Match:            38.1%           Indels:         2
DB:                     3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-978-274A-30 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
```

```
                ||||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 10
US-11-106-187-1
; Sequence 1, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  WANG, PINGER
;  TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
;  FILE REFERENCE: OCIRS 3.9-060 CONT
;  CURRENT APPLICATION NUMBER: US/11/106,187
;  CURRENT FILING DATE:  2005-04-14
;  PRIOR APPLICATION NUMBER: US/09/721,047
;  PRIOR FILING DATE: 2000-11-22
;  PRIOR APPLICATION NUMBER: PCT/US99/11301
;  PRIOR FILING DATE: 1999-05-21
;  PRIOR APPLICATION NUMBER: 60/086,374
;  PRIOR FILING DATE: 1998-05-22
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
;   LENGTH: 1379
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (225)..(1163)
US-11-106-187-1

Alignment Scores:
Pred. No.:              2.98          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     10            Gaps:           1

US-10-758-902-1 (1-30) x US-11-106-187-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 11
US-10-027-632-230755/c
; Sequence 230755, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230755
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230755

Alignment Scores:
Pred. No.:              1.2           Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     5             Gaps:           1

US-10-758-902-1 (1-30) x US-10-027-632-230755 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 12
US-10-027-632-230756/c
; Sequence 230756, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230756
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230756

Alignment Scores:
Pred. No.:              1.2           Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     5             Gaps:           1

US-10-758-902-1 (1-30) x US-10-027-632-230756 (1-596)
```

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                        ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450
```

RESULT 13
US-10-027-632-230757/c
; Sequence 230757, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230757
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-230757

Alignment Scores:

Pred. No.:	1.2	Length:	596
Score:	60.50	Matches:	14
Percent Similarity:	40.9%	Conservative:	4
Best Local Similarity:	31.8%	Mismatches:	7
Query Match:	37.8%	Indels:	19
DB:	5	Gaps:	1

US-10-758-902-1 (1-30) x US-10-027-632-230757 (1-596)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                        ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450
```

RESULT 14
US-10-027-632-230755/c
; Sequence 230755, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230755
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-230755

Alignment Scores:

Pred. No.:	1.2	Length:	596
Score:	60.50	Matches:	14
Percent Similarity:	40.9%	Conservative:	4
Best Local Similarity:	31.8%	Mismatches:	7
Query Match:	37.8%	Indels:	19
DB:	6	Gaps:	1

US-10-758-902-1 (1-30) x US-10-027-632-230755 (1-596)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                        ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450
```

RESULT 15
US-10-027-632-230756/c
; Sequence 230756, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

```
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230756
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230756

Alignment Scores:
Pred. No.:              1.2          Length:        596
Score:                  60.50        Matches:       14
Percent Similarity:     40.9%        Conservative:  4
Best Local Similarity:  31.8%        Mismatches:    7
Query Match:            37.8%        Indels:        19
DB:                     6            Gaps:          1

US-10-758-902-1 (1-30) x US-10-027-632-230756 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                        ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 16
US-10-027-632-230757/c
; Sequence 230757, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230757
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230757

Alignment Scores:
Pred. No.:              1.2          Length:        596
Score:                  60.50        Matches:       14
Percent Similarity:     40.9%        Conservative:  4
Best Local Similarity:  31.8%        Mismatches:    7
Query Match:            37.8%        Indels:        19
DB:                     6            Gaps:          1

US-10-758-902-1 (1-30) x US-10-027-632-230757 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                        ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 17
US-10-424-599-70917
; Sequence 70917, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 70917
;   LENGTH: 526
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_3504C.1
US-10-424-599-70917

Alignment Scores:
Pred. No.:              1.9          Length:        526
Score:                  59.00        Matches:       17
Percent Similarity:     48.7%        Conservative:  2
Best Local Similarity:  43.6%        Mismatches:    8
Query Match:            36.9%        Indels:        12
DB:                     7            Gaps:          2

US-10-758-902-1 (1-30) x US-10-424-599-70917 (1-526)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        311 ACTGTCAACTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 367

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||   |||||||||     |||
Db        368 CAGGCAGAACATGCAGCAGCTGGAGTGGCTCTTAACACTCTTGCAAAAAGAGGTCCC 424

RESULT 18
US-10-437-963-43964
; Sequence 43964, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
```

```
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 43964
;   LENGTH: 1452
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_47070C.1
US-10-437-963-43964

Alignment Scores:
Pred. No.:              17          Length:        1452
Score:                  57.00       Matches:       16
Percent Similarity:     48.7%       Conservative:  3
Best Local Similarity:  41.0%       Mismatches:    8
Query Match:            35.6%       Indels:        12
DB:                     7           Gaps:          2

US-10-758-902-1 (1-30) x US-10-437-963-43964 (1-1452)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        396 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 452

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        453 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 509

RESULT 19
US-09-978-274A-5
; Sequence 5, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 465
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-5

Alignment Scores:
Pred. No.:              5.65        Length:        465
Score:                  56.00       Matches:       11
Percent Similarity:     72.0%       Conservative:  7
Best Local Similarity:  44.0%       Mismatches:    5
Query Match:            35.0%       Indels:        2
DB:                     3           Gaps:          1

US-10-758-902-1 (1-30) x US-09-978-274A-5 (1-465)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||  |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||:::
Db         67 TCTCTTCGTAATCAA 81

RESULT 20
US-10-767-701-6363
; Sequence 6363, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 6363
;   LENGTH: 655
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41259_1
US-10-767-701-6363

Alignment Scores:
Pred. No.:              8.93        Length:        655
Score:                  56.00       Matches:       16
Percent Similarity:     48.7%       Conservative:  3
Best Local Similarity:  41.0%       Mismatches:    8
Query Match:            35.0%       Indels:        12
DB:                     7           Gaps:          2

US-10-758-902-1 (1-30) x US-10-767-701-6363 (1-655)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        530 ACAGTTAATTTCAAT---GGGGAGATGTTCGAGAGCCCCGCGTTTTGTTCTACTTTGCGG 586

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        587 CAGGCGGAGCATGCGGCAGCTGAGGTAGCGCTCAATGAGTTATCGAAGAGGGGCCCT 643

RESULT 21
US-10-425-115-166418
; Sequence 166418, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166418
;   LENGTH: 791
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83354C.1
US-10-425-115-166418

Alignment Scores:
Pred. No.:              11.5        Length:        791
Score:                  56.00       Matches:       16
Percent Similarity:     48.7%       Conservative:  3
Best Local Similarity:  41.0%       Mismatches:    8
Query Match:            35.0%       Indels:        12
DB:                     8           Gaps:          2

US-10-758-902-1 (1-30) x US-10-425-115-166418 (1-791)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        535 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 591

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
```

```
                                                  |||||||||:::|||      |||
Db        592 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 648
```

RESULT 22
US-09-978-274A-3
; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-3

Alignment Scores:

Pred. No.:	11.5	Length:	792
Score:	56.00	Matches:	11
Percent Similarity:	72.0%	Conservative:	7
Best Local Similarity:	44.0%	Mismatches:	5
Query Match:	35.0%	Indels:	2
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-978-274A-3 (1-792)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||        :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                |||||||||:::
Db         67 TCTCTTCGTAATCAA 81
```

RESULT 23
US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-1

Alignment Scores:

Pred. No.:	14.6	Length:	945
Score:	56.00	Matches:	11
Percent Similarity:	72.0%	Conservative:	7
Best Local Similarity:	44.0%	Mismatches:	5
Query Match:	35.0%	Indels:	2
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-978-274A-1 (1-945)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||        :::|||   ||||||::::::
Db         76 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 135

Qy         20 AspLeuArgAsnGlu 24
                |||||||||:::
Db        136 TCTCTTCGTAATCAA 150
```

RESULT 24
US-10-128-713A-15
; Sequence 15, Application US/10128713A
; Publication No. US20030170847A1
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael G
; TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production
; FILE REFERENCE: CL-1788
; CURRENT APPLICATION NUMBER: US/10/128,713A
; CURRENT FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis
US-10-128-713A-15

Alignment Scores:

Pred. No.:	14.6	Length:	945
Score:	56.00	Matches:	10
Percent Similarity:	72.7%	Conservative:	6
Best Local Similarity:	45.5%	Mismatches:	6
Query Match:	35.0%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x US-10-128-713A-15 (1-945)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||:::::      ||||||:::|||:::     :::|||
Db        520 AATCTCGGTGAGGCGTTTCAGCTGACCAACTTCATCCGCGACGTCGGTGAAGACCTCGAC 579

Qy         27 LysGly 28
              :::|||
Db        580 CGGGGA 585
```

RESULT 25
US-10-425-115-166417
; Sequence 166417, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166417
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1020)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_83353C.1

```
US-10-425-115-166417

Alignment Scores:
Pred. No.:              16.1          Length:        1020
Score:                  56.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.0%         Indels:        12
DB:                     8             Gaps:          2

US-10-758-902-1 (1-30) x US-10-425-115-166417 (1-1020)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db        572 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCTACTCTGCGG 628

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||     |||
Db        629 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 685

RESULT 26
US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 1092
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19

Alignment Scores:
Pred. No.:              17.7          Length:        1092
Score:                  56.00         Matches:       11
Percent Similarity:     72.0%         Conservative:  7
Best Local Similarity:  44.0%         Mismatches:    5
Query Match:            35.0%         Indels:        2
DB:                     3             Gaps:          1

US-10-758-902-1 (1-30) x US-09-978-274A-19 (1-1092)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                ||||||||||:::
Db         67 TCTCTTCGTAATCAA 81

RESULT 27
US-09-978-274A-31
; Sequence 31, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 1368
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-31

Alignment Scores:
Pred. No.:              23.9          Length:        1368
Score:                  56.00         Matches:       12
Percent Similarity:     64.0%         Conservative:  4
Best Local Similarity:  48.0%         Mismatches:    7
Query Match:            35.0%         Indels:        2
DB:                     3             Gaps:          1

US-10-758-902-1 (1-30) x US-09-978-274A-31 (1-1368)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCGGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 28
US-10-425-114-31620
; Sequence 31620, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31620
;   LENGTH: 2197
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLB73196E06_FLI
US-10-425-114-31620

Alignment Scores:
Pred. No.:              44.9          Length:        2197
Score:                  56.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.0%         Indels:        12
DB:                     7             Gaps:          2

US-10-758-902-1 (1-30) x US-10-425-114-31620 (1-2197)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db        464 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 520

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||     |||
Db        521 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 577
```

```
RESULT 29
US-10-425-115-166421
; Sequence 166421, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166421
;   LENGTH: 2380
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83357C.1
US-10-425-115-166421

Alignment Scores:
Pred. No.:              50          Length:         2380
Score:                  56.00       Matches:        16
Percent Similarity:     48.7%       Conservative:   3
Best Local Similarity:  41.0%       Mismatches:     8
Query Match:            35.0%       Indels:         12
DB:                     8           Gaps:           2

US-10-758-902-1 (1-30) x US-10-425-115-166421 (1-2380)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||        ||||||
Db        580 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 636

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        637 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 693

RESULT 30
US-10-060-333-3
; Sequence 3, Application US/10060333
; Publication No. US20020115186A1
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL000862DIV
;  CURRENT APPLICATION NUMBER: US/10/060,333
;  CURRENT FILING DATE:  2002-08-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 38844
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-060-333-3

Alignment Scores:
Pred. No.:              2.56e+03    Length:         38844
Score:                  55.50       Matches:        10
Percent Similarity:     48.7%       Conservative:   9
Best Local Similarity:  25.6%       Mismatches:     11
Query Match:            34.7%       Indels:         9
DB:                     5           Gaps:           1

US-10-758-902-1 (1-30) x US-10-060-333-3 (1-38844)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr---------------------- 12
              ||||||::::::   |||:::            |||
Db      38592 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 38651

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::||||||||||   :::      ||||||
Db      38652 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 38708

RESULT 31
US-11-074-697-3
; Sequence 3, Application US/11074697
; Publication No. US20050181414A1
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL000862DIV
;  CURRENT APPLICATION NUMBER: US/11/074,697
;  CURRENT FILING DATE:  2005-03-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 38844
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-074-697-3

Alignment Scores:
Pred. No.:              2.56e+03    Length:         38844
Score:                  55.50       Matches:        10
Percent Similarity:     48.7%       Conservative:   9
Best Local Similarity:  25.6%       Mismatches:     11
Query Match:            34.7%       Indels:         9
DB:                     10          Gaps:           1

US-10-758-902-1 (1-30) x US-11-074-697-3 (1-38844)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr---------------------- 12
              ||||||::::::   |||:::            |||
Db      38592 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 38651

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::||||||||||   :::      ||||||
Db      38652 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 38708

RESULT 32
US-10-450-763-18022/c
; Sequence 18022, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 790CIP3/US
;  CURRENT APPLICATION NUMBER: US/10/450,763
;  CURRENT FILING DATE:  2003-06-11
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 18022
;   LENGTH: 2139
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (562)..(1398)
;   OTHER INFORMATION: 98% homologous to Homo sapiens mono ATP-binding cassette
;   OTHER INFORMATION: protein,accession number AB013380,Smith-Waterman Score=1341.
US-10-450-763-18022
```

Alignment Scores:
Pred. No.: 65.8 Length: 2139
Score: 55.00 Matches: 8
Percent Similarity: 70.8% Conservative: 9
Best Local Similarity: 33.3% Mismatches: 7
Query Match: 34.4% Indels: 0
DB: 9 Gaps: 0

US-10-758-902-1 (1-30) x US-10-450-763-18022 (1-2139)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ::::::|||   |||::::::   |||:::|||:::||||||   :::::::::
Db       1335 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 1276

Qy         27 LysGlyThrPro 30
                ||| |||
Db       1275 TCCGGAGAGCCC 1264
```

RESULT 33
US-10-343-903-34/c
; Sequence 34, Application US/10343903
; Publication No. US20040224911A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry;
; APPLICANT: THORNTON, Michael; RAMKUMAR, Jayalaxmi;
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; YANG, Junming;
; APPLICANT: YAO, Monique G.; LAL, Preeti G.;
; APPLICANT: CHAWLA, Narinder K.; GANDHI, Ameena R.;
; APPLICANT: HAFALIA, April J.A.; NGUYEN, Danniel B.;
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: TRIBOULEY, Catherine M.; LU, Dyung Aina M.;
; APPLICANT: XU, Yuming; REDDY, Roopa;
; APPLICANT: HERNANDEZ, Roberto; BOROWSKY, Mark L.;
; APPLICANT: LO, Terence P.; LU, Yan;
; APPLICANT: POLICKY, Jennifer L.; GREENE, Barrie D.;
; APPLICANT: SANJANWALA, Madhusudan M.; RAUMANN, Brigette E.;
; APPLICANT: BURFORD, Neil; ISON, Craig H.;
; APPLICANT: LEE, Ernestine A.; DING, Li;
; APPLICANT: DAS, Debopriya; KALLICK, Deborah A.;
; APPLICANT: KHAN, Farrah A.; SEILHAMER, Jeffrey J.;
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0183 USN
; CURRENT APPLICATION NUMBER: US/10/343,903
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: PCT/US01/24217
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/231,434
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/230,067
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/228,140
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/226,410
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/224,456
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/223,269
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 2558
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 3105257CB1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2523
; OTHER INFORMATION: a, t, c, g, or other

US-10-343-903-34

Alignment Scores:
Pred. No.: 83.6 Length: 2558
Score: 55.00 Matches: 8
Percent Similarity: 70.8% Conservative: 9
Best Local Similarity: 33.3% Mismatches: 7
Query Match: 34.4% Indels: 0
DB: 8 Gaps: 0

US-10-758-902-1 (1-30) x US-10-343-903-34 (1-2558)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ::::::|||   |||::::::   |||:::|||:::||||||   :::::::::
Db       1041 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 982

Qy         27 LysGlyThrPro 30
                ||| |||
Db        981 TCCGGAGAGCCC 970
```

RESULT 34
US-10-424-599-131861
; Sequence 131861, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 131861
; LENGTH: 1142
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90078C.1
US-10-424-599-131861

Alignment Scores:
Pred. No.: 35.1 Length: 1142
Score: 54.50 Matches: 12
Percent Similarity: 58.1% Conservative: 6
Best Local Similarity: 38.7% Mismatches: 12
Query Match: 34.1% Indels: 1
DB: 7 Gaps: 1

US-10-758-902-1 (1-30) x US-10-424-599-131861 (1-1142)

```
Qy          1 TyrAsnThrValSerPheAsnLeu---GlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||       :::   ||||||      ||||||   ::::::||||||   |||
Db        328 TACACCTTTCTTGAATTCAACACGCAGGGCGAGGATTTCGACTACCCCGAGTTCCGCGAC 387

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                :::|||:::   :::|||      ||||||
Db        388 CCGATTAGGTCGCCGGTTGCCTGGCCCACGCCG 420
```

RESULT 35
US-10-425-115-72394/c
; Sequence 72394, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B

```
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 72394
;   LENGTH: 333
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_166022C.1
US-10-425-115-72394

Alignment Scores:
Pred. No.:              8.35          Length:         333
Score:                  54.00         Matches:        11
Percent Similarity:     59.3%         Conservative:   5
Best Local Similarity:  40.7%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-1 (1-30) x US-10-425-115-72394 (1-333)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              :::|||      :::   :::||||||   |||      ||||||      :::||||||
Db        100 TTGTCTTGACGTGTCGCTCAGGCCTACAATTATTAAAATTTTATTGCATCAATCAGAAAT 41

Qy         24 GluLeuAlaLysGlyThrPro 30
              :::      ||||||   |||
Db         40 AAAAAAAAGAAAGGGCATCCG 20

RESULT 36
US-09-925-065A-373047
; Sequence 373047, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 373047
;   LENGTH: 546
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(546)
;   OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-373047

Alignment Scores:
Pred. No.:              16.2          Length:         546
Score:                  54.00         Matches:        10
Percent Similarity:     70.6%         Conservative:   2
Best Local Similarity:  58.8%         Mismatches:     5
Query Match:            33.8%         Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-373047 (1-546)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
                ||||||||||||          |||   ||||||   ||||||:::|||:::
Db        111 TCATTTAATCTTCACAACAACTATAACTATCCCCATTTTATAGAGGATGTA 161

RESULT 37
US-09-925-065A-748607
; Sequence 748607, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748607
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748607

Alignment Scores:
Pred. No.:              17.1          Length:         569
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-748607 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||      |||:::      |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 38
US-09-925-065A-748608
; Sequence 748608, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 748608
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748608

Alignment Scores:
Pred. No.:              17.1          Length:         569
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-748608 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 39
US-09-925-065A-748609
; Sequence 748609, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748609
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748609

Alignment Scores:
Pred. No.:              17.1          Length:         569
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-748609 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 40
US-09-925-065A-799267
; Sequence 799267, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799267
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799267

Alignment Scores:
Pred. No.:              17.1          Length:         570
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-799267 (1-570)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         63 TTGAGAAATAAATTGGCAAAG 83


Search completed: February 20, 2006, 02:30:14
Job time : 234.084 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:49:47 ; Search time 89.3296 Seconds
(without alignments)
712.890 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160811_3886/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss08
-USER=US10758902_@CGN_1_1_380_@runat_17022006_160811_3886 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	61	38.1	1360	12	US-11-010-795-19	Sequence 19, Appl
c	2	55	34.4	2776	8	US-10-750-185-24916	Sequence 24916, A
c	3	55	34.4	2776	8	US-10-750-623-24916	Sequence 24916, A
	4	54	33.8	546	6	US-09-925-065A-373047	Sequence 373047,
	5	54	33.8	569	6	US-09-925-065A-748607	Sequence 748607,
	6	54	33.8	569	6	US-09-925-065A-748608	Sequence 748608,
	7	54	33.8	569	6	US-09-925-065A-748609	Sequence 748609,
	8	54	33.8	570	6	US-09-925-065A-799267	Sequence 799267,
	9	54	33.8	570	6	US-09-925-065A-799268	Sequence 799268,
	10	54	33.8	570	6	US-09-925-065A-799269	Sequence 799269,
	11	54	33.8	592	6	US-09-925-065A-891048	Sequence 891048,
	12	54	33.8	593	6	US-09-925-065A-871708	Sequence 871708,
c	13	52	32.5	593	6	US-09-925-065A-382110	Sequence 382110,
	14	51.5	32.2	109974	12	US-11-117-187-204	Sequence 204, App
	15	51	31.9	505	6	US-09-925-065A-826328	Sequence 826328,
	16	51	31.9	505	6	US-09-925-065A-826329	Sequence 826329,
	17	51	31.9	511	6	US-09-925-065A-852041	Sequence 852041,
	18	51	31.9	511	6	US-09-925-065A-852042	Sequence 852042,
c	19	51	31.9	513	6	US-09-925-065A-828656	Sequence 828656,
c	20	51	31.9	513	6	US-09-925-065A-828657	Sequence 828657,
c	21	51	31.9	536	6	US-09-925-065A-272151	Sequence 272151,
c	22	51	31.9	628	6	US-09-925-065A-97405	Sequence 97405, A
c	23	51	31.9	159146	12	US-11-121-086-49	Sequence 49, Appl
c	24	51	31.9	203467	12	US-11-121-086-50	Sequence 50, Appl
	25	50.5	31.6	4606	8	US-10-750-185-50060	Sequence 50060, A
	26	50.5	31.6	4606	8	US-10-750-623-50060	Sequence 50060, A
c	27	50	31.2	503	6	US-09-925-065A-454821	Sequence 454821,
	28	50	31.2	522	6	US-09-925-065A-449581	Sequence 449581,
	29	50	31.2	538	6	US-09-925-065A-318790	Sequence 318790,
	30	50	31.2	581	6	US-09-925-065A-261114	Sequence 261114,
	31	50	31.2	581	6	US-09-925-065A-261115	Sequence 261115,
c	32	50	31.2	604	6	US-09-925-065A-886124	Sequence 886124,
c	33	50	31.2	623	6	US-09-925-065A-533904	Sequence 533904,
	34	50	31.2	649	6	US-09-925-065A-705318	Sequence 705318,
c	35	49.5	30.9	578	6	US-09-925-065A-392827	Sequence 392827,
c	36	49.5	30.9	578	6	US-09-925-065A-392828	Sequence 392828,
	37	49	30.6	558	6	US-09-925-065A-252059	Sequence 252059,
	38	49	30.6	558	6	US-09-925-065A-252060	Sequence 252060,
c	39	49	30.6	2468	6	US-09-925-065A-702979	Sequence 702979,
	40	48.5	30.3	559	6	US-09-925-065A-289057	Sequence 289057,
c	41	48.5	30.3	718	6	US-09-925-065A-940929	Sequence 940929,
c	42	48.5	30.3	718	6	US-09-925-065A-940930	Sequence 940930,
	43	48.5	30.3	832	6	US-09-925-065A-924252	Sequence 924252,
c	44	48.5	30.3	127917	8	US-10-775-169-82	Sequence 82, Appl
c	45	48	30.0	388	6	US-09-925-065A-247522	Sequence 247522,
	46	48	30.0	405	12	US-11-108-172-194	Sequence 194, App
	47	48	30.0	421	12	US-11-108-172-624	Sequence 624, App
c	48	48	30.0	516	6	US-09-925-065A-383973	Sequence 383973,
c	49	48	30.0	516	6	US-09-925-065A-383974	Sequence 383974,
	50	48	30.0	533	6	US-09-925-065A-593647	Sequence 593647,
	51	48	30.0	575	6	US-09-925-065A-436594	Sequence 436594,
	52	48	30.0	575	6	US-09-925-065A-436595	Sequence 436595,
	53	48	30.0	575	6	US-09-925-065A-436596	Sequence 436596,
	54	48	30.0	577	6	US-09-925-065A-416541	Sequence 416541,
	55	48	30.0	610	6	US-09-925-065A-215370	Sequence 215370,
	56	48	30.0	629	6	US-09-925-065A-909199	Sequence 909199,
	57	48	30.0	319608	12	US-11-145-703-1	Sequence 1, Appli
	58	47.5	29.7	201	8	US-10-995-561-62740	Sequence 62740, A
c	59	47.5	29.7	201	8	US-10-995-561-82660	Sequence 82660, A
c	60	47.5	29.7	586	6	US-09-925-065A-101302	Sequence 101302,
c	61	47.5	29.7	586	6	US-09-925-065A-101303	Sequence 101303,
c	62	47.5	29.7	628	6	US-09-925-065A-635382	Sequence 635382,
c	63	47.5	29.7	1016	8	US-10-750-185-26648	Sequence 26648, A
c	64	47.5	29.7	1016	8	US-10-750-623-26648	Sequence 26648, A
	65	47.5	29.7	15056	9	US-11-166-234-14	Sequence 14, Appl
	66	47.5	29.7	15056	12	US-11-153-458-10	Sequence 10, Appl
c	67	47.5	29.7	27240	8	US-10-995-561-13499	Sequence 13499, A
	68	47.5	29.7	52520	8	US-10-995-561-13360	Sequence 13360, A
	69	47	29.4	375	6	US-09-925-065A-338743	Sequence 338743,
	70	47	29.4	375	6	US-09-925-065A-338744	Sequence 338744,
	71	47	29.4	375	6	US-09-925-065A-338745	Sequence 338745,
	72	47	29.4	414	6	US-09-925-065A-428155	Sequence 428155,
c	73	47	29.4	557	6	US-09-925-065A-462150	Sequence 462150,
	74	47	29.4	563	6	US-09-925-065A-843025	Sequence 843025,
	75	47	29.4	563	6	US-09-925-065A-843026	Sequence 843026,
	76	47	29.4	563	6	US-09-925-065A-843027	Sequence 843027,
	77	47	29.4	563	6	US-09-925-065A-843028	Sequence 843028,

	78	47	29.4	581	6	US-09-925-065A-22641 Sequence 22641, A
c	79	47	29.4	583	6	US-09-925-065A-493151 Sequence 493151,
c	80	47	29.4	584	6	US-09-925-065A-636762 Sequence 636762,
	81	47	29.4	628	6	US-09-925-065A-741720 Sequence 741720,
	82	47	29.4	631	6	US-09-925-065A-745180 Sequence 745180,
	83	47	29.4	658	6	US-09-925-065A-75177 Sequence 75177, A
c	84	47	29.4	663	6	US-09-925-065A-630276 Sequence 630276,
c	85	47	29.4	691	6	US-09-925-065A-14239 Sequence 14239, A
c	86	47	29.4	691	6	US-09-925-065A-14240 Sequence 14240, A
c	87	47	29.4	1089	6	US-09-925-065A-10989 Sequence 10989, A
c	88	47	29.4	1089	6	US-09-925-065A-10990 Sequence 10990, A
c	89	47	29.4	1089	6	US-09-925-065A-10991 Sequence 10991, A
c	90	47	29.4	1089	6	US-09-925-065A-10992 Sequence 10992, A
c	91	47	29.4	1089	6	US-09-925-065A-10993 Sequence 10993, A
	92	47	29.4	1114	8	US-10-750-185-37163 Sequence 37163, A
	93	47	29.4	1114	8	US-10-750-623-37163 Sequence 37163, A
	94	47	29.4	12233	12	US-11-124-367A-5008 Sequence 5008, Ap
c	95	47	29.4	30258	8	US-10-995-561-13228 Sequence 13228, A
	96	46.5	29.1	548	6	US-09-925-065A-16828 Sequence 16828, A
	97	46.5	29.1	588	6	US-09-925-065A-510784 Sequence 510784,
	98	46.5	29.1	631	6	US-09-925-065A-729828 Sequence 729828,
	99	46.5	29.1	647	6	US-09-925-065A-388051 Sequence 388051,
	100	46.5	29.1	669	8	US-10-793-626-127 Sequence 127, App

ALIGNMENTS

```
RESULT 1
US-11-010-795-19
; Sequence 19, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  DI, RONG
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
;  TITLE OF INVENTION:  RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
;  FILE REFERENCE: OCIRS 3.0-085
;  CURRENT APPLICATION NUMBER: US/11/010,795
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: 60/529,348
;  PRIOR FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
;   LENGTH: 1360
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (207)..(1145)
US-11-010-795-19

Alignment Scores:
Pred. No.:              3.07          Length:        1360
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     12            Gaps:          1

US-10-758-902-1 (1-30) x US-11-010-795-19 (1-1360)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        276 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 335

Qy         20 AspLeuArgAsnGlu 24
              |||||||||||||||
Db        336 GATCTTCGTAATGAA 350

RESULT 2
US-10-750-185-24916/c
; Sequence 24916, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 24916
;   LENGTH: 2776
;   TYPE: DNA
;   ORGANISM: Bovine  19866881045177
US-10-750-185-24916

Alignment Scores:
Pred. No.:              81.4          Length:        2776
Score:                  55.00         Matches:       11
Percent Similarity:     59.1%         Conservative:  2
Best Local Similarity:  50.0%         Mismatches:    9
Query Match:            34.4%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x US-10-750-185-24916 (1-2776)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::     |||||||||          |||:::|||      |||   |||
Db        692 GGGTCAGCCCACTCCATGCCCACCTTCTTTGCCCGGCTCCAGAATGCAAGTGCCATGGGC 633

Qy         29 ThrPro 30
              ||||||
Db        632 ACGCCC 627

RESULT 3
US-10-750-623-24916/c
; Sequence 24916, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 24916
;   LENGTH: 2776
;   TYPE: DNA
;   ORGANISM: Bovine  19866881045177
US-10-750-623-24916

Alignment Scores:
Pred. No.:              81.4          Length:        2776
Score:                  55.00         Matches:       11
Percent Similarity:     59.1%         Conservative:  2
Best Local Similarity:  50.0%         Mismatches:    9
Query Match:            34.4%         Indels:        0
```

```
DB:                    8             Gaps:          0

US-10-758-902-1 (1-30) x US-10-750-623-24916 (1-2776)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::     |||||||||         |||:::|||      |||   |||
Db        692 GGGTCAGCCCACTCCATGCCCACCTTCTTTGCCCGGCTCCAGAATGCAAGTGCCATGGGC 633

Qy         29 ThrPro 30
              ||||||
Db        632 ACGCCC 627

RESULT 4
US-09-925-065A-373047
; Sequence 373047, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 373047
;   LENGTH: 546
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(546)
;   OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-373047

Alignment Scores:
Pred. No.:              16.6          Length:        546
Score:                  54.00         Matches:       10
Percent Similarity:     70.6%         Conservative:  2
Best Local Similarity:  58.8%         Mismatches:    5
Query Match:            33.8%         Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-373047 (1-546)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||||||||         |||   ||||||   ||||||:::|||:::
Db        111 TCATTTAATCTTCACAACAACTATAACTATCCCCATTTTATAGAGGATGTA 161

RESULT 5
US-09-925-065A-748607
; Sequence 748607, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748607
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748607

Alignment Scores:
Pred. No.:              17.4          Length:        569
Score:                  54.00         Matches:       13
Percent Similarity:     59.3%         Conservative:  3
Best Local Similarity:  48.1%         Mismatches:    11
Query Match:            33.8%         Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-748607 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::      |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 6
US-09-925-065A-748608
; Sequence 748608, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748608
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748608

Alignment Scores:
Pred. No.:              17.4          Length:        569
Score:                  54.00         Matches:       13
Percent Similarity:     59.3%         Conservative:  3
Best Local Similarity:  48.1%         Mismatches:    11
Query Match:            33.8%         Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-748608 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
```

```
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 7
US-09-925-065A-748609
; Sequence 748609, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748609
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748609

Alignment Scores:
Pred. No.:              17.4          Length:         569
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-748609 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 8
US-09-925-065A-799267
; Sequence 799267, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799267
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799267

Alignment Scores:
Pred. No.:              17.5          Length:         570
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-799267 (1-570)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         63 TTGAGAAATAAATTGGCAAAG 83

RESULT 9
US-09-925-065A-799268
; Sequence 799268, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799268
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799268

Alignment Scores:
Pred. No.:              17.5          Length:         570
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-799268 (1-570)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
```

```
Db         63 TTGAGAAATAAATTGGCAAAG 83

RESULT 10
US-09-925-065A-799269
; Sequence 799269, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799269
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799269

Alignment Scores:
Pred. No.:              17.5          Length:         570
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-799269 (1-570)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         63 TTGAGAAATAAATTGGCAAAG 83

RESULT 11
US-09-925-065A-891048
; Sequence 891048, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 891048
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-891048

Alignment Scores:
Pred. No.:              18.3          Length:         592
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-891048 (1-592)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db        162 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 221

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db        222 TTGAGAAATAAATTGGCAAAG 242

RESULT 12
US-09-925-065A-871708
; Sequence 871708, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 871708
;   LENGTH: 593
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-871708

Alignment Scores:
Pred. No.:              18.3          Length:         593
Score:                  54.00         Matches:        13
Percent Similarity:     59.3%         Conservative:   3
Best Local Similarity:  48.1%         Mismatches:     11
Query Match:            33.8%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-871708 (1-593)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db        162 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 221

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db        222 TTGAGAAATAAATTGGCAAAG 242

RESULT 13
US-09-925-065A-382110/c
; Sequence 382110, Application US/09925065A
```

```
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 382110
;   LENGTH: 593
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-382110

Alignment Scores:
Pred. No.:              40.8          Length:         593
Score:                  52.00         Matches:        11
Percent Similarity:     57.7%         Conservative:   4
Best Local Similarity:  42.3%         Mismatches:     11
Query Match:            32.5%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-382110 (1-593)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||:  |||:::|||   |||||||||   |||            ||||||
Db        445 TTTAATATGGTCAATTTCATGCTAGGTGAATTATATACCAATAAGCCTTTCATTACAAAA 386

Qy         21 LeuArgAsnGluLeuAla 26
                 :::   |||:::|||
Db        385 AGTAAAAAGGAAATAGCT 368

RESULT 14
US-11-117-187-204
; Sequence 204, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
;  APPLICANT: PREUSS, DAPHNE
;  APPLICANT:  COPENHAVER, GREGORY
;  TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
;  FILE REFERENCE: ARCD:309US
;  CURRENT APPLICATION NUMBER: US/11/117,187
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: US/09/531,120
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,219
;  PRIOR FILING DATE: 1999-03-18
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 204
;   LENGTH: 109974
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-11-117-187-204

Alignment Scores:
Pred. No.:              3e+04         Length:         109974
Score:                  51.50         Matches:        10
Percent Similarity:     69.6%         Conservative:   6
Best Local Similarity:  43.5%         Mismatches:     4
Query Match:            32.2%         Indels:         3
DB:                     12            Gaps:           1

US-10-758-902-1 (1-30) x US-11-117-187-204 (1-109974)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAsp---------LeuArgAsnGluLeuAlaLys 27
              |||   :::|||||||||||||   ::::::         |||||:::   ::::::
Db      23327 GCCGAGAAGTATCCTACCTTCTTTGAAGAACTCCTCACACTGAGAAGTTCAATCAGTTCG 23386

Qy         28 GlyThrPro 30
              |||||||||
Db      23387 GGAACCCCG 23395

RESULT 15
US-09-925-065A-826328
; Sequence 826328, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 826328
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-826328

Alignment Scores:
Pred. No.:              50.1          Length:         505
Score:                  51.00         Matches:        10
Percent Similarity:     66.7%         Conservative:   6
Best Local Similarity:  41.7%         Mismatches:     8
Query Match:            31.9%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-826328 (1-505)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::   :::|||            :::   :::||||||||||||
Db        228 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 287

Qy         27 LysGlyThrPro 30
              :::||||||||||
Db        288 AGAGGGACACCA 299

RESULT 16
US-09-925-065A-826329
; Sequence 826329, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
```

```
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 826329
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-826329

Alignment Scores:
Pred. No.:                50.1          Length:          505
Score:                    51.00         Matches:         10
Percent Similarity:       66.7%         Conservative:    6
Best Local Similarity:    41.7%         Mismatches:      8
Query Match:              31.9%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-826329 (1-505)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::   :::|||           :::   :::||||||||||||
Db        228 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 287

Qy         27 LysGlyThrPro 30
              :::||||||||||
Db        288 AGAGGGACACCA 299

RESULT 17
US-09-925-065A-852041
; Sequence 852041, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 852041
;   LENGTH: 511
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-852041

Alignment Scores:
Pred. No.:                50.8          Length:          511
Score:                    51.00         Matches:         10
Percent Similarity:       66.7%         Conservative:    6
Best Local Similarity:    41.7%         Mismatches:      8
Query Match:              31.9%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-852041 (1-511)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::   :::|||           :::   :::||||||||||||
Db        228 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 287

Qy         27 LysGlyThrPro 30
              :::||||||||||
Db        288 AGAGGGACACCA 299

RESULT 18
US-09-925-065A-852042
; Sequence 852042, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 852042
;   LENGTH: 511
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-852042

Alignment Scores:
Pred. No.:                50.8          Length:          511
Score:                    51.00         Matches:         10
Percent Similarity:       66.7%         Conservative:    6
Best Local Similarity:    41.7%         Mismatches:      8
Query Match:              31.9%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-852042 (1-511)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::   :::|||           :::   :::||||||||||||
Db        228 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 287

Qy         27 LysGlyThrPro 30
              :::||||||||||
Db        288 AGAGGGACACCA 299

RESULT 19
US-09-925-065A-828656/c
; Sequence 828656, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
```

```
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 828656
;    LENGTH: 513
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-925-065A-828656

Alignment Scores:
Pred. No.:              51              Length:         513
Score:                  51.00           Matches:        10
Percent Similarity:     66.7%           Conservative:   6
Best Local Similarity:  41.7%           Mismatches:     8
Query Match:            31.9%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-828656 (1-513)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::   :::|||           :::   :::||||||||||||
Db        286 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 227

Qy         27 LysGlyThrPro 30
              :::||||||||||
Db        226 AGAGGGACACCA 215

RESULT 20
US-09-925-065A-828657/c
; Sequence 828657, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 828657
;    LENGTH: 513
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-925-065A-828657

Alignment Scores:
Pred. No.:              51              Length:         513
Score:                  51.00           Matches:        10
Percent Similarity:     66.7%           Conservative:   6
Best Local Similarity:  41.7%           Mismatches:     8
Query Match:            31.9%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-828657 (1-513)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::   :::|||           :::   :::||||||||||||
Db        286 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 227

Qy         27 LysGlyThrPro 30
              :::||||||||||
Db        226 AGAGGGACACCA 215

RESULT 21
US-09-925-065A-272151/c
; Sequence 272151, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272151
;    LENGTH: 536
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-925-065A-272151

Alignment Scores:
Pred. No.:              53.9            Length:         536
Score:                  51.00           Matches:        9
Percent Similarity:     73.3%           Conservative:   2
Best Local Similarity:  60.0%           Mismatches:     4
Query Match:            31.9%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-272151 (1-536)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              ::::::   ||||||   ||||||||||||   ||||||   |||
Db        517 TCTTTTCCCTATCCATTGTTTATCCAGGATTGTAGAAACTCCCTA 473

RESULT 22
US-09-925-065A-97405/c
; Sequence 97405, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97405
;    LENGTH: 628
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-925-065A-97405
```

```
Alignment Scores:
Pred. No.:              65.4          Length:         628
Score:                  51.00         Matches:        10
Percent Similarity:     57.7%         Conservative:   5
Best Local Similarity:  38.5%         Mismatches:     11
Query Match:            31.9%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-97405 (1-628)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              |||   |||   |||       |||   ::::::||||||   |||:::|||
Db        355 ACGTGTTCAATCAATTCAAGAGAAAATTTCAAATATCCAGTGTTTTTGCAGAAATGTTTA 296

Qy         23 AsnGluLeuAlaLysGly 28
              |||   :::   :::|||
Db        295 AATTTCATGTTAGAGGGT 278

RESULT 23
US-11-121-086-49/c
; Sequence 49, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
;  APPLICANT: POULSEN, TIM S.
;  APPLICANT:  NIELSEN, KIRSTEN V.
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
;  FILE REFERENCE: 09138.6000-00000
;  CURRENT APPLICATION NUMBER: US/11/121,086
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,570
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
;   LENGTH: 159146
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-121-086-49

Alignment Scores:
Pred. No.:              5.76e+04      Length:         159146
Score:                  51.00         Matches:        11
Percent Similarity:     60.9%         Conservative:   3
Best Local Similarity:  47.8%         Mismatches:     9
Query Match:            31.9%         Indels:         0
DB:                     12            Gaps:           0

US-10-758-902-1 (1-30) x US-11-121-086-49 (1-159146)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              |||||||||||||   :::               ||||||   |||:::::|||   |||
Db       5213 ACAGTGTCTTTTTAAGTAGCATTACTCTTGTTTTACCCTATCTTTGTTGAAGATACTAGA 5154

Qy         23 AsnGluLeu 25
              |||||||
Db       5153 ACTGAGCTA 5145

RESULT 24
US-11-121-086-50/c
; Sequence 50, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
;  APPLICANT: POULSEN, TIM S.
;  APPLICANT:  NIELSEN, KIRSTEN V.
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
;  FILE REFERENCE: 09138.6000-00000
;  CURRENT APPLICATION NUMBER: US/11/121,086
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,570
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50
;   LENGTH: 203467
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-121-086-50

Alignment Scores:
Pred. No.:              7.78e+04      Length:         203467
Score:                  51.00         Matches:        11
Percent Similarity:     60.9%         Conservative:   3
Best Local Similarity:  47.8%         Mismatches:     9
Query Match:            31.9%         Indels:         0
DB:                     12            Gaps:           0

US-10-758-902-1 (1-30) x US-11-121-086-50 (1-203467)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              |||||||||||   :::               ||||||   |||:::::|||   |||
Db     169122 ACAGTGTCTTTTTAAGTAGCATTACTCTTGTTTTACCCTATCTTTGTTGAAGATACTAGA 169063

Qy         23 AsnGluLeu 25
              |||||||
Db     169062 ACTGAGCTA 169054

RESULT 25
US-10-750-185-50060
; Sequence 50060, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 50060
;   LENGTH: 4606
;   TYPE: DNA
;   ORGANISM: Bovine  19866881244156
US-10-750-185-50060

Alignment Scores:
Pred. No.:              917           Length:         4606
Score:                  50.50         Matches:        13
Percent Similarity:     50.0%         Conservative:   6
Best Local Similarity:  34.2%         Mismatches:     11
Query Match:            31.6%         Indels:         8
DB:                     8             Gaps:           1

US-10-758-902-1 (1-30) x US-10-750-185-50060 (1-4606)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::       |||   |||   ||||||   ||||||   ||| :::|||||
Db       3348 TATTCGAGAATACGAATCAATTTTGGCAATGCGTATGTGTATCCTCCCTTCCCTCCAAGA 3407

Qy         20 p----------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                       :::   :::||||||:::       |||
Db       3408 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 3459

RESULT 26
US-10-750-623-50060
; Sequence 50060, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 50060
;   LENGTH: 4606
;   TYPE: DNA
;   ORGANISM: Bovine  19866881244156
US-10-750-623-50060

Alignment Scores:
Pred. No.:              917          Length:        4606
Score:                  50.50        Matches:       13
Percent Similarity:     50.0%        Conservative:  6
Best Local Similarity:  34.2%        Mismatches:    11
Query Match:            31.6%        Indels:        8
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-10-750-623-50060 (1-4606)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::     |||   |||   ||||||   ||||||   ||| :::|||||
Db       3348 TATTCGAGAATACGAATCAATTTTGGCAATGCGTATGTGTATCCTCCCTTCCCTCCAAGA 3407

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                    :::   :::||||||:::      |||
Db       3408 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 3459

RESULT 27
US-09-925-065A-454821/c
; Sequence 454821, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 454821
;   LENGTH: 503
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-454821

Alignment Scores:
Pred. No.:              74.4         Length:        503
Score:                  50.00        Matches:       11
Percent Similarity:     56.7%        Conservative:  6
Best Local Similarity:  36.7%        Mismatches:    11
Query Match:            31.2%        Indels:        2
DB:                     6            Gaps:          1

US-10-758-902-1 (1-30) x US-09-925-065A-454821 (1-503)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp------ 20
              |||:::      :::|||   |||        |||||||||::::::|||
Db        162 ACCATTAGGAGTGACCTGAAGGAGACTYCTAGCTATCCAACCTATGTACAGCCTCCATTC 103

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
                |||::::::|||      |||   |||
Db        102 CCACGTAGCCAATTGGTCTCTGGGGGTCCG 73

RESULT 28
US-09-925-065A-449581
; Sequence 449581, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 449581
;   LENGTH: 522
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-449581

Alignment Scores:
Pred. No.:              77.8         Length:        522
Score:                  50.00        Matches:       12
Percent Similarity:     56.7%        Conservative:  5
Best Local Similarity:  40.0%        Mismatches:    9
Query Match:            31.2%        Indels:        4
DB:                     6            Gaps:          1

US-10-758-902-1 (1-30) x US-09-925-065A-449581 (1-522)

Qy          4 ValSerPheAsnLeuGlyGluAla-----------TyrGluTyrProThrPheIleGln 19
              :::||||||   ||||||   |||          |||   :::   |||   :::
Db        301 TTATCTTTTCAGTTAGGCCATGCCAAATATAGAGGCTATGCATTTTTCACTGTGGTACCC 360

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThr 29
                |||:::|||:::   |||   ||||||
Db        361 AGTCTCCAAAATAAAACAGCATCTGGCACA 390

RESULT 29
US-09-925-065A-318790
; Sequence 318790, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
```

```
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 318790
;   LENGTH: 538
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-318790

Alignment Scores:
Pred. No.:                80.7          Length:         538
Score:                    50.00         Matches:        6
Percent Similarity:       73.9%         Conservative:   11
Best Local Similarity:    26.1%         Mismatches:     6
Query Match:              31.2%         Indels:         0
DB:                       6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-318790 (1-538)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||::::::   |||:::::::|||:::   ::::::   |||   ::::::   :::
Db         86 TACAATAGCATCCCCTTTTCCATAGGGGATACATTCCAAGATCCCCAGTGGATGCTTGAA 145

Qy         21 LeuArgAsn 23
              :::   |||
Db        146 ATTATGAAT 154

RESULT 30
US-09-925-065A-261114
; Sequence 261114, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261114
;   LENGTH: 581
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-261114

Alignment Scores:
Pred. No.:                88.7          Length:         581
Score:                    50.00         Matches:        7
Percent Similarity:       82.4%         Conservative:   7
Best Local Similarity:    41.2%         Mismatches:     3
Query Match:              31.2%         Indels:         0
DB:                       6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-261114 (1-581)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              ||||||:::   |||:::   |||:::   :::::::::|||||||||:::
Db         64 AATACATTGAAATTTTCTAAAGGACAATTTTTTCAATTTCCAACTTTTATG 114

RESULT 31
US-09-925-065A-261115
; Sequence 261115, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261115
;   LENGTH: 581
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-261115

Alignment Scores:
Pred. No.:                88.7          Length:         581
Score:                    50.00         Matches:        7
Percent Similarity:       82.4%         Conservative:   7
Best Local Similarity:    41.2%         Mismatches:     3
Query Match:              31.2%         Indels:         0
DB:                       6             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-261115 (1-581)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              ||||||:::   |||:::   |||:::   :::::::::|||||||||:::
Db         64 AATACATTGAAATTTTCTAAAGGACAATTTTTTCAATTTCCAACTTTTATG 114

RESULT 32
US-09-925-065A-886124/c
; Sequence 886124, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 886124
;   LENGTH: 604
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
US-09-925-065A-886124

Alignment Scores:
Pred. No.:              93          Length:         604
Score:                  50.00       Matches:        11
Percent Similarity:     57.7%       Conservative:   4
Best Local Similarity:  42.3%       Mismatches:     11
Query Match:            31.2%       Indels:         0
DB:                     6           Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-886124 (1-604)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||:::|||:::   |||||||||:::           |||      ||||||:::
Db        585 TACAACTCAGTCACTCTAAACCTAGGTCAACCTAGGTATTTACCTAGAAAAATACAAGAA 526

Qy         21 LeuArgAsnGluLeuAla 26
                 |||      |||
Db        525 TATGCCAATACAAAGGCA 508

RESULT 33
US-09-925-065A-533904/c
; Sequence 533904, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 533904
;   LENGTH: 623
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-533904

Alignment Scores:
Pred. No.:              96.6        Length:         623
Score:                  50.00       Matches:        12
Percent Similarity:     56.7%       Conservative:   5
Best Local Similarity:  40.0%       Mismatches:     9
Query Match:            31.2%       Indels:         4
DB:                     6           Gaps:           1

US-10-758-902-1 (1-30) x US-09-925-065A-533904 (1-623)

Qy          4 ValSerPheAsnLeuGlyGluAla----------TyrGluTyrProThrPheIleGln 19
              :::||||||   ||||||   |||           |||   :::   |||   :::
Db        384 TTATCTTTTCAGTTAGGCCATGCCAAATATAGAGGCTATGCATTTTTCACTGTGGTACCC 325

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThr 29
                 |||:::|||:::   |||   ||||||
Db        324 AGTCTCCAAAATAAAACAGCATCTGGCACA 295

RESULT 34
US-09-925-065A-705318
; Sequence 705318, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 705318
;   LENGTH: 649
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-705318

Alignment Scores:
Pred. No.:              102         Length:         649
Score:                  50.00       Matches:        7
Percent Similarity:     82.4%       Conservative:   7
Best Local Similarity:  41.2%       Mismatches:     3
Query Match:            31.2%       Indels:         0
DB:                     6           Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-705318 (1-649)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe 17
              :::||||||:::   |||::::::|||   ||||||::::::   :::|||
Db        344 CACAACACGCTTAAGTTTTCCATTGGCCATGCCTATGATTTTGTGTCCTTT 394

RESULT 35
US-09-925-065A-392827/c
; Sequence 392827, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 392827
;   LENGTH: 578
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-392827

Alignment Scores:
Pred. No.:              108         Length:         578
Score:                  49.50       Matches:        13
Percent Similarity:     65.2%       Conservative:   2
Best Local Similarity:  56.5%       Mismatches:     5
Query Match:            30.9%       Indels:         3
```

```
DB:                    6             Gaps:          1

US-10-758-902-1 (1-30) x US-09-925-065A-392827 (1-578)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyr---------GluTyrProThrPheIle 18
              ||||||          ||||||   |||||||||          :::|||   |||||||||
Db        153 AATACTGAATAAGTTAATTTATCTGAAGCTTATAACAATGTCAAATATATTACTTTTATA 94

Qy         19 GlnAspLeu 21
              :::|||||
Db         93 AGGGATCTT 85

RESULT 36
US-09-925-065A-392828/c
; Sequence 392828, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 392828
;   LENGTH: 578
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-392828

Alignment Scores:
Pred. No.:              108           Length:        578
Score:                  49.50         Matches:       13
Percent Similarity:     65.2%         Conservative:  2
Best Local Similarity:  56.5%         Mismatches:    5
Query Match:            30.9%         Indels:        3
DB:                     6             Gaps:          1

US-10-758-902-1 (1-30) x US-09-925-065A-392828 (1-578)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyr---------GluTyrProThrPheIle 18
              ||||||          ||||||   |||||||||          :::|||   |||||||||
Db        153 AATACTGAATAAGTTAATTTATCTGAAGCTTATAACAATGTCAAATATATTACTTTTATA 94

Qy         19 GlnAspLeu 21
              :::|||||
Db         93 AGGGATCTT 85

RESULT 37
US-09-925-065A-252059
; Sequence 252059, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 252059
;   LENGTH: 558
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(558)
;   OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-252059

Alignment Scores:
Pred. No.:              126           Length:        558
Score:                  49.00         Matches:       11
Percent Similarity:     58.1%         Conservative:  7
Best Local Similarity:  35.5%         Mismatches:    7
Query Match:            30.6%         Indels:        6
DB:                     6             Gaps:          1

US-10-758-902-1 (1-30) x US-09-925-065A-252059 (1-558)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThr------------ 16
              |||   ::::::|||   |||   |||:::|||:::|||:::|||:::
Db        394 TATATGAGCATCTCAATAAACACAGGAAAAGCATTTGAGTGGCCTAGTAATCAACTTTCT 453

Qy         17 ------PheIleGlnAspLeuArgAsnGluLeu 25
                    ||||||          |||:::   |||
Db        454 GATTTCTTTATCTGGCAATTCAGAGATCTTCTT 486

RESULT 38
US-09-925-065A-252060
; Sequence 252060, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 252060
;   LENGTH: 558
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(558)
;   OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-252060

Alignment Scores:
Pred. No.:              126           Length:        558
Score:                  49.00         Matches:       11
```

```
Percent Similarity:    58.1%          Conservative:  7
Best Local Similarity: 35.5%          Mismatches:    7
Query Match:           30.6%          Indels:        6
DB:                    6              Gaps:          1

US-10-758-902-1 (1-30) x US-09-925-065A-252060 (1-558)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThr---------- 16
              |||   ::::::|||   |||   |||:::|||:::|||:::|||:::
Db        394 TATATGAGCATCTCAATAAACACAGGAAAAGCATTTGAGTGGCCTAGTAATCAACTTTCT 453

Qy         17 ------PheIleGlnAspLeuArgAsnGluLeu 25
                  ||||||       |||:::   |||
Db        454 GATTTCTTTATCTGGCAATTCAGAGATCTTCTT 486

RESULT 39
US-09-925-065A-702979/c
; Sequence 702979, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 702979
;   LENGTH: 2468
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-702979

Alignment Scores:
Pred. No.:             779            Length:        2468
Score:                 49.00          Matches:       13
Percent Similarity:    62.1%          Conservative:  5
Best Local Similarity: 44.8%          Mismatches:    7
Query Match:           30.6%          Indels:        4
DB:                    6              Gaps:          2

US-10-758-902-1 (1-30) x US-09-925-065A-702979 (1-2468)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe------IleGlnAspLeu 21
              :::|||||||||||||||      |||:::::::|||   |||      |||   :::|||
Db       1491 CTATCATTTAATTTGGGC------TATAAGCACCCACTCTTTGATCTAATTACTGAACTC 1438

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
                 |||:::      |||      |||
Db       1437 AGTAATAAGAAATGCAAAGATTTTCCC 1411

RESULT 40
US-09-925-065A-289057
; Sequence 289057, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 289057
;   LENGTH: 559
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-289057

Alignment Scores:
Pred. No.:             154            Length:        559
Score:                 48.50          Matches:       11
Percent Similarity:    71.4%          Conservative:  4
Best Local Similarity: 52.4%          Mismatches:    5
Query Match:           30.3%          Indels:        1
DB:                    6              Gaps:          1

US-10-758-902-1 (1-30) x US-09-925-065A-289057 (1-559)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp---LeuArg 22
              :::|||||||||||||||      :::      |||:::||||||   |||   |||:::
Db        302 TTGTCCTTTAATTTAGGCCCTTGCTTTTACATACCTTCATTTATCTTTGATTGTCTTAAG 361

Qy         23 Asn 23
              |||
Db        362 AAC 364


Search completed: February 20, 2006, 01:03:09
Job time : 98.3296 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:12:50 ; Search time 1055.7 Seconds
(without alignments)
1329.558 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160802_3709/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10758902_@CGN_1_1_10172_@runat_17022006_160802_3709 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	76	47.5	506	1	AI043519	AI043519 L30-519T3
2	76	47.5	644	6	CA838401	CA838401 MCT016B04
3	76	47.5	667	6	CA838446	CA838446 MCT016F04
4	76	47.5	672	1	AW053585	AW053585 L30-2143T
5	76	47.5	678	6	CA840373	CA840373 MCT036G03
6	76	47.5	698	6	CA838926	CA838926 MCT021H09
7	69	43.1	811	2	BE034055	BE034055 MG04C05 M
8	69	43.1	1021	2	BE036639	BE036639 MP03B03 M
9	59	36.9	520	11	DE052179	DE052179 Oryzias l
10	58	36.2	814	7	CV472618	CV472618 45989.1 C
c 11	58	36.2	945	8	DN923351	DN923351 45989.3 C
12	57	35.6	378	9	BZ839949	BZ839949 CH240_261
c 13	57	35.6	508	9	AQ277060	AQ277060 CITBI-E1-
14	57	35.6	527	6	CD215509	CD215509 pgp2n.pk0
15	57	35.6	527	11	CR920825	CR920825 Sus scrof
16	57	35.6	603	3	BM426222	BM426222 pgf2n.pk0
17	57	35.6	659	3	BI392858	BI392858 pgp1n.pk0
18	57	35.6	673	3	BM488278	BM488278 pgm2n.pk0
c 19	57	35.6	760	9	AQ354093	AQ354093 CITBI-E1-
c 20	57	35.6	779	11	CNS03K0S	AL247573 Tetraodon
21	57	35.6	782	10	AG520129	AG520129 Mus muscu
22	57	35.6	939	10	DU009707	DU009707 241569 To
c 23	56.5	35.3	578	10	CE644685	CE644685 tigr-gss-
24	56	35.0	271	7	CR528387	CR528387 CR528387
25	56	35.0	284	6	CA533718	CA533718 C0405D02-
26	56	35.0	423	1	AA783170	AA783170 c1g09a1.r
c 27	56	35.0	451	5	BY555839	BY555839 BY555839
28	56	35.0	506	9	BH879393	BH879393 ht46b11.b
29	56	35.0	529	2	BG556183	BG556183 EM1_68_G0
30	56	35.0	657	6	CF428375	CF428375 PH1_14_B0
31	56	35.0	665	9	AZ364827	AZ364827 1M0111E17
32	56	35.0	684	8	DR801301	DR801301 ZM_BFb002
c 33	56	35.0	731	10	CW658238	CW658238 OG_BBa000
34	56	35.0	857	7	CF933557	CF933557 TrEST-B09
c 35	56	35.0	911	9	BZ814229	BZ814229 PUFGM69TD
c 36	56	35.0	949	5	BU161967	BU161967 AGENCOURT
37	56	35.0	963	5	BQ952169	BQ952169 AGENCOURT
c 38	56	35.0	970	10	CZ994983	CZ994983 183000 To
39	56	35.0	991	10	CL999228	CL999228 ZMMBHf001
40	56	35.0	994	10	CL987992	CL987992 ZMMBHe000
41	56	35.0	995	10	CL996830	CL996830 ZMMBHf000
42	56	35.0	1031	9	CC636648	CC636648 OGULM19TV
43	56	35.0	1047	10	CL998940	CL998940 ZMMBHf001
c 44	56	35.0	1291	10	AG500004	AG500004 Mus muscu
c 45	56	35.0	1330	8	DR747390	DR747390 C08_AECAL
c 46	55.5	34.7	421	7	CV190488	CV190488 she01-4ms
47	55.5	34.7	694	2	BG963962	BG963962 602828687
c 48	55.5	34.7	3806	4	CR859132	CR859132 Pongo pyg
49	55	34.4	374	6	CA398556	CA398556 EL01N0306
50	55	34.4	392	1	AJ689331	AJ689331 AJ689331
51	55	34.4	654	10	CZ222642	CZ222642 AIAA-aad0
52	55	34.4	700	3	BJ255634	BJ255634 BJ255634
53	55	34.4	751	6	CD624153	CD624153 56060565J
54	55	34.4	807	6	CD853964	CD853964 DH0AMM24Z
c 55	55	34.4	847	3	BQ212581	BQ212581 AGENCOURT
c 56	55	34.4	901	10	CL392280	CL392280 ZMMBBb039
c 57	55	34.4	1700	11	DQ030691	DQ030691 Homo sapi
58	54.5	34.1	430	7	CN847299	CN847299 PG07031B0
59	54.5	34.1	500	9	CE132168	CE132168 tigr-gss-
60	54.5	34.1	517	3	BP063495	BP063495 BP063495
61	54.5	34.1	528	10	CE360894	CE360894 tigr-gss-
c 62	54.5	34.1	550	9	CE116221	CE116221 tigr-gss-
63	54.5	34.1	574	9	CC816360	CC816360 1O0001A19
64	54.5	34.1	586	9	CE162608	CE162608 tigr-gss-
c 65	54.5	34.1	633	10	CE819631	CE819631 tigr-gss-
c 66	54.5	34.1	635	9	CE002151	CE002151 tigr-gss-
67	54.5	34.1	637	9	CE097460	CE097460 tigr-gss-
c 68	54.5	34.1	648	9	CE238170	CE238170 tigr-gss-
c 69	54.5	34.1	682	9	CE153948	CE153948 tigr-gss-
c 70	54.5	34.1	718	10	CE583908	CE583908 tigr-gss-
c 71	54.5	34.1	752	10	CE270899	CE270899 tigr-gss-
c 72	54.5	34.1	897	10	CW949798	CW949798 TcB34.4_B
c 73	54.5	34.1	898	10	CW943936	CW943936 TcB25.4_F
74	54.5	34.1	975	11	CT021248	CT021248 KBrH131P0
75	54	33.8	201	9	BZ203831	BZ203831 CH230-436
c 76	54	33.8	374	7	CR773662	CR773662 DKFZp459F
77	54	33.8	376	9	AZ925651	AZ925651 4910.ez34
c 78	54	33.8	383	6	CD980757	CD980757 QAI16c03.
79	54	33.8	411	1	AI872103	AI872103 wm55c05.x
c 80	54	33.8	425	9	AQ683450	AQ683450 HS_5432_B

	81	54	33.8	438	5	BU579130	BU579130 sar54d08.
	82	54	33.8	494	7	CN600715	CN600715 EG-F01_00
c	83	54	33.8	513	6	CD981131	CD981131 QAI20c11.
c	84	54	33.8	513	8	DN350106	DN350106 LIB3579-0
c	85	54	33.8	514	6	CD980619	CD980619 QAI14e02.
c	86	54	33.8	515	8	DN400321	DN400321 LIB4004-0
c	87	54	33.8	542	1	AW055395	AW055395 614080D06
c	88	54	33.8	550	6	CD981119	CD981119 QAI20b06.
	89	54	33.8	553	7	CK769069	CK769069 Gm-r1030-
c	90	54	33.8	570	6	CD980539	CD980539 QAI13d11.
c	91	54	33.8	590	6	CD980426	CD980426 QAI11h03.
	92	54	33.8	602	9	CC671744	CC671744 OGWBT26TV
	93	54	33.8	605	11	CT010984	CT010984 KBrH118E2
	94	54	33.8	606	1	AV901145	AV901145 AV901145
c	95	54	33.8	638	8	DN222290	DN222290 MEST1126_
c	96	54	33.8	643	8	DN224397	DN224397 MEST1158_
	97	54	33.8	645	7	CN662368	CN662368 A0732H06-
c	98	54	33.8	662	5	BW295982	BW295982 BW295982
	99	54	33.8	662	5	BW492501	BW492501 BW492501
c	100	54	33.8	676	10	CL580929	CL580929 OB__Ba004

ALIGNMENTS

RESULT 1
AI043519
LOCUS AI043519 506 bp mRNA linear EST 20-FEB-2001
DEFINITION L30-519T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-519 5', mRNA sequence.
ACCESSION AI043519
VERSION AI043519.1 GI:3290302
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 506)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T7
BACKWARD: T3
Plate: L30-6 row: C column: 3
Seq primer: T3
High quality sequence stop: 310.
FEATURES Location/Qualifiers
source 1. .506
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L30-519"
/tissue_type="Leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.: 0.032 Length: 506
Score: 76.00 Matches: 15
Percent Similarity: 69.0% Conservative: 5
Best Local Similarity: 51.7% Mismatches: 9
Query Match: 47.5% Indels: 0
DB: 1 Gaps: 0

US-10-758-902-1 (1-30) x AI043519 (1-506)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        199 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 258

Qy         21 LeuArgAsnGluLeuAlaLysGlyThr 29
              |||:::   ||||||      ||||||
Db        259 CTCCAAACTGAACTATTCTCCGGCACA 285
```

RESULT 2
CA838401
LOCUS CA838401 644 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT016B04_166733 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT016B04 5, mRNA sequence.
ACCESSION CA838401
VERSION CA838401.1 GI:26566166
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 644)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 016 row: B column: 04
Seq primer: T3 20mer
High quality sequence stop: 644.
FEATURES Location/Qualifiers
source 1. .644
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT016B04"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.: 0.0426 Length: 644
Score: 76.00 Matches: 15
Percent Similarity: 69.0% Conservative: 5
Best Local Similarity: 51.7% Mismatches: 9
Query Match: 47.5% Indels: 0
DB: 6 Gaps: 0

US-10-758-902-1 (1-30) x CA838401 (1-644)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        202 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 261

Qy         21 LeuArgAsnGluLeuAlaLysGlyThr 29
              |||:::   ||||||      ||||||
Db        262 CTCCAAACTGAACTATTCTCCGGCACA 288
```

RESULT 3
CA838446
LOCUS CA838446 667 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT016F04_166823 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT016F04 5, mRNA sequence.
ACCESSION CA838446
VERSION CA838446.1 GI:26566211
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 667)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 016 row: F column: 04
Seq primer: T3 20mer
High quality sequence stop: 667.
FEATURES Location/Qualifiers
source 1. .667
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT016F04"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:

Pred. No.:	0.0448	Length:	667
Score:	76.00	Matches:	15
Percent Similarity:	69.0%	Conservative:	5
Best Local Similarity:	51.7%	Mismatches:	9
Query Match:	47.5%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x CA838446 (1-667)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        200 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 259

Qy         21 LeuArgAsnGluLeuAlaLysGlyThr 29
              |||:::   ||||||      ||||||
Db        260 CTCCAAACTGAACTATTCTCCGGCACA 286
```

RESULT 4
AW053585
LOCUS AW053585 672 bp mRNA linear EST 20-FEB-2001
DEFINITION L30-2143T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-2143 5', mRNA sequence.
ACCESSION AW053585
VERSION AW053585.1 GI:5916778
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 672)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T7
BACKWARD: T3
Plate: L30-22 row: D column: 11
Seq primer: T3
High quality sequence stop: 450.
FEATURES Location/Qualifiers
source 1. .672
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L30-2143"
/tissue_type="Leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:

Pred. No.:	0.0448	Length:	672
Score:	76.00	Matches:	15
Percent Similarity:	69.0%	Conservative:	5
Best Local Similarity:	51.7%	Mismatches:	9
Query Match:	47.5%	Indels:	0
DB:	1	Gaps:	0

US-10-758-902-1 (1-30) x AW053585 (1-672)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        196 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 255

Qy         21 LeuArgAsnGluLeuAlaLysGlyThr 29
              |||:::   ||||||      ||||||
Db        256 CTCCAAACTGAACTATTCTCCGGCACA 282
```

RESULT 5
CA840373
LOCUS CA840373 678 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT036G03_173841 Ice plant Lambda Uni-Zap XR expression library, 5

```
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
            (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT036G03 5,
            mRNA sequence.
ACCESSION   CA840373
VERSION     CA840373.1  GI:26568138
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 036  row: G  column: 03
            Seq primer: T3 20mer
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
     source          1. .678
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCT036G03"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase IV (5:30 PM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.:              0.0453          Length:         678
Score:                  76.00           Matches:        15
Percent Similarity:     69.0%           Conservative:   5
Best Local Similarity:  51.7%           Mismatches:     9
Query Match:            47.5%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x CA840373 (1-678)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        202 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 261

Qy         21 LeuArgAsnGluLeuAlaLysGlyThr 29
              |||:::   ||||||      ||||||
Db        262 CTCCAAACTGAACTATTCTCCGGCACA 288

RESULT 6
CA838926
LOCUS       CA838926                 698 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  MCT021H09_170947 Ice plant Lambda Uni-Zap XR expression library, 5
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
            (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT021H09 5,
            mRNA sequence.
ACCESSION   CA838926
VERSION     CA838926.1  GI:26566691
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 021  row: H  column: 09
            Seq primer: T3 20mer
            High quality sequence stop: 698.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCT021H09"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase IV (5:30 PM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.:              0.0469          Length:         698
Score:                  76.00           Matches:        15
Percent Similarity:     69.0%           Conservative:   5
Best Local Similarity:  51.7%           Mismatches:     9
Query Match:            47.5%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x CA838926 (1-698)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        197 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 256

Qy         21 LeuArgAsnGluLeuAlaLysGlyThr 29
              |||:::   ||||||      ||||||
Db        257 CTCCAAACTGAACTATTCTCCGGCACA 283

RESULT 7
BE034055
LOCUS       BE034055                 811 bp    mRNA    linear   EST 07-JUN-2000
DEFINITION  MG04C05 MG Mesembryanthemum crystallinum cDNA 5' similar to
            ribosome-inactivating protein gelonin, mRNA sequence.
ACCESSION   BE034055
VERSION     BE034055.1  GI:8329064
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 811)
```

```
  AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
  TITLE     Functional Genomics of Plant Stress Tolerance
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Michalowski,C.B.
            University of Arizona
            Bio Sciences West room 513, Tucson, AZ 85721, USA
            Tel: 520-621-7982
            Fax: 520-621-1697
            Email: cbm@u.arizona.edu
            An open reading frame exists.
            Insert Length: 1   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .811
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /tissue_type="roots"
                     /dev_stage="5-6 weeks"
                     /clone_lib="MG"
                     /note="grown in hydroponics, stress 400 mM NaCl (in 0.5
                     Hoagland's), 30 h stress"
ORIGIN

Alignment Scores:
Pred. No.:                0.834          Length:         811
Score:                    69.00          Matches:        14
Percent Similarity:       65.5%          Conservative:   5
Best Local Similarity:    48.3%          Mismatches:     10
Query Match:              43.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-758-902-1 (1-30) x BE034055 (1-811)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||||||||   :::         |||   ||||||:::
Db        243 TACAACACCGTGACATTCAACCTCGCCCAACCCAACACATATTCCACATTCATGACATCT 302

Qy         21 LeuArgAsnGluLeuAlaLysGlyThr 29
              ||||||   :::|||:::      |||
Db        303 CTCCGAGCTCAACTCTCTGGCACAACC 329

RESULT 8
BE036639
LOCUS       BE036639               1021 bp    mRNA    linear   EST 07-JUN-2000
DEFINITION  MP03B03 MP Mesembryanthemum crystallinum cDNA 5' similar to
            ribosome-inactivating protein gelonin, mRNA sequence.
ACCESSION   BE036639
VERSION     BE036639.1  GI:8331648
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
  TITLE     Functional Genomics of Plant Stress Tolerance
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Michalowski,C.B.
            University of Arizona
            Bio Sciences West room 513, Tucson, AZ 85721, USA
            Tel: 520-621-7982
            Fax: 520-621-1697
            Email: cbm@u.arizona.edu
            An open reading frame exists.
            Insert Length: 1   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .1021
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /tissue_type="apical meristem and leaf primordia"
                     /dev_stage="6 weeks"
                     /clone_lib="MP"
                     /note="3 d 500mM NaCl"
ORIGIN

Alignment Scores:
Pred. No.:                1.1            Length:         1021
Score:                    69.00          Matches:        14
Percent Similarity:       65.5%          Conservative:   5
Best Local Similarity:    48.3%          Mismatches:     10
Query Match:              43.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-758-902-1 (1-30) x BE036639 (1-1021)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||||||||   :::         |||   ||||||:::
Db        216 TACAACACCGTGACATTCAACCTCGCCCAACCCAACACATATTCCACATTCATGACATCT 275

Qy         21 LeuArgAsnGluLeuAlaLysGlyThr 29
              ||||||   :::|||:::      |||
Db        276 CTCCGAGCTCAACTCTCTGGCACAACC 302

RESULT 9
DE052179
LOCUS       DE052179               520 bp    DNA     linear   GSS 25-MAY-2005
DEFINITION  Oryzias latipes DNA, clone: ola1-021G08.R, genomic survey sequence.
ACCESSION   DE052179
VERSION     DE052179.1  GI:62563723
KEYWORDS    GSS.
SOURCE      Oryzias latipes (Japanese medaka)
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1
  AUTHORS   Fujiyama,A., Toyoda,A., Kuroki,Y. and Sakaki,Y.
  TITLE     BAC end sequences of Ola1 Oryzias latipes Library
  JOURNAL   Published Only in Database (2005)
REFERENCE   2  (bases 1 to 520)
  AUTHORS   Fujiyama,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2005) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:afujiyam@gsc.riken.jp, URL:http://stt.gsc.riken.jp/,
            Tel:81-3-4212-2558, Fax:81-3-3556-1916)
COMMENT     This work was done in collaboration with Takeda, H. (1), Naruse, K.
            (2)
            and Narita, T. (3)
            (1) Department of Biological Science,
            University of Tokyo
            Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, JAPAN
            Phone: +81-3-5841-4431
            Fax: +81-3-5841-4993
            E-mail: htakeda.s.u-tokyo.ac.jp
            (2) Department of Biological Science,
            University of Tokyo
            Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, JAPAN
            Phone: +81-3-5841-4431
            Fax: +81-3-5841-4993
            E-mail: naruse.s.u-tokyo.ac.jp
            (3) Department of Biological Science,
            University of Tokyo
            Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, JAPAN
            Phone: +81-3-5841-4431
            Fax: +81-3-5841-4993
            E-mail: tanarita.s.u-tokyo.ac.jp
            PRIMERS
```

```
            Sequencing : Forward
         LIBRARY
            Vector     : pKS145
            R.Site 1   : SacI
            L.Site 2   : SacI.
FEATURES             Location/Qualifiers
     source          1. .520
                     /organism="Oryzias latipes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:8090"
                     /clone="ola1-021G08.R"
                     /sex="male"
                     /cell_type="whole body"
                     /clone_lib="BAC end sequences of Ola1 Oryzias latipes
                     library"
ORIGIN

Alignment Scores:
Pred. No.:              23.4          Length:        520
Score:                  59.00         Matches:       12
Percent Similarity:     57.1%         Conservative:  4
Best Local Similarity:  42.9%         Mismatches:    12
Query Match:            36.9%         Indels:        0
DB:                     11            Gaps:          0

US-10-758-902-1 (1-30) x DE052179 (1-520)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              |||:::                :::      |||   |||||||||      |||||||||
Db        413 ACTATAAAAATTAAAAAAAGTAAAAAATGTGAACCTCCTACTTTTCAAGATGACTTAAGA 472

Qy         23 AsnGluLeuAlaLysGlyThrPro 30
              |||   |||:::|||   :::|||
Db        473 AATCCTTTATCGAAATCTAGTCCC 496

RESULT 10
CV472618
LOCUS       CV472618                 814 bp    mRNA    linear   EST 01-OCT-2004
DEFINITION  45989.1 Common Scab-Challenged Tubers Solanum tuberosum cDNA clone
            45989 5', mRNA sequence.
ACCESSION   CV472618
VERSION     CV472618.1  GI:53697394
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 814)
  AUTHORS   Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De
            Koeyer,D., Audy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S.
  TITLE     Generation of ESTs from common scab-challenged potato tubers
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Barry Flinn
            The Canadian Potato Genome Project - BioAtlantech
            921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
            Email: bflinn@bioatlantech.nb.ca
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .814
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Shepody"
                     /db_xref="taxon:4113"
                     /clone="45989"
                     /tissue_type="Tubers"
                     /lab_host="XL10-Gold"
                     /clone_lib="Common Scab-Challenged Tubers"
                     /note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
                     Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
                     from pathogen-free Solanum tuberosum var. Shepody, clone
                     1756, were inoculated with Streptomyces scabei EF-35, by
                     applying 1 ml of a spore stock (OD650 = 0.7). Tubers were
                     placed in trays of sand and watered from the bottom for
                     the remainder of the experiment. Inoculated tubers were
                     sampled at 2 days, 1 week, 2 weeks and 4 weeks
                     post-infection. Harvested tubers were washed in distilled
                     water, blotted dry, cut into small pieces and frozen in
                     liquid nitrogen. RNA was isolated from each sample
                     collection, pooled and used for cDNA library
                     construction."
ORIGIN

Alignment Scores:
Pred. No.:              58.5          Length:        814
Score:                  58.00         Matches:       10
Percent Similarity:     68.4%         Conservative:  3
Best Local Similarity:  52.6%         Mismatches:    6
Query Match:            36.2%         Indels:        0
DB:                     7             Gaps:          0

US-10-758-902-1 (1-30) x CV472618 (1-814)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              ||||||::::::   |||||||||         ||||||:::      |||||||||
Db        679 TATAATAGCATTAGGTTTAATCTCCATCGTGTTTATGAATTCAAACGCTTCATTCAA 735

RESULT 11
DN923351/c
LOCUS       DN923351                 945 bp    mRNA    linear   EST 26-APR-2005
DEFINITION  45989.3 Common Scab-Challenged Tubers Solanum tuberosum cDNA clone
            45989 3', mRNA sequence.
ACCESSION   DN923351
VERSION     DN923351.1  GI:62909684
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De
            Koeyer,D., Audy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S.
  TITLE     Generation of ESTs from common scab-challenged potato tubers
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Barry Flinn
            The Canadian Potato Genome Project - BioAtlantech
            921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
            Email: bflinn@bioatlantech.nb.ca
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .945
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Shepody"
                     /db_xref="taxon:4113"
                     /clone="45989"
                     /tissue_type="Tubers"
                     /lab_host="XL10-Gold"
                     /clone_lib="Common Scab-Challenged Tubers"
                     /note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
                     Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
                     from pathogen-free Solanum tuberosum var. Shepody, clone
                     1756, were inoculated with Streptomyces scabei EF-35, by
                     applying 1 ml of a spore stock (OD650 = 0.7). Tubers were
                     placed in trays of sand and watered from the bottom for
                     the remainder of the experiment. Inoculated tubers were
                     sampled at 2 days, 1 week, 2 weeks and 4 weeks
                     post-infection. Harvested tubers were washed in distilled
                     water, blotted dry, cut into small pieces and frozen in
                     liquid nitrogen. RNA was isolated from each sample
                     collection, pooled and used for cDNA library
                     construction."
ORIGIN

Alignment Scores:
```

```
Pred. No.:              69.7          Length:         945
Score:                  58.00         Matches:        10
Percent Similarity:     68.4%         Conservative:   3
Best Local Similarity:  52.6%         Mismatches:     6
Query Match:            36.2%         Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-1 (1-30) x DN923351 (1-945)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              ||||||::::::   |||||||||         ||||||:::      |||||||||
Db        309 TATAATAGCATTAGGTTTAATCTCCATCGTGTTTATGAATTCAAACGCTTCATTCAA 253

RESULT 12
BZ839949
LOCUS       BZ839949                 378 bp    DNA     linear   GSS 18-MAR-2003
DEFINITION  CH240_261N13.TJ CHORI-240 Bos taurus genomic clone CH240_261N13,
            genomic survey sequence.
ACCESSION   BZ839949
VERSION     BZ839949.1  GI:29067308
KEYWORDS    GSS.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 378)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Chen,D., Riggs,F., de Jong,P.,
            Crawford,A.M. and McEwan,J.C.
  TITLE     Bovine BAC End Sequences from Library CHORI-240
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the bovine BAC library CHORI-240
            (http://www.chori.org/bacpac/bovine240.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/ordering_information.htm). This work
            was undertaken as part of the International Bovine BAC Mapping
            Consortium (IBBMC) by AgResearch Ltd., New Zealand and The
            Institute of Genomic Research (TIGR), USA.
            Plate: 261  row: N  column: 13
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .378
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Hereford"
                     /db_xref="taxon:9913"
                     /clone="CH240_261N13"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-240"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
                     library (Male) produced by Pieter de Jong"
ORIGIN

Alignment Scores:
Pred. No.:              34.7          Length:         378
Score:                  57.00         Matches:        12
Percent Similarity:     50.0%         Conservative:   3
Best Local Similarity:  40.0%         Mismatches:     15
Query Match:            35.6%         Indels:         0
DB:                     9             Gaps:           0

US-10-758-902-1 (1-30) x BZ839949 (1-378)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||   |||||||||:::   |||:::        |||              |||
Db        281 TACAATGAGGTGTCATTTCACAATGGTCAGAATGGCCATTATCAAAATGTCTACAATGAT 340

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
                        :::   ||||||||||||
Db        341 GCTGAAAAGGGTGTGGAGAAAGGGACCCCT 370

RESULT 13
AQ277060/c
LOCUS       AQ277060                 508 bp    DNA     linear   GSS 22-NOV-1998
DEFINITION  CITBI-E1-2516A17.TR CITBI-E1 Homo sapiens genomic clone 2516A17,
            genomic survey sequence.
ACCESSION   AQ277060
VERSION     AQ277060.1  GI:3903256
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
            Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of a random human BAC End Sequence Database for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1998)
COMMENT     Other_GSSs: CITBI-E1-2516A17.TF
            Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2516A17"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

Alignment Scores:
Pred. No.:              49.2          Length:         508
Score:                  57.00         Matches:        11
Percent Similarity:     60.0%         Conservative:   4
Best Local Similarity:  44.0%         Mismatches:     10
Query Match:            35.6%         Indels:         0
DB:                     9             Gaps:           0

US-10-758-902-1 (1-30) x AQ277060 (1-508)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||      :::      |||||||||     |||::::::|||      ||||||
Db        134 TATAGAGTAATACATTAGAATCTGGGAAGGTTATATGACTTTCCCAATGGCATACAGATG 75

Qy         21 LeuArgAsnGluLeu 25
              :::   |||||||||
Db         74 GTTAGTAATGAGCTG 60
```

```
RESULT 14
CD215509
LOCUS       CD215509                527 bp    mRNA    linear   EST 20-MAY-2003
DEFINITION  pgp2n.pk008.a17 Normalized chicken pituitary/hypothalamus/pineal
            cDNA library (pgp2n) Gallus gallus cDNA clone pgp2n.pk008.a17 5'
            similar to ref|XP_008393.3 (XM_008393) neurexin 4 [Homo sapiens],
            mRNA sequence.
ACCESSION   CD215509
VERSION     CD215509.1  GI:30955508
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 527)
  AUTHORS   Porter,T.E. and Cogburn,L.A.
  TITLE     Chicken ESTs from pituitary/hypothalamus/pineal gland
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Larry A. Cogburn
            University of Delaware
            Townsend Hall, Newark, DE 19717, USA
            Tel: 302-831-1335
            Fax: 302-831-2822
            Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES             Location/Qualifiers
     source          1. .527
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Commercial broiler chickens"
                     /db_xref="taxon:9031"
                     /clone="pgp2n.pk008.a17"
                     /sex="Male and Female"
                     /tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
                     /dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,9
                     weeks)"
                     /lab_host="E. Coli EMDH10B"
                     /clone_lib="Normalized chicken
                     pituitary/hypothalamus/pineal cDNA library (pgp2n)"
                     /note="Vector: pCMVSPORT6; Library made from equivalent
                     pools of total RNA isolated from each tissue at different
                     ages. Single pass sequencing from 5'-end"
ORIGIN

Alignment Scores:
Pred. No.:              51.4          Length:         527
Score:                  57.00         Matches:        11
Percent Similarity:     76.5%         Conservative:   2
Best Local Similarity:  64.7%         Mismatches:     4
Query Match:            35.6%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x CD215509 (1-527)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe 17
              :::||||||||||||||||||   |||   |||      :::|||||||||
Db        208 TGGAACACCGTCTCCTTCAACAGAGGTGCAGCCCTGCTCTTCCCCACCTTC 258

RESULT 15
CR920825
LOCUS       CR920825                527 bp    DNA     linear   GSS 24-NOV-2004
DEFINITION  Sus scrofa BES, genomic survey sequence.
ACCESSION   CR920825
VERSION     CR920825.1  GI:56261562
KEYWORDS    GSS; Bac-end sequence BES; Genome Survey Sequence.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 527)
  AUTHORS   Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
            Chardon,P.
  TITLE     Construction of a swine BAC library: application to the
            characterization and mapping of porcine type C endoviral elements
  JOURNAL   Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
  PUBMED    10449899
REFERENCE   2  (bases 1 to 527)
  AUTHORS   Chardon,P., Iannuccelli,N., Roig,A., Dossat,C., Demars,J.,
            Rogel-Gaillard,C., Roy,A., Schibler,L. and Milan,D.
  TITLE     A physical map of the swine genome
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 527)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
FEATURES             Location/Qualifiers
     source          1. .527
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /strain="Large White"
                     /db_xref="taxon:9823"
                     /clone="bI0617C08"
                     /sex="male"
                     /cell_type="fibroblast"
                     /clone_lib="SBAB"
                     /note="Genoscope sequence ID : IH0AAA61BB07FM1"
ORIGIN

Alignment Scores:
Pred. No.:              51.4          Length:         527
Score:                  57.00         Matches:        12
Percent Similarity:     59.3%         Conservative:   4
Best Local Similarity:  44.4%         Mismatches:     11
Query Match:            35.6%         Indels:         0
DB:                     11            Gaps:           0

US-10-758-902-1 (1-30) x CR920825 (1-527)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              :::|||||||||   |||       |||   |||:::         |||:::|||   |||
Db        220 GATACTGTGAGTCACAACTTCCTGGAAAAATATGATATTACTTATTTTCTGCAGGGGTTA 279

Qy         22 ArgAsnGluLeuAlaLysGly 28
              :::|||       ||||||
Db        280 AAAAACAGATGCCTTAAGGGA 300

RESULT 16
BM426222
LOCUS       BM426222                603 bp    mRNA    linear   EST 30-JAN-2002
DEFINITION  pgf2n.pk002.a19 Normalized Chicken Abdominal Fat Library (pgf2n)
            Gallus gallus cDNA clone pgf2n.pk002.a19 5' similar to gi|13652383
            ref|XP_008393.3| neurexin 4 [Homo sapiens], mRNA sequence.
ACCESSION   BM426222
VERSION     BM426222.1  GI:18430364
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 603)
  AUTHORS   Cogburn,L.A., Morgan,R. and Burnside,J.
  TITLE     ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS Animal
            Genome Project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Larry A. Cogburn
            University of Delaware
            Townsend Hall, Newark, DE 19717, USA
            Tel: 302-831-1335
            Fax: 302-831-2822
            Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES             Location/Qualifiers
```

```
     source          1. .603
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Commercial broiler, Ottawa Research Centre,
                     leghorn"
                     /db_xref="taxon:9031"
                     /clone="pgf2n.pk002.a19"
                     /sex="Male and Female"
                     /tissue_type="Abdominal Fat"
                     /dev_stage="Embryonic (d18,d19); post-hatch
                     (d1,w3,w7,w9,w16,1yr)"
                     /lab_host="E. coli EMDH10B"
                     /clone_lib="Normalized Chicken Abdominal Fat Library
                     (pgf2n)"
                     /note="Vector: pCMVSPORT6; Library made from equivalent
                     pools of total RNA isolated  from each developmental age
                     (across strains); Single pass sequencing from 5'-end"
ORIGIN

Alignment Scores:
Pred. No.:                60.3          Length:         603
Score:                    57.00         Matches:        11
Percent Similarity:       76.5%         Conservative:   2
Best Local Similarity:    64.7%         Mismatches:     4
Query Match:              35.6%         Indels:         0
DB:                       3             Gaps:           0

US-10-758-902-1 (1-30) x BM426222 (1-603)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe 17
              :::||||||||||||||||||    |||   |||      :::||||||||||
Db        265 TGGAACACCGTCTCCTTCAACAGAGGTGCAGCCCTGCTCTTCCCCACCTTC 315

RESULT 17
BI392858
LOCUS       BI392858                659 bp    mRNA    linear   EST 06-AUG-2001
DEFINITION  pgp1n.pk009.f23 Normalized Chicken Pituitary/Hypothalamus/Pineal
            Library Gallus gallus cDNA clone pgp1n.pk009.f23 5' similar to
            gi|13652383 ref|XP_008393.3| neurexin 4 [Homo sapiens], mRNA
            sequence.
ACCESSION   BI392858
VERSION     BI392858.1  GI:15086140
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 659)
  AUTHORS   Porter,T.E. and Cogburn,L.A.
  TITLE     ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
            library USDA/IFAFS Animal Genome Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Larry A. Cogburn
            University of Delaware
            Townsend Hall, Newark, DE 19717, USA
            Tel: 302-831-1335
            Fax: 302-831-2822
            Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES             Location/Qualifiers
     source          1. .659
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Commercial broiler chicken"
                     /db_xref="taxon:9031"
                     /clone="pgp1n.pk009.f23"
                     /sex="Male and Female"
                     /tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
                     /dev_stage="Embryonic (d12,d14,d19); post-hatch
                     (w1,w3,w5,w7,w9)"
                     /lab_host="E. Coli EMDH10B"
                     /clone_lib="Normalized Chicken
                     Pituitary/Hypothalamus/Pineal Library"
                     /note="Vector: pCMVSPORT6; Library made from equivalent
                     pools of total RNA isolated from each  tissue at different
                     ages. Single pass sequencing from 5'-end"
ORIGIN

Alignment Scores:
Pred. No.:                67            Length:         659
Score:                    57.00         Matches:        11
Percent Similarity:       76.5%         Conservative:   2
Best Local Similarity:    64.7%         Mismatches:     4
Query Match:              35.6%         Indels:         0
DB:                       3             Gaps:           0

US-10-758-902-1 (1-30) x BI392858 (1-659)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe 17
              :::||||||||||||||||||    |||   |||      :::||||||||||
Db        348 TGGAACACCGTCTCCTTCAACAGAGGTGCAGCCCTGCTCTTCCCCACCTTC 398

RESULT 18
BM488278
LOCUS       BM488278                673 bp    mRNA    linear   EST 07-FEB-2002
DEFINITION  pgm2n.pk007.c10 Normalized Chicken Breast Muscle, Leg Muscle, and
            Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA
            clone pgm2n.pk007.c10 5' similar to ref|XP_008393.3 (XM_008393)
            neurexin 4 [Homo sapiens], mRNA sequence.
ACCESSION   BM488278
VERSION     BM488278.1  GI:18609209
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 673)
  AUTHORS   Cogburn,L.A. and Monsonego-Ornan,E.
  TITLE     ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
            Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
            Project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Larry A. Cogburn
            University of Delaware
            Townsend Hall, Newark, DE 19717, USA
            Tel: 302-831-1335
            Fax: 302-831-2822
            Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES             Location/Qualifiers
     source          1. .673
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Commercial broiler and  Ottawa Res. Centre
                     Strains 90 & 21"
                     /db_xref="taxon:9031"
                     /clone="pgm2n.pk007.c10"
                     /sex="Male and Female"
                     /tissue_type="Breast muscle, leg muscle and epiphyseal
                     growth plate"
                     /dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9
                     ,11 weeks);growth plate(1d,7d,14d post-hatch)"
                     /lab_host="E. coli EMDH10B"
                     /clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
                     and Epiphyseal Growth Plate cDNA library (pgm2n)"
                     /note="Vector: pCMVSPORT6; Library made from equivalent
                     pools of total RNA isolated from each tissue (embryonic
                     muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
                     plate 33.3% of the final RNA pool). Single pass sequencing
                     from 5'-end"
ORIGIN

Alignment Scores:
Pred. No.:                68.6          Length:         673
Score:                    57.00         Matches:        11
Percent Similarity:       76.5%         Conservative:   2
```

```
Best Local Similarity:  64.7%          Mismatches:    4
Query Match:            35.6%          Indels:        0
DB:                     3              Gaps:          0

US-10-758-902-1 (1-30) x BM488278 (1-673)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe 17
              :::|||||||||||||||||||   |||   |||      :::|||||||||
Db         49 TGGAACACCGTCTCCTTCAACAGAGGTGCAGCCCTGCTCTTCCCCACCTTC 99

RESULT 19
AQ354093/c
LOCUS       AQ354093                760 bp    DNA     linear   GSS 24-JAN-1999
DEFINITION  CITBI-E1-2530G10.TR CITBI-E1 Homo sapiens genomic clone 2530G10,
            genomic survey sequence.
ACCESSION   AQ354093
VERSION     AQ354093.1  GI:4181266
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2530G10.TF
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .760
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2530G10"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

Alignment Scores:
Pred. No.:              79.3           Length:        760
Score:                  57.00          Matches:       11
Percent Similarity:     60.0%          Conservative:  4
Best Local Similarity:  44.0%          Mismatches:    10
Query Match:            35.6%          Indels:        0
DB:                     9              Gaps:          0

US-10-758-902-1 (1-30) x AQ354093 (1-760)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||      :::      ||||||||      |||::::::|||      ||||||
Db        156 TATAGAGTAATACATTAGAATCTGGGGAGGTTATATGACTTTCCCAATGGCATACAGATG 97

Qy         21 LeuArgAsnGluLeu 25
              :::   |||||||||
Db         96 GTTAGTAATGAGCTG 82
```

```
RESULT 20
CNS03K0S/c
LOCUS       CNS03K0S                779 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            032B21 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL247573
VERSION     AL247573.1  GI:7968585
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
   PUBMED   10899143
REFERENCE   3  (bases 1 to 779)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .779
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="032B21"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG032CA11LP1
                     end : T7"
ORIGIN

Alignment Scores:
Pred. No.:              81.6           Length:        779
Score:                  57.00          Matches:       9
Percent Similarity:     60.0%          Conservative:  6
Best Local Similarity:  36.0%          Mismatches:    10
Query Match:            35.6%          Indels:        0
DB:                     11             Gaps:          0

US-10-758-902-1 (1-30) x CNS03K0S (1-779)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||   :::   |||||||||         :::::::::||||||:::      |||
Db        626 TACAACAAATTGGACTTTAACCTCAATGGGGTGTTTGACCACCCCACCTACGCCAGTGAC 567

Qy         21 LeuArgAsnGluLeu 25
              :::   |||
Db        566 GCCACCGACCGCCTG 552

RESULT 21
AG520129
LOCUS       AG520129                782 bp    DNA     linear   GSS 22-DEC-2004
```

```
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-426M07.TJ, genomic survey
            sequence.
ACCESSION   AG520129
VERSION     AG520129.1  GI:48227542
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
  TITLE     Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
  JOURNAL   Genome Res. 14 (12), 2439-2447 (2004)
   PUBMED   15574823
REFERENCE   2  (bases 1 to 782)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : TJ
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .782
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-426M07.TJ"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

Alignment Scores:
Pred. No.:              82              Length:         782
Score:                  57.00           Matches:        12
Percent Similarity:     56.0%           Conservative:   2
Best Local Similarity:  48.0%           Mismatches:     11
Query Match:            35.6%           Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-1 (1-30) x AG520129 (1-782)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||   |||||||||||||      |||      |||:::||||||   |||      |||

Db        679 TATAAAACTGTCTCTTTCACCCCCGGTACCATTTACAAATACCCTATCTTTTCCTTGGAC 738

Qy         21 LeuArgAsnGluLeu 25
                :::      |||

Db        739 TCTAAATATCCCCTT 753

RESULT 22
DU009707
LOCUS       DU009707                939 bp    DNA     linear   GSS 12-AUG-2005
DEFINITION  241569 Tomato MboI BAC Library Lycopersicon esculentum genomic
            clone SL_MboI0047E19 5, genomic survey sequence.
ACCESSION   DU009707
VERSION     DU009707.1  GI:72406779
KEYWORDS    GSS.
SOURCE      Lycopersicon esculentum (Solanum lycopersicum)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Mueller,L.A., Buels,R.M., Wang,Y., Tanksley,S.D., Giovannoni,J.J.,
            Van Eck,J. and Stack,S.
  TITLE     BAC end sequencing from three Solanum lycopersicon libraries
  JOURNAL   Unpublished (2005)
COMMENT     Other_GSSs: 301867
            Contact: Lukas Mueller
            Tanksley Lab, Dept. of Plant Breeding
            Cornell University
            251 Emerson Hall, Ithaca, NY 14853, USA
            Tel: 607-255-6557
            Fax: 607-255-6683
            Email: sgn-feedback@sgn.cornell.edu
            Plate: 47  row: E  column: 19
            Seq primer: T7
            Class: BAC ends
            High quality sequence start: 25
            High quality sequence stop: 578.
FEATURES             Location/Qualifiers
     source          1. .939
                     /organism="Lycopersicon esculentum"
                     /mol_type="genomic DNA"
                     /cultivar="Heinz 1706"
                     /db_xref="taxon:4081"
                     /clone="SL_MboI0047E19"
                     /lab_host="E. coli"
                     /clone_lib="Tomato MboI BAC Library"
                     /note="Vector: pBeloBAC11; Site_1: MboI"
ORIGIN

Alignment Scores:
Pred. No.:              102             Length:         939
Score:                  57.00           Matches:        13
Percent Similarity:     59.3%           Conservative:   3
Best Local Similarity:  48.1%           Mismatches:     9
Query Match:            35.6%           Indels:         2
DB:                     10              Gaps:           1

US-10-758-902-1 (1-30) x DU009707 (1-939)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              |||:::   |||   |||   ||||||||||||                |||:::|||:::

Db        294 ACAATCAAATTTCAATTGTCTGAAGCTTATGAG------AAAAGCTTTCAGGAGTTGAAA 347

Qy         23 AsnGluLeuAlaLysGlyThr 29
                |||   |||      ||||||

Db        348 AATAGATTGATGACAGGAACT 368

RESULT 23
CE644685/c
LOCUS       CE644685                578 bp    DNA     linear   GSS 29-SEP-2003
DEFINITION  tigr-gss-dog-17000367128444 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE644685
VERSION     CE644685.1  GI:36963105
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
```

```
          Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
          Venter,J.C.
  TITLE   The dog genome: survey sequencing and comparative analysis
  JOURNAL Science 301 (5641), 1898-1903 (2003)
   PUBMED 14512627
COMMENT   Contact: Kirkness EF
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0200
          Fax: 301-838-0208
          Email: ekirknes@tigr.org
          Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .578
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

Alignment Scores:
Pred. No.:              69.5          Length:       578
Score:                  56.50         Matches:      12
Percent Similarity:     63.3%         Conservative: 7
Best Local Similarity:  40.0%         Mismatches:   10
Query Match:            35.3%         Indels:       1
DB:                     10            Gaps:         1

US-10-758-902-1 (1-30) x CE644685 (1-578)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||||||||:::      :::   ||||||:::      ||||||      :::   |||
Db        572 TACAATACTATGTTGAATAGCAGTGGTGAGAGT---GGATATCCCTGTCTTGTTCCTGAT 516

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
                ||||||   ::::::|||      :::|||
Db        515 CTTAGGGGAAAGGTTGCCAGTGCTTCCCCA 486

RESULT 24
CR528387
LOCUS       CR528387                271 bp    mRNA    linear   EST 07-JUL-2004
DEFINITION  CR528387 Normalized Anopheles Head (NAH) Library Anopheles gambiae
            cDNA clone AGAGP45TR, mRNA sequence.
ACCESSION   CR528387
VERSION     CR528387.1  GI:49926364
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 271)
  AUTHORS   Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.
  TITLE     Anopheles gambiae EST, Center for Tropical Disease Research and
            Training
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Frank H. Collins
            Center for Tropical Disease Research and Training
            University of Notre Dame
            Notre Dame, IN 46556, USA
            Tel: 574-631-9245
            Fax: 574-631-3996
            Email: frank.h.collins.75@nd.edu
            Contact: Frank H. Collins
            Center for Tropical Disease Research and Training
            University of Notre Dame, Notre Dame, IN 46556, USA. Tel: 574-631-
            9245
            Fax: 574-631-3996
            Email: frank.h.collins.75@nd.edu.
FEATURES             Location/Qualifiers
     source          1. .271
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /db_xref="taxon:7165"
                     /clone="AGAGP45TR"
                     /lab_host="E. coli DH10B"
                     /clone_lib="Normalized Anopheles Head (NAH) Library"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoR1 (5'end); Site_2: Not1 (3'end); a
                     directionally cloned and normalized, oligo-T primed cDNA
                     library constructed from strain 4arr adult mosquito heads.
                     Equal numbers of sugar fed males, sugar fed females and 6,
                     24 and 48 hr post blood meal females were used: Bonaldo,
                     Lennon & Soares (1996): Normalization and Subtraction: Two
                     Approaches To Facilitate Gene Discovery, Genome Research
                     6, 791-806. ESTs sequenced from the M13 reverse priming
                     site reading from the 5' ends of the cDNAs are indicated
                     by 'R' in the clone name. ESTs sequenced from the M13
                     forward priming site reading from the 3' ends of the cDNAs
                     are indicated by 'F' in the clone name."
ORIGIN

Alignment Scores:
Pred. No.:              34.4          Length:       271
Score:                  56.00         Matches:      10
Percent Similarity:     93.3%         Conservative: 4
Best Local Similarity:  66.7%         Mismatches:   1
Query Match:            35.0%         Indels:       0
DB:                     7             Gaps:         0

US-10-758-902-1 (1-30) x CR528387 (1-271)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
                :::|||||||||||||    |||:::||||||:::|||:::||||||
Db         96 AAATATCCGACCTTCCAGCAGGAGCTGCGCGATGAAATTGCAAAG 140

RESULT 25
CA533718
LOCUS       CA533718                284 bp    mRNA    linear   EST 18-NOV-2002
DEFINITION  C0405D02-5N NIA Mouse ES Cell (LIF-) cDNA Library (Long) Mus
            musculus cDNA clone NIA:C0405D02 IMAGE:30010117 5', mRNA sequence.
ACCESSION   CA533718
VERSION     CA533718.1  GI:25065088
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 284)
  AUTHORS   Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K.,
            Jaradat,S.A., Boheler,K.R. and Ko,M.S.H.
  TITLE     Systematic Analyses of NIA Mouse ES Cell (LIF-) cDNA Library (Long)
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: C0405D02-3
            Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: C0405  row: D  column: 02
            Seq primer: M13 Reverse
            High quality sequence stop: 284
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .284
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129/Sv x 129/Sv-CP"
                     /db_xref="niaEST:C0405D02-5N"
                     /db_xref="taxon:10090"
                     /clone="NIA:C0405D02 IMAGE:30010117"
```

/tissue_type="ES Cell (LIF-)"
/cell_line="R1 ES cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse ES Cell (LIF-) cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Kenneth R. Boheler (National Institute on Aging, USA). ES cells were cultured without feeder cells in the absence of LIF for 4 hours or 18 hours. Equimolar mixture of these RNA samples was used for the library construction. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from 21 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao (NIA)."
ORIGIN

Alignment Scores:

Pred. No.:	36.4	Length:	284
Score:	56.00	Matches:	11
Percent Similarity:	64.0%	Conservative:	5
Best Local Similarity:	44.0%	Mismatches:	9
Query Match:	35.0%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x CA533718 (1-284)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::          |||
Db        133 TCCCATGAGTTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGGTTCCGAGAA 192

Qy         25 LeuAlaLysGlyThr 29
                |||:::||||||
Db        193 TTTGCTCGAGGCACA 207
```

RESULT 26
AA783170
LOCUS AA783170 423 bp mRNA linear EST 29-JUL-1998
DEFINITION c1g09a1.r2 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone c1g09a1 5', mRNA sequence.
ACCESSION AA783170
VERSION AA783170.1 GI:2843338
KEYWORDS EST.
SOURCE Emericella nidulans (anamorph: Aspergillus nidulans)
ORGANISM Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
REFERENCE 1 (bases 1 to 423)
AUTHORS Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: c1g09a1.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: SK
High quality sequence stop: 394.
FEATURES Location/Qualifiers
source 1. .423
/organism="Emericella nidulans"
/mol_type="mRNA"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="c1g09a1"
/tissue_type="vegetative mycelia, asexual structures"
/clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"
ORIGIN

Alignment Scores:

Pred. No.:	58.3	Length:	423
Score:	56.00	Matches:	11
Percent Similarity:	64.0%	Conservative:	5
Best Local Similarity:	44.0%	Mismatches:	9
Query Match:	35.0%	Indels:	0
DB:	1	Gaps:	0

US-10-758-902-1 (1-30) x AA783170 (1-423)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||   |||   ::::::|||         |||      ||||||   ::::::|||||||
Db        237 AACATCGTATTCTACCATCTCCTTCATCTCTACGCTAACCCGACGCTCCTGGAGGATCTT 296

Qy         22 ArgAsnGluLeuAla 26
              |||   |||:::|||
Db        297 CGAAAGGAGATCGCC 311
```

RESULT 27
BY555839/c
LOCUS BY555839 451 bp mRNA linear EST 14-DEC-2002
DEFINITION BY555839 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730313G11 3', mRNA sequence.
ACCESSION BY555839
VERSION BY555839.1 GI:26890218
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 451)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,

```
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="F730313G11"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
ORIGIN

Alignment Scores:
Pred. No.:              62.9          Length:         451
Score:                  56.00         Matches:        12
Percent Similarity:     50.0%         Conservative:   2
Best Local Similarity:  42.9%         Mismatches:     14
Query Match:            35.0%         Indels:         0
DB:                     5             Gaps:           0

US-10-758-902-1 (1-30) x BY555839 (1-451)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||   :::   |||||||||      ||||||   ||||||   ||||||
Db        100 AATCCTCTTGGCTTCAACCTCCCGAGTGCATATACATACCCGGCATTCATCACCCTGTGC 41

Qy         22 ArgAsnGluLeuAlaLysGlyThr 29
                  |||       |||:::
Db         40 TACCAGCATCTGGTCCCAGGATCA 17

RESULT 28
BH879393
LOCUS       BH879393                506 bp    DNA     linear   GSS 05-AUG-2002
DEFINITION  ht46b11.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
            genomic clone ht46b11 5', genomic survey sequence.
ACCESSION   BH879393
VERSION     BH879393.1  GI:22115290
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
            Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
            Zutavern,T., McCombie,W.R. and Martienssen,R.A.
  TITLE     Genomic shotgun sequences from Zea mays (methyl-filtered)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: ht46  row: b  column: 11
            Seq primer: -21M13UnivFwd
            Class: shotgun
            High quality sequence stop: 506.
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ht46b11"
                     /lab_host="JM107 or DH5a"
                     /clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
                     /note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
                     The vector was digested with XbaI and one nucleotide was
                     added by  fill in in the recessive 3' end. The genomic DNA
                     was nebulized, end  repaired, adaptor ligated and size
                     fractionated using sephadex. The  resulting fragments were
                     between 0.8 and 3 kb and were cloned into  the vector
                     (.x/y reads in M13mp19, .b/g reads in pUC19). The same
                     ligation was transformed in either JM107 or DH5a. "
ORIGIN

Alignment Scores:
Pred. No.:              72            Length:         506
Score:                  56.00         Matches:        16
Percent Similarity:     48.7%         Conservative:   3
Best Local Similarity:  41.0%         Mismatches:     8
Query Match:            35.0%         Indels:         12
DB:                     9             Gaps:           2

US-10-758-902-1 (1-30) x BH879393 (1-506)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        280 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 336

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        337 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 393

RESULT 29
```

```
BG556183
LOCUS       BG556183                529 bp    mRNA    linear   EST 10-APR-2001
DEFINITION  EM1_68_G08.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
            sequence.
ACCESSION   BG556183
VERSION     BG556183.1  GI:13585181
KEYWORDS    EST.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 529)
  AUTHORS   Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
  TITLE     An EST database from Sorghum: developing embryos
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: JEN REV
            High quality sequence stop: 516
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .529
                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /db_xref="taxon:4558"
                     /clone_lib="Embryo 1 (EM1)"
                     /note="Organ: Embryos germinated for 24 hr; Vector:
                     pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
                     EcoRI; The library was made from poly-A RNA in the cloning
                     vector lambda ZAP II.  Clones to be sequenced were
                     prepared by mass excision."
ORIGIN

Alignment Scores:
Pred. No.:                75.9          Length:         529
Score:                    56.00         Matches:        16
Percent Similarity:       48.7%         Conservative:   3
Best Local Similarity:    41.0%         Mismatches:     8
Query Match:              35.0%         Indels:         12
DB:                       2             Gaps:           2

US-10-758-902-1 (1-30) x BG556183 (1-529)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        404 ACAGTTAATTTCAAT---GGGGAGATGTTCGAGAGCCCCGCGTTTTGTTCTACTTTGCGG 460

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        461 CAGGCGGAGCATGCGGCAGCTGAGGTAGCGCTCAATGAGTTATCGAAGAGGGGCCCT 517

RESULT 30
CF428375
LOCUS       CF428375                657 bp    mRNA    linear   EST 03-SEP-2003
DEFINITION  PH1_14_B02.g1_A002 Phosphorous-deficient seedlings Sorghum bicolor
            cDNA clone PH1_14_B02_A002 5', mRNA sequence.
ACCESSION   CF428375
VERSION     CF428375.1  GI:34441076
KEYWORDS    EST.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 657)
  AUTHORS   Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C.,
            Sun,F., Sullivan,R., Harris,K., Eastman,A. and Pratt,L.H.
  TITLE     An EST database from Sorghum: phosphorous-deficient seedlings
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: PH1_14_B02.b1_A002
            Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
            the Human Genome Center, University of Tokyo Institute of Medical
            Science; plant material and RNA prepared at Texas A & M University;
            sequencing done in the Laboratory for Genomics and Bioinformatics,
            University of Georgia. Sequence ends have been trimmed to exclude
            vector and regions below Phred quality 16. Three-prime sequences
            are presented as their reverse complement and have been trimmed to
            exclude polyA.
            Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
FEATURES             Location/Qualifiers
     source          1. .657
                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /cultivar="BTx623"
                     /db_xref="taxon:4558"
                     /clone="PH1_14_B02_A002"
                     /lab_host="DH10B-T1 phage-resistant E. coli"
                     /clone_lib="Phosphorous-deficient seedlings"
                     /note="Vector: pME18S-FL3; Site_1: XhoI; Site_2: XhoI; The
                     library was prepared from polyA+ RNA from BTx623 seedlings
                     grown hydroponically in the absence of added phosphorous.
                     At 14 days of age, roots and shoots were harvested and
                     stored at -80 C until RNA was isolated. Double-stranded
                     cDNA was cloned unidirectionally into different DraIII
                     sites of the pME18S-FL3 vector (5-prime DraIII site is
                     CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises
                     the cDNA insert."
ORIGIN

Alignment Scores:
Pred. No.:                98.1          Length:         657
Score:                    56.00         Matches:        16
Percent Similarity:       48.7%         Conservative:   3
Best Local Similarity:    41.0%         Mismatches:     8
Query Match:              35.0%         Indels:         12
DB:                       6             Gaps:           2

US-10-758-902-1 (1-30) x CF428375 (1-657)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        393 ACAGTTAATTTCAAT---GGGGAGATGTTCGAGAGCCCCGCGTTTTGTTCTACTTTGCGG 449

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        450 CAGGCGGAGCATGCGGCAGCTGAGGTAGCGCTCAATGAGTTATCGAAGAGGGGCCCT 506

RESULT 31
AZ364827
LOCUS       AZ364827                665 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0111E17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0111E17 F, genomic survey sequence.
ACCESSION   AZ364827
VERSION     AZ364827.1  GI:10478527
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
```

```
REFERENCE   1  (bases 1 to 665)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0111  row: E  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 665.
FEATURES             Location/Qualifiers
     source          1. .665
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0111E17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

Alignment Scores:
Pred. No.:              99.6          Length:        665
Score:                  56.00         Matches:       14
Percent Similarity:     75.0%         Conservative:  7
Best Local Similarity:  50.0%         Mismatches:    4
Query Match:            35.0%         Indels:        3
DB:                     9             Gaps:          1

US-10-758-902-1 (1-30) x AZ364827 (1-665)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              ::::::||||||||||||:::|||   |||   |||      ||||||   :::|||:::
Db         69 TTAAATTTTAACCTGGGGCAAGCAACTGAGGTGCCT------ATTCAACAGATCAGATCA 122

Qy         24 GluLeuAlaLys-GlyThrPro 30
              :::|||||||   |||:::|||
Db        123 GACCTGGCCTCCAGGTTCTCCC 144

RESULT 32
DR801301
LOCUS       DR801301                684 bp    mRNA    linear   EST 27-JUL-2005
DEFINITION  ZM_BFb0025A18.r ZM_BFb Zea mays cDNA 5', mRNA sequence.
ACCESSION   DR801301
VERSION     DR801301.1  GI:71329184
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
            Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
  TITLE     Maize Full-length cDNA Project
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yeisoo Yu
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9585
            Fax: 520 621 1259
            Email: yeisoo@genome.arizona.edu
            Plate: 0025  row: A  column: 18.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /tissue_type="mixed (silks, husks, ears, pollen, shoot
                     tips, leaf, root tips, whole seed, embryo)"
                     /dev_stage="varies by tissue"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="ZM_BFb"
                     /note="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
                     NotI; Maize Full length cDNA library (3530 library)
                     created by Invitrogen from multiple tissues; Organ: silks,
                     husks, ears, pollen, shoot tips, leaf, root tips, whole
                     seed, embryo. This is a Gateway compatible vector,
                     permitting clone movement to new vector backbones for
                     expression in diverse host cells using recombination
                     rather than restriction enzymes. poly(A)+ mRNA was
                     prepared by Invitrogen, and equimolar amounts of RNA from
                     each of the 12 tissue samples were mixed together for
                     selection of mRNA with a 5' cap. After synthesis of cDNA,
                     a normalization step was conducted against the mixture of
                     RNA sources. Tissues prepared: 1. just emerging silks; 2.
                     inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
                     immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
                     2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
                     15 day old seedlings; all leaves with an expanded or
                     partially expanded sheath were removed; 8. mature leaf
                     tissue; 9. 0.5 cm long root tips from 15 day old
                     seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
                     embryo; 12. 17 dap endosperm and embryo. All of the
                     sequenced clones in Maize Full-length cDNA Project will be
                     archived at the University of Arizona. Clones, high
                     density filters and amplified library can be ordered from
                     the University of Arizona
                     (http://www.genome.arizona.edu/orders/)."
ORIGIN

Alignment Scores:
Pred. No.:              103           Length:        684
Score:                  56.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.0%         Indels:        12
DB:                     8             Gaps:          2

US-10-758-902-1 (1-30) x DR801301 (1-684)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
```

```
Db        363 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 419

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        420 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 476

RESULT 33
CW658238/c
LOCUS       CW658238                731 bp    DNA     linear   GSS 28-OCT-2004
DEFINITION  OG_BBa0009M05.f OG_BBa Oryza glaberrima genomic clone OG_BBa0009M05
            5', genomic survey sequence.
ACCESSION   CW658238
VERSION     CW658238.1  GI:54787983
KEYWORDS    GSS.
SOURCE      Oryza glaberrima (African rice)
  ORGANISM  Oryza glaberrima
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Kim,H., Yu,Y., Wissotski,M., Byrne,M., Stum,D., Smart,D., Rao,K.,
            Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C.
            and Wing,R.
  TITLE     OMAP
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0009  row: M  column: 05
            Seq primer: TAA TAC GAC TCA CTA TAG GG
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .731
                     /organism="Oryza glaberrima"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4538"
                     /clone="OG_BBa0009M05"
                     /tissue_type="young leaves"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="OG_BBa"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Alignment Scores:
Pred. No.:              111           Length:        731
Score:                  56.00         Matches:       11
Percent Similarity:     58.3%         Conservative:  3
Best Local Similarity:  45.8%         Mismatches:    10
Query Match:            35.0%         Indels:        0
DB:                     10            Gaps:          0

US-10-758-902-1 (1-30) x CW658238 (1-731)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              |||||||||      ||||||   |||||||||   ||||||:::      |||
Db        613 GTATCGTTCACCACCGGTGAGGGCTACGAATATTGGACATTTGTATTGAGCCTCGGAGGT 554

Qy         24 GluLeuAlaLys 27
              :::      :::
Db        553 CAGTATACAAGG 542

RESULT 34
CF933557
LOCUS       CF933557                857 bp    mRNA    linear   EST 17-NOV-2003
DEFINITION  TrEST-B09H03.g TrEST-B Hypocrea jecorina cDNA clone Tr-B09H03.g 5',
            mRNA sequence.
ACCESSION   CF933557
VERSION     CF933557.1  GI:38353378
KEYWORDS    EST.
SOURCE      Hypocrea jecorina (anamorph: Trichoderma reesei)
  ORGANISM  Hypocrea jecorina
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE   1  (bases 1 to 857)
  AUTHORS   Bonaccorsi,E.D., Chambergo,F.S. and El-Dorry,H.
  TITLE     TrEST-B
  JOURNAL   Unpublished (2003)
COMMENT     Contact: El-Dorry, Hamza
            Department of Biochemistry
            Institute of Chemistry. University of Sao Paulo
            Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,
            BRASIL
            Tel: (55) 11-38183848
            Fax: (55) 11-38183848
            Email: dorry@iq.usp.br
            PCR PRimers
            FORWARD: Universal M13 forward primer
            BACKWARD: Universal M13 reverse primer
            Plate: 09  row: H  column: 03
            Seq primer: M13 reverse primer
            High quality sequence start: 32
            High quality sequence stop: 484
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .857
                     /organism="Hypocrea jecorina"
                     /mol_type="mRNA"
                     /strain="QM9414 (ATCC26921)"
                     /db_xref="taxon:51453"
                     /clone="Tr-B09H03.g"
                     /sex="Asexual"
                     /tissue_type="Mycelia"
                     /dev_stage="Mycelial culture grown from 100 mM and
                     harvested to 80 mM glicose concentrations."
                     /lab_host="E. coli DH10B cells (streptomycin resistant)"
                     /clone_lib="TrEST-B"
                     /note="Vector: pUC18; cDNA cloned into SmaI site of pUC18.
                     Average insert size: 1 kb"
ORIGIN

Alignment Scores:
Pred. No.:              134           Length:        857
Score:                  56.00         Matches:       10
Percent Similarity:     75.0%         Conservative:  5
Best Local Similarity:  50.0%         Mismatches:    5
Query Match:            35.0%         Indels:        0
DB:                     7             Gaps:          0

US-10-758-902-1 (1-30) x CF933557 (1-857)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||:::      ||||||:::||||||:::||||||      |||::::::|||   |||
Db        520 GCATGGAGCACGCCTACATGGATCCAGGAGTTGCGCGGCTCCCTATCCAGAGGGAGGCCT 579

RESULT 35
BZ814229/c
LOCUS       BZ814229                911 bp    DNA     linear   GSS 17-MAR-2003
DEFINITION  PUFGM69TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa314K17,
            genomic survey sequence.
ACCESSION   BZ814229
VERSION     BZ814229.1  GI:29026582
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 911)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
```

```
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFGM69TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .911
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa314K17"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

Alignment Scores:
Pred. No.:              145           Length:        911
Score:                  56.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.0%         Indels:        12
DB:                     9             Gaps:          2

US-10-758-902-1 (1-30) x BZ814229 (1-911)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        810 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 754

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||     |||
Db        753 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 697

RESULT 36
BU161967/c
LOCUS       BU161967                949 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_7971897 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6169906
            5', mRNA sequence.
ACCESSION   BU161967
VERSION     BU161967.1  GI:22675877
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 949)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13535  row: m  column: 11
            High quality sequence stop: 606.
FEATURES             Location/Qualifiers
     source          1. .949
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6169906"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_67"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb.   Library constructed by Life
                     Technologies."
ORIGIN

Alignment Scores:
Pred. No.:              152           Length:        949
Score:                  56.00         Matches:       13
Percent Similarity:     53.3%         Conservative:  3
Best Local Similarity:  43.3%         Mismatches:    12
Query Match:            35.0%         Indels:        2
DB:                     5             Gaps:          1

US-10-758-902-1 (1-30) x BU161967 (1-949)

Qy          3 ThrValSerPheAsnLeuGly------GluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||   ||||||   ||||||      :::   |||:::||||||   |||
Db        830 ACCACCAGTTTCCCTCTGGGCCAACAGGACCAGTACCAATACCCCCCATTTTGTAGCCAT 771

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||            |||:::|||   |||
Db        770 CTGGAAGAGGCAGGCGCAAGGGGTTGTCCA 741

RESULT 37
BQ952169
LOCUS       BQ952169                963 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8945692 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6459826
            5', mRNA sequence.
ACCESSION   BQ952169
VERSION     BQ952169.1  GI:22367647
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 963)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2645  row: i  column: 11
            High quality sequence stop: 601.
FEATURES             Location/Qualifiers
     source          1. .963
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6459826"
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_101"
                     /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
                     XhoI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
```

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	154	Length:	963
Score:	56.00	Matches:	11
Percent Similarity:	63.6%	Conservative:	3
Best Local Similarity:	50.0%	Mismatches:	8
Query Match:	35.0%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-1 (1-30) x BQ952169 (1-963)

```
Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              ||||||||||||      :::|||   |||:::   |||       |||       |||:::
Db        680 CTGGGGGAAGCGAATGTCCACCCTTGATTCGTCCATGATTTTGCGAATGCCTTTGCCCGC 739

Qy         28 GlyThr 29
              ||||||
Db        740 GGCACC 745
```

RESULT 38
CZ994983/c
LOCUS CZ994983 970 bp DNA linear GSS 11-AUG-2005
DEFINITION 183000 Tomato MboI BAC Library Lycopersicon esculentum genomic clone SL_MboI0088N11 5, genomic survey sequence.
ACCESSION CZ994983
VERSION CZ994983.1 GI:72346628
KEYWORDS GSS.
SOURCE Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 970)
AUTHORS Mueller,L.A., Buels,R.M., Wang,Y., Tanksley,S.D., Giovannoni,J.J., Van Eck,J. and Stack,S.
TITLE BAC end sequencing from three Solanum lycopersicon libraries
JOURNAL Unpublished (2005)
COMMENT Other_GSSs: 320666
Contact: Lukas Mueller
Tanksley Lab, Dept. of Plant Breeding
Cornell University
251 Emerson Hall, Ithaca, NY 14853, USA
Tel: 607-255-6557
Fax: 607-255-6683
Email: sgn-feedback@sgn.cornell.edu
Plate: 88 row: N column: 11
Seq primer: T7
Class: BAC ends
High quality sequence start: 13
High quality sequence stop: 444.

FEATURES Location/Qualifiers
source 1. .970
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/cultivar="Heinz 1706"
/db_xref="taxon:4081"
/clone="SL_MboI0088N11"
/lab_host="E. coli"
/clone_lib="Tomato MboI BAC Library"
/note="Vector: pBeloBAC11; Site_1: MboI"

ORIGIN

Alignment Scores:

Pred. No.:	156	Length:	970
Score:	56.00	Matches:	12
Percent Similarity:	51.7%	Conservative:	3
Best Local Similarity:	41.4%	Mismatches:	14
Query Match:	35.0%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-1 (1-30) x CZ994983 (1-970)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||||||||      ||||||:::      |||   |||       |||       |||
Db        875 TATAATACTAGAAAATTCAATGTGAGGGTTGAATATATTTATGGACTCTTCTATAGTGAT 816

Qy         21 LeuArgAsnGluLeuAlaLysGlyThr 29
              |||       |||       :::|||:::
Db        815 CTGATGAGGGAATGGAAAAGAGGTAGT 789
```

RESULT 39
CL999228
LOCUS CL999228 991 bp DNA linear GSS 23-SEP-2004
DEFINITION ZMMBHf0012p04.r ZMMBHf Zea mays genomic clone ZMMBHf0012p04 3', genomic survey sequence.
ACCESSION CL999228
VERSION CL999228.1 GI:52571609
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 991)
AUTHORS Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and Bennetzen,J.
TITLE ZMMBH sequences
JOURNAL Unpublished (2004)
COMMENT Contact: Jeff Bennetzen
Bennetzen Lab
The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, GA 30602, USA
Tel: 706-542-3698
Fax: 706-583-0972
Email: maize@uga.edu
Plate: 0012 row: p column: 04
Class: BAC ends.

FEATURES Location/Qualifiers
source 1. .991
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBHf0012p04"
/tissue_type="immature ear"
/dev_stage="6-8 weeks"
/lab_host="DH10B"
/clone_lib="ZMMBHf"
/note="Vector: TOPOpcr4; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Alignment Scores:

Pred. No.:	160	Length:	991
Score:	56.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.0%	Indels:	12
DB:	10	Gaps:	2

US-10-758-902-1 (1-30) x CL999228 (1-991)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||           ||||||
Db        542 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 598

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||       |||
Db        599 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 655
```

RESULT 40
CL987992

```
LOCUS       CL987992                994 bp    DNA     linear   GSS 23-SEP-2004
DEFINITION  ZMMBHe0004n18.r ZMMBHe Zea mays genomic clone ZMMBHe0004n18 3',
            genomic survey sequence.
ACCESSION   CL987992
VERSION     CL987992.1  GI:52556070
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 994)
  AUTHORS   Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and
            Bennetzen,J.
  TITLE     ZMMBH sequences
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Jeff Bennetzen
            Bennetzen Lab
            The University of Georgia
            Department of Genetics, C426a Life Sciences Building, Athens, GA
            30602, USA
            Tel: 706-542-3698
            Fax: 706-583-0972
            Email: maize@uga.edu
            Plate: 0004  row: n  column: 18
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .994
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBHe0004n18"
                     /tissue_type="immature ear"
                     /dev_stage="6-8 weeks"
                     /lab_host="DH10B"
                     /clone_lib="ZMMBHe"
                     /note="Vector: TOPOpcr4; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              160           Length:        994
Score:                  56.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.0%         Indels:        12
DB:                     10            Gaps:          2

US-10-758-902-1 (1-30) x CL987992 (1-994)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db        440 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 496

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        497 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 553

Search completed: February 20, 2006, 02:07:37
Job time : 1065.7 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:54:27 ; Search time 1211.56 Seconds
(without alignments)
1407.522 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 30
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgappp 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 1

Total number of hits satisfying chosen parameters: 11757716

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160833_4016/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10758902_@CGN_1_1_5142_@runat_17022006_160833_4016 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30	100.0	1085	15	AY437531	AY437531 Bougainvi
2	30	100.0	1387	15	AF445416	AF445416 Bougainvi
3	21	70.0	65	6	A82770	A82770 Sequence 5
4	21	70.0	65	6	AR454120	AR454120 Sequence
5	14	46.7	363	6	A82773	A82773 Sequence 8
6	14	46.7	363	6	AR454123	AR454123 Sequence
c 7	9	30.0	1637	5	BC086634	BC086634 Xenopus l
c 8	9	30.0	191191	8	AC000119	AC000119 Homo sapi
9	9	30.0	198134	14	AC024117	AC024117 Homo sapi
10	8	26.7	1238	6	AX069004	AX069004 Sequence
11	8	26.7	2108	8	BC069192	BC069192 Homo sapi
12	8	26.7	2134	8	AF374416	AF374416 Homo sapi
13	8	26.7	2291	6	CQ845798	CQ845798 Sequence
14	8	26.7	2291	8	AK131393	AK131393 Homo sapi
c 15	8	26.7	7046	5	BC084217	BC084217 Xenopus l
16	8	26.7	15626	2	AF507073	AF507073 Trypanoso
17	8	26.7	17981	14	AC153364_5	Continuation (6 of
c 18	8	26.7	42282	2	CEC08H9	Z54342 Caenorhabdi
19	8	26.7	47872	14	AC106844	AC106844 Mus muscu
c 20	8	26.7	78680	8	AC010228	AC010228 Homo sapi
21	8	26.7	110000	14	AC153364_4	Continuation (5 of
c 22	8	26.7	110000	14	TANN3_10	Continuation (11 o
23	8	26.7	110000	15	CR380954_08	Continuation (9 of
c 24	8	26.7	138187	2	AC159438	AC159438 Trypanoso
25	8	26.7	142422	9	AL844588	AL844588 Mouse DNA
c 26	8	26.7	148008	14	AC130471	AC130471 Homo sapi
c 27	8	26.7	148142	8	AC011421	AC011421 Homo sapi
c 28	8	26.7	155629	14	AC108196	AC108196 Felis cat
29	8	26.7	165802	8	AL135914	AL135914 Human DNA
c 30	8	26.7	172714	9	AC112269	AC112269 Mus muscu
31	8	26.7	175178	14	AC011783	AC011783 Homo sapi
c 32	8	26.7	187816	9	AL606919	AL606919 Mouse DNA
c 33	8	26.7	189341	14	AC147190	AC147190 Otolemur
34	8	26.7	194520	9	AL691424	AL691424 Mouse DNA
c 35	8	26.7	196162	9	AC108508	AC108508 Genomic s
36	8	26.7	206806	14	AC147189	AC147189 Otolemur
c 37	8	26.7	207845	14	AC108507	AC108507 Mus muscu
38	8	26.7	230706	14	AC134261	AC134261 Rattus no
39	8	26.7	258088	14	AC131516	AC131516 Rattus no
40	8	26.7	265438	14	AC129451	AC129451 Rattus no
41	8	26.7	283054	14	AC160292	AC160292 Bos tauru
c 42	8	26.7	307462	14	AC112828	AC112828 Rattus no
43	7	23.3	23	6	A82768	A82768 Sequence 3
c 44	7	23.3	23	6	A82769	A82769 Sequence 4
45	7	23.3	23	6	AR454118	AR454118 Sequence
c 46	7	23.3	23	6	AR454119	AR454119 Sequence
47	7	23.3	25	6	A82771	A82771 Sequence 6
48	7	23.3	25	6	AR454121	AR454121 Sequence
49	7	23.3	194	1	AF500162	AF500162 Salmonell
c 50	7	23.3	431	6	CQ486483	CQ486483 Sequence
51	7	23.3	439	6	AR128236	AR128236 Sequence
c 52	7	23.3	484	6	CQ892691	CQ892691 Sequence
c 53	7	23.3	484	15	NTA538552	AJ538552 Nicotiana
c 54	7	23.3	498	6	CQ516297	CQ516297 Sequence
c 55	7	23.3	511	10	BV366443	BV366443 S231P6131
c 56	7	23.3	513	4	AF536282	AF536282 Equus cab
c 57	7	23.3	537	10	G79395	G79395 S209P6132RD
c 58	7	23.3	543	6	AX462317	AX462317 Sequence
c 59	7	23.3	574	15	PAB292701	AJ292701 Picea abi
60	7	23.3	588	6	CQ523157	CQ523157 Sequence
61	7	23.3	588	6	AX436488	AX436488 Sequence
62	7	23.3	596	10	BV004188	BV004188 S208P6407
c 63	7	23.3	605	10	BV258337	BV258337 S235P6343
64	7	23.3	651	6	AR393990	AR393990 Sequence
c 65	7	23.3	654	10	BV295335	BV295335 S232P613F
66	7	23.3	690	10	BV455485	BV455485 pzr79d02.
67	7	23.3	693	6	AX436495	AX436495 Sequence
c 68	7	23.3	709	10	BV616484	BV616484 S215P6135
69	7	23.3	731	6	AR655413	AR655413 Sequence
c 70	7	23.3	745	10	BV591022	BV591022 G591P6420
71	7	23.3	778	10	BV495826	BV495826 S217P6165
c 72	7	23.3	787	10	BV481469	BV481469 svu15c06.
c 73	7	23.3	806	10	BV564499	BV564499 qzh19d12.
c 74	7	23.3	834	10	BV658812	BV658812 S215P6148
75	7	23.3	946	10	BV573697	BV573697 G591P6055
76	7	23.3	1048	10	BV179291	BV179291 sqnm10472

c 77	7	23.3	1143	6	BD062321	BD062321 Solution-
78	7	23.3	1145	15	AY507353	AY507353 Fossombro
c 79	7	23.3	1146	8	CR542268	CR542268 Homo sapi
c 80	7	23.3	1146	11	AY335755	AY335755 Synthetic
c 81	7	23.3	1357	6	CQ722265	CQ722265 Sequence
c 82	7	23.3	1360	6	AX330198	AX330198 Sequence
c 83	7	23.3	1360	6	AX409622	AX409622 Sequence
c 84	7	23.3	1360	8	HUMCKB	M16364 Human creat
85	7	23.3	1364	15	DQ013264	DQ013264 Bougainvi
c 86	7	23.3	1372	8	HUMCKBBA	M16451 Human creat
c 87	7	23.3	1386	8	HUMCKBR	L47647 Homo sapien
c 88	7	23.3	1400	15	CSRIO1GEN	X96739 S.cerevisia
c 89	7	23.3	1418	8	BC004914	BC004914 Homo sapi
c 90	7	23.3	1424	8	BC008323	BC008323 Homo sapi
c 91	7	23.3	1426	8	BC001190	BC001190 Homo sapi
c 92	7	23.3	1426	8	BC019259	BC019259 Homo sapi
c 93	7	23.3	1431	6	CS115048	CS115048 Sequence
c 94	7	23.3	1431	6	CS119660	CS119660 Sequence
c 95	7	23.3	1432	6	CS080610	CS080610 Sequence
c 96	7	23.3	1432	6	CS119176	CS119176 Sequence
c 97	7	23.3	1440	8	BC010002	BC010002 Homo sapi
c 98	7	23.3	1447	8	BC019281	BC019281 Homo sapi
99	7	23.3	1554	6	AX416290	AX416290 Sequence
100	7	23.3	1710	15	DQ000309	DQ000309 Nicotiana
101	7	23.3	1778	5	AY049813	AY049813 Callorhin
c 102	7	23.3	1912	6	E38307	E38307 Gene encodi
c 103	7	23.3	1917	6	E38306	E38306 Gene encodi
104	7	23.3	1965	5	BC090219	BC090219 Xenopus l
105	7	23.3	2167	15	BT013813	BT013813 Lycopersi
106	7	23.3	2172	15	NTGLUTLIG	X83524 N.tabacum m
c 107	7	23.3	2184	2	AY147845	AY147845 Taenia sa
108	7	23.3	2211	1	AF112480	AF112480 Anaplasma
c 109	7	23.3	2218	2	AJ616851	AJ616851 Taenia sa
110	7	23.3	2229	1	AF110808	AF110808 Anaplasma
111	7	23.3	2232	1	AF111197	AF111197 Anaplasma
112	7	23.3	2235	1	AF111195	AF111195 Anaplasma
113	7	23.3	2260	15	AK120017	AK120017 Oryza sat
114	7	23.3	2274	1	AY841153	AY841153 Anaplasma
115	7	23.3	2289	1	AF348137	AF348137 Anaplasma
c 116	7	23.3	2320	14	AC019380	AC019380 Drosophil
c 117	7	23.3	2343	6	AR084972	AR084972 Sequence
118	7	23.3	2410	1	AF221693	AF221693 Anaplasma
119	7	23.3	2470	15	AF267870	AF267870 Schizophy
120	7	23.3	2553	15	SCYOR119C	Z75027 S.cerevisia
121	7	23.3	2556	6	AR264297	AR264297 Sequence
c 122	7	23.3	2704	2	AB073429	AB073429 Ciona sav
c 123	7	23.3	2730	1	ATVIRAL	X05241 Agrobacteri
c 124	7	23.3	2822	5	BC057538	BC057538 Danio rer
125	7	23.3	2845	1	LHPRLSABC	Z30709 L.helveticu
126	7	23.3	2980	1	APMMSP1B	M59845 Anaplasma m
c 127	7	23.3	3016	6	AR379714	AR379714 Sequence
c 128	7	23.3	3023	1	AF116773	AF116773 Salmonell
c 129	7	23.3	3035	13	AF134509	AF134509 Kadipiro
c 130	7	23.3	3216	6	E38305	E38305 Gene encodi
c 131	7	23.3	3216	15	AB018407	AB018407 Coriolus
c 132	7	23.3	3224	6	E38304	E38304 Gene encodi
c 133	7	23.3	3224	15	AB018406	AB018406 Coriolus
134	7	23.3	3225	6	AR047984	AR047984 Sequence
135	7	23.3	3225	6	AR064703	AR064703 Sequence
136	7	23.3	3225	6	AR087767	AR087767 Sequence
137	7	23.3	3225	6	AX968570	AX968570 Sequence
138	7	23.3	3640	15	AY311527	AY311527 Solanum t
c 139	7	23.3	3679	14	AC018083	AC018083 Drosophil
c 140	7	23.3	4261	5	BC084220	BC084220 Xenopus l
c 141	7	23.3	4534	13	BLCMPOLY	M21951 Germiston b
c 142	7	23.3	4590	14	AC014474	AC014474 Drosophil
143	7	23.3	4772	1	AF221692	AF221692 Anaplasma
144	7	23.3	4962	6	CQ598061	CQ598061 Sequence
145	7	23.3	4995	6	CQ598058	CQ598058 Sequence
c 146	7	23.3	5648	9	AK172922	AK172922 Mus muscu
147	7	23.3	6249	8	HSM808726	BX648575 Homo sapi
c 148	7	23.3	7893	6	BD193634	BD193634 Enterococ
149	7	23.3	8245	9	AF388573	AF388573 Mus muscu
150	7	23.3	9471	6	AR264288	AR264288 Sequence
c 151	7	23.3	9720	1	PSDNGC	Z73914 Pseudomonas
152	7	23.3	9804	6	CQ598055	CQ598055 Sequence
153	7	23.3	10029	1	AE006253	AE006253 Lactococc
154	7	23.3	10100	8	AP005897	AP005897 Homo sapi
c 155	7	23.3	10475	6	I08101	I08101 Sequence 4
c 156	7	23.3	10475	6	I08711	I08711 Sequence 9
c 157	7	23.3	10476	6	AX334892	AX334892 Sequence
c 158	7	23.3	10476	6	AX335346	AX335346 Sequence
c 159	7	23.3	10476	8	HUMSPBAA	M24461 Human pulmo
c 160	7	23.3	10968	6	AR029638	AR029638 Sequence
c 161	7	23.3	10968	6	AR157372	AR157372 Sequence
c 162	7	23.3	10968	15	LEU65391	U65391 Lycopersico
c 163	7	23.3	11095	1	AE010229	AE010229 Pyrococcu
c 164	7	23.3	11807	8	AF400074	AF400074 Homo sapi
c 165	7	23.3	12828	1	LLCPJW565	Y12736 Lactococcus
166	7	23.3	20922	1	AE008726	AE008726 Salmonell
167	7	23.3	24684	14	AC133917	AC133917 Homo sapi
168	7	23.3	27188	2	U61950	U61950 Caenorhabdi
c 169	7	23.3	31466	8	AC003955	AC003955 Homo sapi
170	7	23.3	32900	2	AF025469	AF025469 Caenorhab
c 171	7	23.3	36502	2	CEF17B5	Z81066 Caenorhabdi
172	7	23.3	37754	2	U23519	U23519 Caenorhabdi
c 173	7	23.3	40124	14	AY714840	AY714840 Unculture
174	7	23.3	40679	7	AY052766	AY052766 Salmonell
175	7	23.3	40705	14	AC017405	AC017405 Drosophil
176	7	23.3	41391	7	AB102868	AB102868 Salmonell
c 177	7	23.3	41700	8	AC108140	AC108140 Homo sapi
178	7	23.3	42021	2	CEC05D12	Z50872 Caenorhabdi
179	7	23.3	42809	14	AC018237	AC018237 Drosophil
c 180	7	23.3	43254	2	AF016443	AF016443 Caenorhab
181	7	23.3	46463	2	U49830	U49830 Caenorhabdi
c 182	7	23.3	50916	14	AC068439	AC068439 Homo sapi
183	7	23.3	50984	15	SCXVORFS	X90518 S.cerevisia
184	7	23.3	52954	14	AC103677	AC103677 Homo sapi
c 185	7	23.3	53951	8	AC092866	AC092866 Homo sapi
c 186	7	23.3	54886	14	AC166396	AC166396 Bos tauru
187	7	23.3	55640	8	AB001914	AB001914 Homo sapi
c 188	7	23.3	57598	8	AL513526	AL513526 Human DNA
c 189	7	23.3	58778	14	AP001959	AP001959 Homo sapi
c 190	7	23.3	60831	15	AF220602	AF220602 Lycopersi
191	7	23.3	64643	14	AC102078	AC102078 Mus muscu
192	7	23.3	68185	14	AC151900_3	Continuation (4 of
193	7	23.3	69718	8	AC006474	AC006474 Homo sapi
c 194	7	23.3	71120	14	AC124800	AC124800 Homo sapi
c 195	7	23.3	71302	14	AC087760	AC087760 Homo sapi
c 196	7	23.3	71506	8	AC092452	AC092452 Homo sapi
197	7	23.3	73872	14	AC133558	AC133558 Homo sapi
c 198	7	23.3	75388	5	BX936441	BX936441 Zebrafish
199	7	23.3	79438	8	HSDJ547C9	AL109927 Human DNA
200	7	23.3	79729	14	AC165503	AC165503 Bos tauru
c 201	7	23.3	81404	13	AY653733_11	Continuation (12 o
c 202	7	23.3	85237	8	HSDJ653C5	AL049743 Human DNA
c 203	7	23.3	87135	14	AC023808	AC023808 Mus muscu
c 204	7	23.3	88746	8	AC009321	AC009321 Homo sapi
c 205	7	23.3	90406	14	AC133297	AC133297 Rattus no
c 206	7	23.3	90417	14	AC156055	AC156055 Bos tauru
207	7	23.3	90594	14	AC116126	AC116126 Mus muscu
c 208	7	23.3	90594	14	AC116126	AC116126 Mus muscu
c 209	7	23.3	91206	2	AC005735	AC005735 Drosophil
c 210	7	23.3	92488	14	AP007315	AP007315 Lotus cor
c 211	7	23.3	93156	8	AY640177	AY640177 Homo sapi
212	7	23.3	93324	8	AL139119	AL139119 Human DNA
213	7	23.3	94081	8	HSJ820B18	AL109946 Human DNA
214	7	23.3	94410	8	AL355275	AL355275 Human DNA
215	7	23.3	95665	15	AP004163	AP004163 Oryza sat
c 216	7	23.3	96348	2	AC165428_7	Continuation (8 of
c 217	7	23.3	96597	6	AX695698	AX695698 Sequence
218	7	23.3	99033	8	AC005704	AC005704 Homo sapi
c 219	7	23.3	99399	15	AC135103	AC135103 Medicago
c 220	7	23.3	99606	14	AP007816	AP007816 Lotus cor
221	7	23.3	100259	8	AC005800	AC005800 Homo sapi
c 222	7	23.3	102484	8	HS510H16	AL008635 Human DNA

c	223	7	23.3	102752	8	AC110288 AC110288 Homo sapi
c	224	7	23.3	103532	14	AC166916 AC166916 Bos tauru
	225	7	23.3	103699	8	AC034305 AC034305 Homo sapi
	226	7	23.3	105643	8	AC005629 AC005629 Homo sapi
	227	7	23.3	106710	8	HSB7L1C4 AL078476 Homo sapi
c	228	7	23.3	107121	15	AP005559 AP005559 Oryza sat
c	229	7	23.3	107482	15	BX908789 BX908789 Neurospor
c	230	7	23.3	108932	8	AF067845 AF067845 Homo sapi
	231	7	23.3	108937	8	AC098593 AC098593 Homo sapi
	232	7	23.3	109179	14	CR962121 CR962121 Medicago
	233	7	23.3	110000	1	AE016827_09 Continuation (10 o
	234	7	23.3	110000	1	AE016853_53 Continuation (54 o
	235	7	23.3	110000	1	AE017220_07 Continuation (8 of
	236	7	23.3	110000	1	AE017225_47 Continuation (48 o
	237	7	23.3	110000	1	AE017334_47 Continuation (48 o
c	238	7	23.3	110000	1	AE017340_18 Continuation (19 o
	239	7	23.3	110000	1	AE017340_27 Continuation (28 o
c	240	7	23.3	110000	1	AE017354_26 Continuation (27 o
	241	7	23.3	110000	1	AE017355_47 Continuation (48 o
	242	7	23.3	110000	1	AP006618_35 Continuation (36 o
	243	7	23.3	110000	1	AP006627_04 Continuation (5 of
c	244	7	23.3	110000	1	BA000004_11 Continuation (12 o
	245	7	23.3	110000	1	BA000019_33 Continuation (34 o
	246	7	23.3	110000	1	BA000031_26 Continuation (27 o
c	247	7	23.3	110000	1	BA000037_22 Continuation (23 o
	248	7	23.3	110000	1	CP000001_48 Continuation (49 o
c	249	7	23.3	110000	1	CP000021_03 Continuation (4 of
c	250	7	23.3	110000	1	CP000026_21 Continuation (22 o
c	251	7	23.3	110000	1	CP000030_00 CP000030 Anaplasma
	252	7	23.3	110000	1	CP000030_01 Continuation (2 of
c	253	7	23.3	110000	1	CP000030_01 Continuation (2 of
c	254	7	23.3	110000	1	CP000083_17 Continuation (18 o
c	255	7	23.3	110000	14	AC087331_3 Continuation (4 of
	256	7	23.3	110000	14	CR954209_0 CR954209 Ostreococ
	257	7	23.3	110000	14	CR954209_1 Continuation (2 of
c	258	7	23.3	110000	14	CR954213_2 Continuation (3 of
c	259	7	23.3	110000	14	CT005257_4 Continuation (5 of
c	260	7	23.3	110000	14	CT005269_08 Continuation (9 of
	261	7	23.3	110000	14	LMFLCHR18_06 Continuation (7 of
c	262	7	23.3	110000	14	TANN2_00 CR940348 Theileria
	263	7	23.3	110000	15	AP008214_273 Continuation (274
c	264	7	23.3	110000	15	AP008215_168 Continuation (169
	265	7	23.3	110000	15	AP008217_176 Continuation (177
	266	7	23.3	110000	15	AP008217_239 Continuation (240
c	267	7	23.3	110000	15	AP008218_069 Continuation (70 o
	268	7	23.3	110000	15	CR380950_4 Continuation (5 of
c	269	7	23.3	110000	15	CR380956_00 CR380956 Candida g
c	270	7	23.3	110000	15	CR382129_13 Continuation (14 o
	271	7	23.3	110000	15	CR382138_14 Continuation (15 o
c	272	7	23.3	110000	15	AE017351_06 Continuation (7 of
	273	7	23.3	110000	15	AP008207_422 Continuation (423
c	274	7	23.3	110000	15	AP008210_085 Continuation (86 o
	275	7	23.3	110000	15	AP008212_129 Continuation (130
c	276	7	23.3	110000	15	AP008212_266 Continuation (267
	277	7	23.3	110885	8	HS191E19 AL034451 Human DNA
	278	7	23.3	113613	8	AC097524 AC097524 Homo sapi
c	279	7	23.3	116621	8	AL596106 AL596106 Human DNA
	280	7	23.3	116960	8	AL356362 AL356362 Human DNA
c	281	7	23.3	117481	14	AC160617 AC160617 Loxodonta
	282	7	23.3	118889	14	AC017230 AC017230 Drosophil
	283	7	23.3	119296	8	HS836E8 AL031679 Human DNA
	284	7	23.3	121088	15	AP004326 AP004326 Oryza sat
	285	7	23.3	121884	15	AC123975 AC123975 Medicago
c	286	7	23.3	122289	8	AL389925 AL389925 Human DNA
	287	7	23.3	122504	14	AC147508 AC147508 Phytophth
c	288	7	23.3	122504	14	AC147508 AC147508 Phytophth
	289	7	23.3	122523	4	CR956361 CR956361 Pig DNA s
	290	7	23.3	123176	9	AC156934 AC156934 Mus muscu
	291	7	23.3	124025	8	AL160169 AL160169 Human DNA
c	292	7	23.3	124181	14	AC166228 AC166228 Sorex ara
c	293	7	23.3	125792	8	AC090365 AC090365 Homo sapi
c	294	7	23.3	126270	8	AC005283 AC005283 Homo sapi
c	295	7	23.3	126541	15	AC124962 AC124962 Medicago
c	296	7	23.3	126581	8	AC003957 AC003957 Homo sapi
	297	7	23.3	126757	15	AP003619 AP003619 Oryza sat
c	298	7	23.3	127039	14	AP001127 AP001127 Homo sapi
c	299	7	23.3	129033	9	AL954701 AL954701 Mouse DNA
	300	7	23.3	129171	5	CR759889 CR759889 Zebrafish
	301	7	23.3	129528	15	SC130KBXV X94335 S.cerevisia
c	302	7	23.3	130119	14	AC160226 AC160226 Loxodonta
	303	7	23.3	130347	14	AC141963 AC141963 Rattus no
	304	7	23.3	132093	14	AC141964 AC141964 Rattus no
c	305	7	23.3	132600	14	AL355675 AL355675 Homo sapi
c	306	7	23.3	132966	14	AP001277 AP001277 Homo sapi
	307	7	23.3	133030	8	AC004863 AC004863 Homo sapi
c	308	7	23.3	133846	14	AP001276 AP001276 Homo sapi
c	309	7	23.3	134108	9	AC102538 AC102538 Mus muscu
c	310	7	23.3	134423	15	AP004803 AP004803 Oryza sat
	311	7	23.3	134896	8	AC006571 AC006571 Homo sapi
	312	7	23.3	134953	14	AC026088 AC026088 Homo sapi
	313	7	23.3	135715	9	AC157803 AC157803 Mus muscu
	314	7	23.3	136613	14	AC090379 AC090379 Homo sapi
	315	7	23.3	138007	14	AC141282 AC141282 Homo sapi
c	316	7	23.3	138412	8	AC117481 AC117481 Homo sapi
	317	7	23.3	139353	14	AC149636 AC149636 Medicago
c	318	7	23.3	139932	14	AC024297 AC024297 Homo sapi
	319	7	23.3	140156	14	AC027261 AC027261 Homo sapi
c	320	7	23.3	142201	8	AC124248 AC124248 Homo sapi
c	321	7	23.3	142762	14	AL391599 AL391599 Homo sapi
	322	7	23.3	142908	5	BX936403 BX936403 Zebrafish
	323	7	23.3	142965	8	AC087528 AC087528 Homo sapi
	324	7	23.3	143036	9	AL732611 AL732611 Mouse DNA
c	325	7	23.3	143597	14	AC151505 AC151505 Dasypus n
	326	7	23.3	143626	4	AJ630366 AJ630366 Canis fam
	327	7	23.3	143834	8	AC004960 AC004960 Homo sapi
	328	7	23.3	144563	15	CNS08C7P AL731740 Oryza sat
	329	7	23.3	145481	8	AL356862 AL356862 Human DNA
	330	7	23.3	146099	14	AC121625 AC121625 Rattus no
	331	7	23.3	146189	15	AC121244 AC121244 Medicago
c	332	7	23.3	146453	4	AY152827 AY152827 Felis cat
c	333	7	23.3	146843	8	AC096761 AC096761 Homo sapi
c	334	7	23.3	146928	14	AC135775 AC135775 Homo sapi
c	335	7	23.3	147079	8	AL772262 AL772262 Human DNA
c	336	7	23.3	147592	14	AC122105 AC122105 Rattus no
	337	7	23.3	147801	15	AC136150 AC136150 Oryza sat
	338	7	23.3	148498	15	AC125780 AC125780 Oryza sat
c	339	7	23.3	148952	8	AY679523 AY679523 Homo sapi
	340	7	23.3	149400	15	AC121327 AC121327 Oryza sat
c	341	7	23.3	149542	8	AC011711 AC011711 Homo sapi
c	342	7	23.3	149951	8	AC018375 AC018375 Homo sapi
c	343	7	23.3	150007	15	OSJN00248 AL731598 Oryza sat
c	344	7	23.3	150817	14	AC021762 AC021762 Homo sapi
	345	7	23.3	150986	14	AL139386 AL139386 Homo sapi
c	346	7	23.3	151770	14	CR925754 CR925754 Danio rer
c	347	7	23.3	151941	8	AC108131 AC108131 Homo sapi
c	348	7	23.3	152405	9	AC125318 AC125318 Mus muscu
	349	7	23.3	153094	14	AC096715 AC096715 Homo sapi
c	350	7	23.3	153137	8	AC016995 AC016995 Homo sapi
	351	7	23.3	153304	8	AC084834 AC084834 Homo sapi
c	352	7	23.3	153609	8	HSAJ9617 AJ009617 Homo sapi
	353	7	23.3	153751	2	AC116551 AC116551 Dictyoste
c	354	7	23.3	154227	14	CR628323 CR628323 Danio rer
c	355	7	23.3	154537	15	AP005393 AP005393 Oryza sat
	356	7	23.3	154939	8	AC022537 AC022537 Homo sapi
	357	7	23.3	155112	8	AC144898 AC144898 Homo sapi
c	358	7	23.3	155270	9	AC130837 AC130837 Mus muscu
	359	7	23.3	155313	8	AC006453 AC006453 Homo sapi
	360	7	23.3	155751	9	AC132347 AC132347 Mus muscu
c	361	7	23.3	156024	8	AC104300 AC104300 Homo sapi
c	362	7	23.3	156351	8	AC092133 AC092133 Homo sapi
	363	7	23.3	157248	8	AC002312 AC002312 Human Chr
c	364	7	23.3	157385	8	AC006023 AC006023 Homo sapi
c	365	7	23.3	158052	8	AC027612 AC027612 Homo sapi
	366	7	23.3	158574	15	AP003763 AP003763 Oryza sat
	367	7	23.3	158817	8	AP005353 AP005353 Homo sapi
c	368	7	23.3	158846	9	AC154241 AC154241 Mus muscu

	369	7	23.3	158847	5	AL928619 AL928619 Zebrafish
c	370	7	23.3	159120	14	AC021395 AC021395 Homo sapi
c	371	7	23.3	159575	14	AC141407 AC141407 Homo sapi
c	372	7	23.3	159625	9	AC154717 AC154717 Mus muscu
	373	7	23.3	159691	14	AC132764 AC132764 Rattus no
c	374	7	23.3	159909	14	AC019352 AC019352 Homo sapi
	375	7	23.3	160704	15	AP003238 AP003238 Oryza sat
	376	7	23.3	160780	5	AL935142 AL935142 Zebrafish
	377	7	23.3	161251	14	AC147284 AC147284 Pan trogl
c	378	7	23.3	161387	14	AC016929 AC016929 Homo sapi
c	379	7	23.3	161500	8	AC103778 AC103778 Homo sapi
	380	7	23.3	161567	8	HS594J14 AL445595 Homo sapi
	381	7	23.3	161708	5	CR545467 CR545467 Zebrafish
	382	7	23.3	162107	14	AP002423 AP002423 Homo sapi
	383	7	23.3	162608	8	AC009478 AC009478 Homo sapi
c	384	7	23.3	162810	8	AC006382 AC006382 Homo sapi
c	385	7	23.3	163004	8	AC137675 AC137675 Homo sapi
c	386	7	23.3	163025	14	AC016366 AC016366 Homo sapi
c	387	7	23.3	163260	14	AC091049 AC091049 Homo sapi
	388	7	23.3	163404	5	BX470132 BX470132 Zebrafish
	389	7	23.3	163541	8	AC068954 AC068954 Homo sapi
c	390	7	23.3	163570	8	AC016910 AC016910 Homo sapi
c	391	7	23.3	163579	8	AC093563 AC093563 Homo sapi
c	392	7	23.3	163595	14	AC022076 AC022076 Homo sapi
	393	7	23.3	163835	8	AC136488 AC136488 Homo sapi
c	394	7	23.3	163862	14	AC092911 AC092911 Homo sapi
c	395	7	23.3	163915	14	AC140236 AC140236 Mus muscu
	396	7	23.3	163935	15	OEL271079 AJ271079 Oenothera
c	397	7	23.3	164000	8	AL591682 AL591682 Human DNA
	398	7	23.3	164259	14	AC142091 AC142091 Sus scrof
c	399	7	23.3	164339	14	AC025792 AC025792 Homo sapi
	400	7	23.3	164468	8	AC136489 AC136489 Homo sapi
c	401	7	23.3	164656	14	AC149122 AC149122 Papio anu
	402	7	23.3	164906	8	AC096637 AC096637 Homo sapi
c	403	7	23.3	165082	14	AC026559 AC026559 Homo sapi
	404	7	23.3	165191	8	HSDJ140A9 AL109917 Human DNA
	405	7	23.3	165225	8	AC116050 AC116050 Homo sapi
c	406	7	23.3	165383	5	BX470196 BX470196 Zebrafish
	407	7	23.3	165624	9	AC162918 AC162918 Mus muscu
c	408	7	23.3	165655	8	AL136962 AL136962 Human DNA
	409	7	23.3	165714	9	AC103376 AC103376 Mus muscu
	410	7	23.3	165796	9	AC102401 AC102401 Mus muscu
	411	7	23.3	165833	8	AC012157 AC012157 Homo sapi
c	412	7	23.3	165888	14	AC025555 AC025555 Homo sapi
c	413	7	23.3	165924	4	AC150752 AC150752 Bos tauru
	414	7	23.3	165962	8	AC092185 AC092185 Homo sapi
c	415	7	23.3	166036	14	AC041013 AC041013 Homo sapi
c	416	7	23.3	166449	5	BX548166 BX548166 Zebrafish
c	417	7	23.3	166490	15	AP003712 AP003712 Oryza sat
c	418	7	23.3	166685	14	AL353601 AL353601 Homo sapi
	419	7	23.3	167036	14	AC148855 AC148855 Otolemur
c	420	7	23.3	167053	9	AC124447 AC124447 Mus muscu
	421	7	23.3	167198	14	AC148509 AC148509 Macropus
c	422	7	23.3	167381	5	BX571817 BX571817 Zebrafish
c	423	7	23.3	167831	14	AC027723 AC027723 Homo sapi
c	424	7	23.3	168009	9	AC102342 AC102342 Mus muscu
c	425	7	23.3	168471	9	AC126598 AC126598 Mus muscu
	426	7	23.3	168544	14	AC024334 AC024334 Homo sapi
c	427	7	23.3	168546	8	AC135776 AC135776 Homo sapi
	428	7	23.3	168754	14	AC027487 AC027487 Homo sapi
c	429	7	23.3	168927	14	AC155469 AC155469 Zea mays
c	430	7	23.3	168956	8	AC090286 AC090286 Homo sapi
	431	7	23.3	169442	8	AC110766 AC110766 Homo sapi
	432	7	23.3	170533	14	CR762388 CR762388 Danio rer
c	433	7	23.3	170607	9	AC133650 AC133650 Mus muscu
	434	7	23.3	170720	8	AC009309 AC009309 Homo sapi
	435	7	23.3	171046	14	AC159681 AC159681 Bos tauru
c	436	7	23.3	171058	8	AC138559 AC138559 Lemur cat
	437	7	23.3	171089	8	AC006368 AC006368 Homo sapi
	438	7	23.3	171161	9	AC105980 AC105980 Mus muscu
c	439	7	23.3	171307	14	AL355820 AL355820 Homo sapi
	440	7	23.3	171375	2	AC007082 AC007082 Drosophil
c	441	7	23.3	171501	8	AL359704 AL359704 Human DNA
c	442	7	23.3	171563	2	AC007890 AC007890 Drosophil
c	443	7	23.3	171621	8	AP003177 AP003177 Homo sapi
	444	7	23.3	171856	9	AC126607 AC126607 Mus muscu
	445	7	23.3	172025	9	AC115835 AC115835 Mus muscu
c	446	7	23.3	172460	14	AC079798 AC079798 Homo sapi
	447	7	23.3	172676	8	AC015711 AC015711 Homo sapi
	448	7	23.3	173191	8	AL596114 AL596114 Human DNA
	449	7	23.3	173331	9	AC126022 AC126022 Mus muscu
	450	7	23.3	173988	5	BX072572 BX072572 Zebrafish
c	451	7	23.3	174204	14	AC073956 AC073956 Homo sapi
	452	7	23.3	174239	14	AC073830 AC073830 Homo sapi
c	453	7	23.3	174345	14	AC025236 AC025236 Homo sapi
	454	7	23.3	174646	14	AC087355 AC087355 Homo sapi
	455	7	23.3	174673	8	AC019187 AC019187 Homo sapi
	456	7	23.3	175179	8	AC005237 AC005237 Homo sapi
c	457	7	23.3	175493	9	AC157516 AC157516 Mus muscu
	458	7	23.3	175639	9	AL662931 AL662931 Mouse DNA
c	459	7	23.3	176320	8	AP003028 AP003028 Homo sapi
	460	7	23.3	176320	14	AC158349 AC158349 Mus muscu
c	461	7	23.3	176322	14	AC161096 AC161096 Callicebu
	462	7	23.3	176987	14	AC103356 AC103356 Mus muscu
	463	7	23.3	177160	8	AC019089 AC019089 Homo sapi
c	464	7	23.3	177284	5	BX072575 BX072575 Zebrafish
c	465	7	23.3	177505	14	CR556712 CR556712 Danio rer
c	466	7	23.3	177748	14	AC016185 AC016185 Homo sapi
c	467	7	23.3	177925	14	AC116087 AC116087 Rattus no
	468	7	23.3	177947	14	AC074022 AC074022 Homo sapi
c	469	7	23.3	178201	14	AC019169 AC019169 Homo sapi
	470	7	23.3	178555	14	AC027397 AC027397 Homo sapi
	471	7	23.3	178705	8	AC011131 AC011131 Homo sapi
	472	7	23.3	178895	14	AC148063 AC148063 Bos tauru
c	473	7	23.3	179064	9	AC129081 AC129081 Mus muscu
c	474	7	23.3	179085	8	AC011611 AC011611 Homo sapi
c	475	7	23.3	179096	9	AC110160 AC110160 Mus muscu
	476	7	23.3	179382	9	AC109612 AC109612 Mus muscu
	477	7	23.3	180331	14	CR751602 CR751602 Danio rer
c	478	7	23.3	180465	8	AC074011 AC074011 Homo sapi
	479	7	23.3	180816	14	AC113230 AC113230 Sus scrof
c	480	7	23.3	180816	14	AC113230 AC113230 Sus scrof
	481	7	23.3	180893	14	AC160719 AC160719 Callicebu
c	482	7	23.3	180951	14	AC157665 AC157665 Mus muscu
	483	7	23.3	181041	14	AC087677 AC087677 Homo sapi
c	484	7	23.3	181120	9	AC161148 AC161148 Mus muscu
c	485	7	23.3	181258	14	AC147355 AC147355 Xenopus t
	486	7	23.3	181618	14	AL442129 AL442129 Homo sapi
	487	7	23.3	181642	5	BX890611 BX890611 Zebrafish
	488	7	23.3	182011	9	AC121806 AC121806 Mus muscu
c	489	7	23.3	182137	14	AC150920 AC150920 Bos tauru
	490	7	23.3	182156	9	AC140220 AC140220 Mus muscu
c	491	7	23.3	182295	14	AP001501 AP001501 Homo sapi
	492	7	23.3	182411	8	AC068044 AC068044 Homo sapi
	493	7	23.3	182520	9	AL627392 AL627392 Mouse DNA
c	494	7	23.3	182832	14	AC131529 AC131529 Rattus no
	495	7	23.3	183325	9	AC122256 AC122256 Mus muscu
c	496	7	23.3	183671	8	AC023024 AC023024 Homo sapi
	497	7	23.3	183766	2	AC009845 AC009845 Drosophil
	498	7	23.3	184346	9	AC122283 AC122283 Mus muscu
c	499	7	23.3	184448	8	CNS018OZ AL109766 Human chr
	500	7	23.3	184498	14	AC145823 AC145823 Pan trogl
c	501	7	23.3	184616	5	CR925821 CR925821 Zebrafish
c	502	7	23.3	184767	14	AC084363 AC084363 Homo sapi
	503	7	23.3	184896	14	AC113229 AC113229 Sus scrof
c	504	7	23.3	184896	14	AC113229 AC113229 Sus scrof
c	505	7	23.3	185061	2	AC023750 AC023750 Drosophil
	506	7	23.3	185318	5	AC145963 AC145963 Gallus ga
c	507	7	23.3	185369	9	AL671860 AL671860 Mouse DNA
	508	7	23.3	185512	8	AC012454 AC012454 Homo sapi
	509	7	23.3	185672	14	BX640474 BX640474 Danio rer
	510	7	23.3	185879	14	AC135705 AC135705 Rattus no
	511	7	23.3	186063	14	AC156926 AC156926 Bos tauru
c	512	7	23.3	186491	8	AC148705 AC148705 Macaca mu
c	513	7	23.3	186858	8	AL356585 AL356585 Human DNA
c	514	7	23.3	187081	9	AC124421 AC124421 Mus muscu

c 515	7	23.3	187203	14	AP000832	AP000832 Homo sapi
c 516	7	23.3	187776	14	AC163114	AC163114 Bos tauru
517	7	23.3	188049	14	AC069391	AC069391 Homo sapi
c 518	7	23.3	188193	2	AY449458	AY449458 Oikopleur
519	7	23.3	188335	9	AC118733	AC118733 Mus muscu
520	7	23.3	188359	14	AC141404	AC141404 Homo sapi
c 521	7	23.3	188700	9	AC121525	AC121525 Mus muscu
522	7	23.3	188708	9	AC107710	AC107710 Mus muscu
c 523	7	23.3	188709	9	AC125075	AC125075 Mus muscu
c 524	7	23.3	188802	14	AC113864	AC113864 Rattus no
525	7	23.3	188883	9	AC121257	AC121257 Mus muscu
526	7	23.3	189765	8	HS353E16	AL031591 Human DNA
c 527	7	23.3	190175	14	AC137330	AC137330 Rattus no
c 528	7	23.3	190225	8	AC023983	AC023983 Homo sapi
c 529	7	23.3	190647	9	AC154550	AC154550 Mus muscu
c 530	7	23.3	190651	8	AL353811	AL353811 Human DNA
531	7	23.3	190676	14	CR847904	CR847904 Danio rer
532	7	23.3	190711	8	AF254983	AF254983 Homo sapi
533	7	23.3	190925	14	AL606665	AL606665 Homo sapi
c 534	7	23.3	191176	14	AC162429	AC162429 Bos tauru
c 535	7	23.3	191204	8	AP000843	AP000843 Homo sapi
c 536	7	23.3	191240	14	AC027738	AC027738 Homo sapi
c 537	7	23.3	191698	14	AC141072	AC141072 Homo sapi
538	7	23.3	191847	14	CR735111	CR735111 Danio rer
c 539	7	23.3	191855	9	AC154104	AC154104 Mus muscu
540	7	23.3	192000	1	AE001438	AE001438 Clostridi
c 541	7	23.3	192664	14	AC013466	AC013466 Homo sapi
c 542	7	23.3	192753	5	BX248118	BX248118 Zebrafish
c 543	7	23.3	192912	9	AL607091	AL607091 Mouse DNA
c 544	7	23.3	193093	14	AC146935	AC146935 Canis fam
c 545	7	23.3	193471	14	AC163686	AC163686 Mus muscu
546	7	23.3	193527	14	AC087770	AC087770 Homo sapi
547	7	23.3	193779	14	AP001327	AP001327 Homo sapi
548	7	23.3	194006	8	AC074044	AC074044 Homo sapi
c 549	7	23.3	194321	14	CR936926	CR936926 Danio rer
550	7	23.3	194631	14	AC134314	AC134314 Macaca mu
551	7	23.3	194760	8	CNS01RG7	AL157792 Human chr
552	7	23.3	194916	14	AC129846	AC129846 Rattus no
c 553	7	23.3	194950	14	AC055115	AC055115 Homo sapi
c 554	7	23.3	195529	14	AC025612	AC025612 Homo sapi
c 555	7	23.3	195625	14	AC134809	AC134809 Rattus no
c 556	7	23.3	195985	14	AC141251	AC141251 Homo sapi
557	7	23.3	196206	8	AC012368	AC012368 Homo sapi
558	7	23.3	196320	8	AL731559	AL731559 Human DNA
559	7	23.3	196337	8	AL358975	AL358975 Human DNA
c 560	7	23.3	196509	14	AL928549	AL928549 Danio rer
c 561	7	23.3	196625	9	AC160399	AC160399 Mus muscu
c 562	7	23.3	197109	14	AC141252	AC141252 Homo sapi
c 563	7	23.3	197398	9	AL732360	AL732360 Mouse DNA
564	7	23.3	197652	14	CR956621	CR956621 Sus scrof
565	7	23.3	197720	9	AC121791	AC121791 Mus muscu
566	7	23.3	197761	9	AC022235	AC022235 Mus muscu
c 567	7	23.3	198442	14	AC160256	AC160256 Bos tauru
568	7	23.3	198444	5	BX470065	BX470065 Zebrafish
569	7	23.3	199363	14	BX897749	BX897749 Danio rer
570	7	23.3	199400	9	AC155727	AC155727 Mus muscu
571	7	23.3	199593	9	AL808137	AL808137 Mouse DNA
572	7	23.3	199825	8	AC099570	AC099570 Homo sapi
c 573	7	23.3	200147	14	AC022774	AC022774 Mus muscu
c 574	7	23.3	200237	5	BX548063	BX548063 Zebrafish
c 575	7	23.3	200253	9	AC162382	AC162382 Mus muscu
576	7	23.3	200592	9	AC112789	AC112789 Mus muscu
577	7	23.3	202161	14	AC158808	AC158808 Mus muscu
578	7	23.3	202505	14	AP000912	AP000912 Homo sapi
579	7	23.3	202837	8	AC127384	AC127384 Homo sapi
580	7	23.3	203798	14	CR854931	CR854931 Danio rer
c 581	7	23.3	203875	14	CR848841	CR848841 Danio rer
582	7	23.3	204179	9	AC099607	AC099607 Mus muscu
583	7	23.3	204888	9	AL731800	AL731800 Mouse DNA
584	7	23.3	204964	5	BX545855	BX545855 Zebrafish
585	7	23.3	205666	14	BX511067	BX511067 Danio rer
586	7	23.3	206121	14	AC122362	AC122362 Mus muscu
c 587	7	23.3	207144	9	AC099711	AC099711 Mus muscu
c 588	7	23.3	207840	14	AC142383	AC142383 Homo sapi
c 589	7	23.3	207858	14	AC127132	AC127132 Rattus no
590	7	23.3	208108	14	AC158023	AC158023 Bos tauru
c 591	7	23.3	208181	14	AC016527	AC016527 Homo sapi
592	7	23.3	208232	9	AC119804	AC119804 Mus muscu
593	7	23.3	208313	14	AC120953	AC120953 Rattus no
594	7	23.3	208492	14	AC141767	AC141767 Apis mell
595	7	23.3	208932	14	AC137487	AC137487 Homo sapi
596	7	23.3	208984	9	AC101703	AC101703 Mus muscu
597	7	23.3	209176	14	AC110006	AC110006 Homo sapi
c 598	7	23.3	209448	14	AC137314	AC137314 Rattus no
599	7	23.3	210380	9	AL627238	AL627238 Mouse DNA
c 600	7	23.3	210563	8	AC034154	AC034154 Homo sapi
601	7	23.3	211261	5	BX255940	BX255940 Zebrafish
602	7	23.3	211404	14	AC097764	AC097764 Rattus no
603	7	23.3	211555	14	AC132172	AC132172 Rattus no
604	7	23.3	212001	9	AL845293	AL845293 Mouse DNA
c 605	7	23.3	212522	14	AC166058	AC166058 Mus muscu
606	7	23.3	212995	9	AC107741	AC107741 Mus muscu
607	7	23.3	213085	14	AC095379	AC095379 Rattus no
c 608	7	23.3	213155	9	AC116705	AC116705 Mus muscu
609	7	23.3	213371	9	AC117578	AC117578 Mus muscu
610	7	23.3	213440	14	AC106557	AC106557 Rattus no
611	7	23.3	213540	14	AC112652	AC112652 Homo sapi
c 612	7	23.3	213732	9	AC102110	AC102110 Mus muscu
c 613	7	23.3	213996	8	AC019115	AC019115 Homo sapi
c 614	7	23.3	214113	14	AC159286	AC159286 Mus muscu
c 615	7	23.3	214133	9	AC126261	AC126261 Mus muscu
c 616	7	23.3	214404	5	AL929507	AL929507 Zebrafish
617	7	23.3	214532	9	AC159468	AC159468 Mus muscu
c 618	7	23.3	214895	9	AL845313	AL845313 Mouse DNA
619	7	23.3	215049	14	AC113853	AC113853 Rattus no
c 620	7	23.3	215386	14	AC139261	AC139261 Homo sapi
621	7	23.3	215415	14	AC161502	AC161502 Mus muscu
c 622	7	23.3	215480	14	AC135781	AC135781 Homo sapi
c 623	7	23.3	216211	14	AC091315	AC091315 Mus muscu
c 624	7	23.3	216362	9	AC099692	AC099692 Mus muscu
625	7	23.3	216510	9	AL604062	AL604062 Mouse DNA
c 626	7	23.3	216902	9	AC131719	AC131719 Mus muscu
c 627	7	23.3	217129	9	AC158686	AC158686 Mus muscu
628	7	23.3	217462	14	CR855266	CR855266 Danio rer
629	7	23.3	217642	14	AC111542	AC111542 Rattus no
c 630	7	23.3	217904	14	AC015915	AC015915 Mus muscu
c 631	7	23.3	219139	14	AC084418	AC084418 Homo sapi
c 632	7	23.3	219212	9	AC124502	AC124502 Mus muscu
633	7	23.3	219226	14	AC133847	AC133847 Rattus no
c 634	7	23.3	219847	14	AC112743	AC112743 Rattus no
635	7	23.3	220591	14	AC166829	AC166829 Mus muscu
c 636	7	23.3	220939	14	AC110371	AC110371 Rattus no
c 637	7	23.3	221164	2	AE003722	AE003722 Drosophil
c 638	7	23.3	221467	14	AC020866	AC020866 Mus muscu
c 639	7	23.3	221524	9	AC139040	AC139040 Mus muscu
c 640	7	23.3	221980	9	AC122418	AC122418 Mus muscu
c 641	7	23.3	222888	5	AL928954	AL928954 Zebrafish
642	7	23.3	223025	14	CR854933	CR854933 Danio rer
c 643	7	23.3	224028	14	AC111276	AC111276 Rattus no
c 644	7	23.3	224709	14	AC106153	AC106153 Rattus no
645	7	23.3	224741	14	AC149652	AC149652 Bos tauru
c 646	7	23.3	224828	14	AC157113	AC157113 Bos tauru
647	7	23.3	224908	9	AC154187	AC154187 Mus muscu
c 648	7	23.3	225535	14	AC111381	AC111381 Rattus no
c 649	7	23.3	226093	14	AC098006	AC098006 Rattus no
c 650	7	23.3	226579	9	AC133525	AC133525 Mus muscu
c 651	7	23.3	227011	14	AC147847	AC147847 Otolemur
c 652	7	23.3	227529	14	AC145052	AC145052 Canis fam
c 653	7	23.3	228157	14	AC103187	AC103187 Rattus no
654	7	23.3	228208	14	AC119786	AC119786 Rattus no
c 655	7	23.3	228925	14	AC162604	AC162604 Bos tauru
c 656	7	23.3	229375	14	AC114174	AC114174 Rattus no
657	7	23.3	229396	14	AC024108	AC024108 Homo sapi
658	7	23.3	231271	14	AC117004	AC117004 Rattus no
659	7	23.3	231566	14	AL158811	AL158811 Homo sapi
c 660	7	23.3	231715	14	AC161696	AC161696 Bos tauru

	661	7	23.3	231980	14	AC094305 AC094305 Rattus no
c	662	7	23.3	232120	14	AC135153 AC135153 Rattus no
	663	7	23.3	232508	14	AC116189 AC116189 Rattus no
	664	7	23.3	232564	14	AC120973 AC120973 Rattus no
	665	7	23.3	232863	14	AC097162 AC097162 Rattus no
c	666	7	23.3	234262	14	AC110310 AC110310 Rattus no
c	667	7	23.3	234515	14	AC098639 AC098639 Rattus no
c	668	7	23.3	234812	14	AC111482 AC111482 Rattus no
	669	7	23.3	235282	14	AC152427 AC152427 Bos tauru
	670	7	23.3	236029	14	AC095288 AC095288 Rattus no
	671	7	23.3	236122	14	AC105466 AC105466 Rattus no
	672	7	23.3	236486	14	CR854911 CR854911 Danio rer
c	673	7	23.3	237091	14	AC162979 AC162979 Bos tauru
c	674	7	23.3	238317	14	AC107350 AC107350 Rattus no
	675	7	23.3	238936	14	AC111758 AC111758 Rattus no
c	676	7	23.3	239703	14	AC137015 AC137015 Rattus no
c	677	7	23.3	239994	9	AC122201 AC122201 Mus muscu
	678	7	23.3	240050	1	AL627267 AL627267 Salmonell
	679	7	23.3	240562	14	AC098895 AC098895 Rattus no
	680	7	23.3	241394	14	AC131549 AC131549 Rattus no
c	681	7	23.3	242302	14	AC131200 AC131200 Rattus no
c	682	7	23.3	242633	14	AC108957 AC108957 Rattus no
c	683	7	23.3	244042	14	AC126484 AC126484 Rattus no
c	684	7	23.3	244183	14	AC164178 AC164178 Mus muscu
c	685	7	23.3	244597	14	AC114858 AC114858 Rattus no
	686	7	23.3	244837	14	AC131162 AC131162 Rattus no
c	687	7	23.3	245113	14	AC156927 AC156927 Bos tauru
c	688	7	23.3	245377	14	AC095875 AC095875 Rattus no
c	689	7	23.3	245468	14	AC109534 AC109534 Rattus no
	690	7	23.3	247543	14	AC152283 AC152283 Bos tauru
c	691	7	23.3	247565	14	AC124873 AC124873 Rattus no
	692	7	23.3	247900	14	AC136408 AC136408 Rattus no
	693	7	23.3	248676	14	AC157007 AC157007 Bos tauru
c	694	7	23.3	249086	14	AC165164 AC165164 Mus muscu
	695	7	23.3	249263	14	AC159365 AC159365 Bos tauru
c	696	7	23.3	250033	14	AC120676 AC120676 Rattus no
	697	7	23.3	251426	14	AC111816 AC111816 Rattus no
	698	7	23.3	252914	14	AC097431 AC097431 Rattus no
c	699	7	23.3	255199	9	AL662875 AL662875 Mouse DNA
	700	7	23.3	255522	14	AC129169 AC129169 Rattus no
	701	7	23.3	256016	14	AC114903 AC114903 Mus muscu
c	702	7	23.3	256654	14	AC096311 AC096311 Rattus no
c	703	7	23.3	259798	14	AC103131 AC103131 Rattus no
	704	7	23.3	260993	14	AC127195 AC127195 Rattus no
	705	7	23.3	261198	14	AC106528 AC106528 Rattus no
	706	7	23.3	261236	14	AC119381 AC119381 Rattus no
c	707	7	23.3	261758	14	AC160009 AC160009 Bos tauru
c	708	7	23.3	262164	14	AC097853 AC097853 Rattus no
	709	7	23.3	262875	14	AC120775 AC120775 Rattus no
	710	7	23.3	262895	14	CR387980 CR387980 Danio rer
c	711	7	23.3	263036	14	AC105597 AC105597 Rattus no
c	712	7	23.3	263349	14	AC134358 AC134358 Rattus no
c	713	7	23.3	264198	14	AC156904 AC156904 Bos tauru
	714	7	23.3	265875	14	AC162081 AC162081 Bos tauru
	715	7	23.3	266205	2	AE003662 AE003662 Drosophil
c	716	7	23.3	269263	14	AC097883 AC097883 Rattus no
	717	7	23.3	269877	14	AC112041 AC112041 Rattus no
c	718	7	23.3	271253	9	AC109233 AC109233 Mus muscu
	719	7	23.3	273077	14	AC094884 AC094884 Rattus no
	720	7	23.3	273532	14	AC115408 AC115408 Rattus no
c	721	7	23.3	274551	14	AC123329 AC123329 Rattus no
	722	7	23.3	277047	14	AC137780 AC137780 Homo sapi
	723	7	23.3	281116	8	HS21C001 AL163201 Homo sapi
c	724	7	23.3	282149	14	AC152532 AC152532 Bos tauru
	725	7	23.3	287248	1	AE017280 AE017280 Bacillus
c	726	7	23.3	287560	1	AE017274 AE017274 Bacillus
	727	7	23.3	289569	14	CR382321 CR382321 Danio rer
	728	7	23.3	291205	1	AE017040 AE017040 Bacillus
	729	7	23.3	294329	14	AC159486 AC159486 Bos tauru
c	730	7	23.3	294329	14	AC159486 AC159486 Bos tauru
c	731	7	23.3	297096	14	AC120717 AC120717 Rattus no
c	732	7	23.3	300099	1	AE016841 AE016841 Salmonell
	733	7	23.3	300507	1	AE017146 AE017146 Helicobac
	734	7	23.3	300854	1	AE017014 AE017014 Bacillus
	735	7	23.3	300893	1	AE017006 AE017006 Bacillus
	736	7	23.3	302060	14	AC162075 AC162075 Bos tauru
c	737	7	23.3	302132	1	AE016955 AE016955 Enterococ
c	738	7	23.3	303370	2	AE003598 AE003598 Drosophil
	739	7	23.3	307050	2	BX538351 BX538351 Cryptospo
	740	7	23.3	308833	14	AC106408 AC106408 Rattus no
c	741	7	23.3	315761	14	AL158079 AL158079 Homo sapi
c	742	7	23.3	328965	14	AC152742 AC152742 Bos tauru
c	743	7	23.3	330399	2	AE003575 AE003575 Drosophil
c	744	7	23.3	348299	14	BX855589 BX855589 Danio rer
c	745	6	20.0	29	6	AX956410 AX956410 Sequence
	746	6	20.0	60	6	CQ545869 CQ545869 Sequence
	747	6	20.0	60	6	CQ553471 CQ553471 Sequence
	748	6	20.0	70	6	AR141386 AR141386 Sequence
	749	6	20.0	70	6	AR141401 AR141401 Sequence
	750	6	20.0	93	6	BD038444 BD038444 Sequence
	751	6	20.0	93	6	AX902911 AX902911 Sequence
c	752	6	20.0	105	6	AR029362 AR029362 Sequence
	753	6	20.0	112	10	CR379884 CR379884 Arabidops
	754	6	20.0	112	10	CR384509 CR384509 Arabidops
c	755	6	20.0	114	6	AR615554 AR615554 Sequence
	756	6	20.0	123	6	CS012428 CS012428 Sequence
	757	6	20.0	139	6	BD047424 BD047424 Sequence
	758	6	20.0	139	6	AX911891 AX911891 Sequence
c	759	6	20.0	141	15	ATH528930 AJ528930 Arabidops
	760	6	20.0	147	6	BD032886 BD032886 Sequence
	761	6	20.0	147	6	AX897353 AX897353 Sequence
	762	6	20.0	147	10	CR384726 CR384726 Arabidops
c	763	6	20.0	156	15	WPZ93885 Z93885 W.pratensis
c	764	6	20.0	160	10	AGRPD34T7 Z68680 A.gambiae S
	765	6	20.0	163	10	AB133408 AB133408 Homo sapi
	766	6	20.0	168	13	AY453195 AY453195 HIV-1 iso
	767	6	20.0	176	13	AY751810 AY751810 Human cor
	768	6	20.0	176	13	AY751811 AY751811 Human cor
	769	6	20.0	176	13	AY751812 AY751812 Human cor
	770	6	20.0	178	13	AY453187 AY453187 HIV-1 iso
	771	6	20.0	180	10	G02872 G02872 human STS W
c	772	6	20.0	183	6	CQ112537 CQ112537 Sequence
c	773	6	20.0	183	6	CQ151407 CQ151407 Sequence
c	774	6	20.0	183	6	CQ234792 CQ234792 Sequence
c	775	6	20.0	183	6	CQ346623 CQ346623 Sequence
	776	6	20.0	188	8	AY679929 AY679929 Homo sapi
	777	6	20.0	190	4	HRSAVIASH L29112 Equus cabal
c	778	6	20.0	192	10	HSPE07H07 AL009379 H.sapiens
	779	6	20.0	196	6	AR522190 AR522190 Sequence
c	780	6	20.0	198	6	CQ447279 CQ447279 Sequence
c	781	6	20.0	201	6	CQ927162 CQ927162 Sequence
c	782	6	20.0	201	10	BV175720 BV175720 sqnm83192
	783	6	20.0	208	13	AF293420 AF293420 HIV-1 iso
c	784	6	20.0	219	6	AR557193 AR557193 Sequence
c	785	6	20.0	226	6	AR520271 AR520271 Sequence
	786	6	20.0	232	10	BV118668 BV118668 PZA01268
	787	6	20.0	233	10	BV118675 BV118675 PZA01268
	788	6	20.0	234	10	BV118667 BV118667 PZA01268
	789	6	20.0	234	10	BV118673 BV118673 PZA01268
	790	6	20.0	236	10	BV118672 BV118672 PZA01268
	791	6	20.0	236	10	BV118677 BV118677 PZA01268
	792	6	20.0	239	10	G37747 G37747 SHGC-63466
	793	6	20.0	249	2	AY732238 AY732238 Pyrophoru
c	794	6	20.0	251	6	CQ708182 CQ708182 Sequence
c	795	6	20.0	253	10	BV084721 BV084721 scl287_p5
c	796	6	20.0	253	10	BV084723 BV084723 scl287_p5
c	797	6	20.0	253	10	BV084726 BV084726 scl287_p5
c	798	6	20.0	253	10	BV084727 BV084727 scl287_p5
c	799	6	20.0	254	10	BV084725 BV084725 scl287_p5
c	800	6	20.0	255	10	BV084717 BV084717 scl287_p5
c	801	6	20.0	255	10	BV084718 BV084718 scl287_p5
c	802	6	20.0	255	10	BV084719 BV084719 scl287_p5
c	803	6	20.0	255	10	BV084720 BV084720 scl287_p5
c	804	6	20.0	255	10	BV084722 BV084722 scl287_p5
c	805	6	20.0	255	10	BV084724 BV084724 scl287_p5
c	806	6	20.0	255	10	BV084728 BV084728 scl287_p5

c 807	6	20.0	255	10	BV084729	BV084729 scl287_p5
c 808	6	20.0	255	10	BV084730	BV084730 scl287_p5
c 809	6	20.0	258	6	BD045874	BD045874 Sequence
c 810	6	20.0	258	6	AX910341	AX910341 Sequence
c 811	6	20.0	258	15	AY094310	AY094310 Zea mays
c 812	6	20.0	260	9	AF271158	AF271158 Rattus no
c 813	6	20.0	261	6	CQ658510	CQ658510 Sequence
c 814	6	20.0	269	6	BD060040	BD060040 Secreted
c 815	6	20.0	270	6	AX523999	AX523999 Sequence
c 816	6	20.0	270	6	AX552737	AX552737 Sequence
c 817	6	20.0	274	15	AY021822	AY021822 Oryza sat
c 818	6	20.0	276	15	AY094300	AY094300 Zea mays
c 819	6	20.0	280	15	AY094290	AY094290 Zea mays
820	6	20.0	282	5	AY178152	AY178152 Prunella
c 821	6	20.0	283	15	AY094304	AY094304 Zea mays
822	6	20.0	284	5	AY178150	AY178150 Passer do
823	6	20.0	284	5	AY178151	AY178151 Passer mo
824	6	20.0	284	5	AY178153	AY178153 Prunella
c 825	6	20.0	284	10	BV115039	BV115039 PZA01095
c 826	6	20.0	284	15	AY094289	AY094289 Zea mays
c 827	6	20.0	284	15	AY094297	AY094297 Zea mays
c 828	6	20.0	284	15	AY094312	AY094312 Zea mays
c 829	6	20.0	284	15	AY094313	AY094313 Zea mays
c 830	6	20.0	285	2	AB076031	AB076031 Lymantria
c 831	6	20.0	285	2	AY388527	AY388527 Culex pip
832	6	20.0	285	6	AR548779	AR548779 Sequence
833	6	20.0	286	5	AY178135	AY178135 Agelaius
834	6	20.0	286	5	AY178136	AY178136 Cardinali
835	6	20.0	286	5	AY178139	AY178139 Emberiza
836	6	20.0	286	5	AY178140	AY178140 Emberiza
837	6	20.0	286	5	AY178144	AY178144 Icteria v
838	6	20.0	286	5	AY178158	AY178158 Wilsonia
c 839	6	20.0	286	6	CQ149950	CQ149950 Sequence
c 840	6	20.0	286	6	CQ233248	CQ233248 Sequence
c 841	6	20.0	286	6	CQ271182	CQ271182 Sequence
c 842	6	20.0	286	6	CQ308565	CQ308565 Sequence
c 843	6	20.0	286	6	CQ345326	CQ345326 Sequence
844	6	20.0	286	10	AL831490	AL831490 Arabidops
845	6	20.0	288	5	AF294630	AF294630 Ficedula
c 846	6	20.0	289	15	AY094303	AY094303 Zea mays
847	6	20.0	291	6	AX084086	AX084086 Sequence
848	6	20.0	291	6	AX395147	AX395147 Sequence
849	6	20.0	292	5	AF525981	AF525981 Corvus co
c 850	6	20.0	292	6	CQ670632	CQ670632 Sequence
c 851	6	20.0	292	10	BV210167	BV210167 PCR_WAG-3
c 852	6	20.0	294	15	DQ090734	DQ090734 Cordyceps
853	6	20.0	296	10	BV447444	BV447444 PZA02938
854	6	20.0	299	10	AL831514	AL831514 Arabidops
855	6	20.0	299	10	BV142160	BV142160 PZ02938 Z
856	6	20.0	300	5	AY178149	AY178149 Parus maj
c 857	6	20.0	300	6	CQ660740	CQ660740 Sequence
858	6	20.0	303	10	BV142167	BV142167 PZ02938 Z
c 859	6	20.0	305	6	CQ673421	CQ673421 Sequence
860	6	20.0	308	6	BD041604	BD041604 Sequence
861	6	20.0	308	6	AX906071	AX906071 Sequence
c 862	6	20.0	309	6	AR502233	AR502233 Sequence
c 863	6	20.0	309	6	AR517515	AR517515 Sequence
c 864	6	20.0	309	10	G36124	G36124 STS h14a185
865	6	20.0	309	10	BV142165	BV142165 PZ02938 Z
866	6	20.0	311	5	AF294633	AF294633 Phyllosco
867	6	20.0	311	8	HS22F9R	Z60426 H.sapiens C
868	6	20.0	312	10	BV142153	BV142153 PZ02938 Z
869	6	20.0	313	10	BV142161	BV142161 PZ02938 Z
870	6	20.0	314	10	BV142152	BV142152 PZ02938 Z
871	6	20.0	315	10	AU025342	AU025342 Rattus no
c 872	6	20.0	321	5	AF195842	AF195842 Rana escu
873	6	20.0	321	10	BV142155	BV142155 PZ02938 Z
c 874	6	20.0	328	10	G71831	G71831 A06734334FM
c 875	6	20.0	329	8	HSA333221	AJ333221 Homo sapi
c 876	6	20.0	330	15	AY632678	AY632678 Emericell
877	6	20.0	332	6	BD209611	BD209611 Compositi
878	6	20.0	332	6	AR341417	AR341417 Sequence
879	6	20.0	333	10	BV142154	BV142154 PZ02938 Z
880	6	20.0	333	10	BV142157	BV142157 PZ02938 Z
881	6	20.0	333	10	BV142158	BV142158 PZ02938 Z
882	6	20.0	333	10	BV142163	BV142163 PZ02938 Z
883	6	20.0	333	10	BV142164	BV142164 PZ02938 Z
884	6	20.0	333	10	BV447433	BV447433 PZA02938
885	6	20.0	335	10	BV089435	BV089435 RPAMMSEQ0
886	6	20.0	335	10	BV447449	BV447449 PZA02938
c 887	6	20.0	338	10	BV115041	BV115041 PZA01095
c 888	6	20.0	339	10	BV115040	BV115040 PZA01095
c 889	6	20.0	339	10	BV115048	BV115048 PZA01095
c 890	6	20.0	339	10	BV115049	BV115049 PZA01095
891	6	20.0	339	10	BV447446	BV447446 PZA02938
892	6	20.0	340	10	AB136955	AB136955 Homo sapi
c 893	6	20.0	340	10	BV115035	BV115035 PZA01095
c 894	6	20.0	340	10	BV115037	BV115037 PZA01095
c 895	6	20.0	340	10	BV115044	BV115044 PZA01095
c 896	6	20.0	340	10	BV115046	BV115046 PZA01095
c 897	6	20.0	340	10	BV115050	BV115050 PZA01095
c 898	6	20.0	341	10	BV094714	BV094714 RPAMMSEQ0
c 899	6	20.0	341	10	BV115036	BV115036 PZA01095
c 900	6	20.0	341	10	BV115038	BV115038 PZA01095
c 901	6	20.0	341	10	BV115042	BV115042 PZA01095
c 902	6	20.0	341	10	BV115043	BV115043 PZA01095
c 903	6	20.0	341	10	BV115045	BV115045 PZA01095
c 904	6	20.0	341	10	BV115047	BV115047 PZA01095
905	6	20.0	341	10	BV142156	BV142156 PZ02938 Z
906	6	20.0	341	10	BV142159	BV142159 PZ02938 Z
907	6	20.0	341	10	BV142162	BV142162 PZ02938 Z
908	6	20.0	341	10	BV142166	BV142166 PZ02938 Z
909	6	20.0	341	10	BV447431	BV447431 PZA02938
910	6	20.0	341	10	BV447442	BV447442 PZA02938
911	6	20.0	344	10	BX000021	BX000021 Arabidops
c 912	6	20.0	345	10	G70992	G70992 A06734334FB
913	6	20.0	346	2	AF329666	AF329666 Cicindela
914	6	20.0	347	6	AX508770	AX508770 Sequence
c 915	6	20.0	348	15	AB084856	AB084856 Schizosac
916	6	20.0	355	6	CQ515109	CQ515109 Sequence
917	6	20.0	356	13	AY356849	AY356849 HIV-1 iso
918	6	20.0	360	11	AGLMROP	X54184 Synthetic g
c 919	6	20.0	360	15	AY534935	AY534935 Ophiostom
c 920	6	20.0	360	15	AY534936	AY534936 Ophiostom
921	6	20.0	361	6	AX245157	AX245157 Sequence
c 922	6	20.0	363	8	AY392746	AY392746 Homo sapi
c 923	6	20.0	363	10	HSA081TH9	Z51903 H.sapiens (
924	6	20.0	364	10	AB147389	AB147389 Homo sapi
c 925	6	20.0	364	15	AY534928	AY534928 Leptograp
c 926	6	20.0	364	15	AY534929	AY534929 Leptograp
c 927	6	20.0	364	15	AY534930	AY534930 Leptograp
c 928	6	20.0	364	15	AY534931	AY534931 Leptograp
c 929	6	20.0	367	6	CQ057942	CQ057942 Sequence
c 930	6	20.0	367	6	CQ077250	CQ077250 Sequence
c 931	6	20.0	367	6	CQ108251	CQ108251 Sequence
c 932	6	20.0	367	6	CQ146880	CQ146880 Sequence
c 933	6	20.0	367	6	CQ182291	CQ182291 Sequence
c 934	6	20.0	367	6	CQ206687	CQ206687 Sequence
c 935	6	20.0	367	6	CQ230105	CQ230105 Sequence
c 936	6	20.0	367	6	CQ268253	CQ268253 Sequence
c 937	6	20.0	367	6	CQ305287	CQ305287 Sequence
c 938	6	20.0	367	6	CQ342488	CQ342488 Sequence
939	6	20.0	370	2	AF329658	AF329658 Cicindela
940	6	20.0	370	2	AF329659	AF329659 Cicindela
941	6	20.0	370	2	AF329662	AF329662 Cicindela
942	6	20.0	372	8	AF087425	AF087425 Homo sapi
943	6	20.0	374	10	AB141280	AB141280 Homo sapi
c 944	6	20.0	376	2	AF329656	AF329656 Cicindela
945	6	20.0	377	6	CQ417912	CQ417912 Sequence
946	6	20.0	377	13	AY356854	AY356854 HIV-1 iso
c 947	6	20.0	378	6	CQ436297	CQ436297 Sequence
c 948	6	20.0	378	8	AY499140	AY499140 Homo sapi
949	6	20.0	380	10	BV016801	BV016801 S212P6597
950	6	20.0	384	6	CQ485286	CQ485286 Sequence
951	6	20.0	385	6	AX779475	AX779475 Sequence
952	6	20.0	385	15	AF012660	AF012660 Arabidops

953	6	20.0	389	6	AX072165	AX072165 Sequence
c 954	6	20.0	390	6	BD162325	BD162325 Novel pol
c 955	6	20.0	390	6	AX120208	AX120208 Sequence
c 956	6	20.0	394	6	AX587845	AX587845 Sequence
957	6	20.0	394	13	AY356861	AY356861 HIV-1 iso
958	6	20.0	395	8	AF283067	AF283067 Homo sapi
959	6	20.0	398	10	G22257	G22257 human STS W
960	6	20.0	398	13	AY441845	AY441845 HIV-1 iso
961	6	20.0	401	10	BV189477	BV189477 sqnm16383
962	6	20.0	401	13	AY356860	AY356860 HIV-1 iso
963	6	20.0	402	6	AX618656	AX618656 Sequence
964	6	20.0	403	13	AY356847	AY356847 HIV-1 iso
965	6	20.0	403	13	AY356848	AY356848 HIV-1 iso
966	6	20.0	404	6	CQ448321	CQ448321 Sequence
967	6	20.0	407	13	AY356853	AY356853 HIV-1 iso
968	6	20.0	413	6	CQ093254	CQ093254 Sequence
969	6	20.0	413	6	CQ170611	CQ170611 Sequence
970	6	20.0	413	6	CQ253837	CQ253837 Sequence
971	6	20.0	413	6	CQ327953	CQ327953 Sequence
972	6	20.0	419	6	AX314656	AX314656 Sequence
973	6	20.0	420	13	AY587968	AY587968 HIV-1 iso
c 974	6	20.0	421	15	AY674433	AY674433 Eupenicil
975	6	20.0	423	13	AY356856	AY356856 HIV-1 iso
976	6	20.0	424	13	AY356857	AY356857 HIV-1 iso
977	6	20.0	424	13	AY356858	AY356858 HIV-1 iso
978	6	20.0	424	13	AY356859	AY356859 HIV-1 iso
979	6	20.0	426	6	AX778776	AX778776 Sequence
c 980	6	20.0	426	10	BV197347	BV197347 sqnm19282
c 981	6	20.0	426	15	AY999143	AY999143 Zopfiella
982	6	20.0	427	13	AY356852	AY356852 HIV-1 iso
983	6	20.0	428	6	CQ527083	CQ527083 Sequence
984	6	20.0	430	13	AY356850	AY356850 HIV-1 iso
985	6	20.0	430	13	AY535665	AY535665 HIV-1 iso
986	6	20.0	431	10	CR381988	CR381988 Arabidops
987	6	20.0	431	13	AY356851	AY356851 HIV-1 iso
988	6	20.0	433	10	AB139792	AB139792 Homo sapi
989	6	20.0	434	13	AY356855	AY356855 HIV-1 iso
c 990	6	20.0	437	15	AY999142	AY999142 Podospora
991	6	20.0	441	13	AY484786	AY484786 HIV-1 iso
992	6	20.0	441	15	AY066057	AY066057 Arabidops
c 993	6	20.0	443	10	BV104662	BV104662 MARC 5883
994	6	20.0	445	10	AB153524	AB153524 Homo sapi
c 995	6	20.0	446	6	CQ097218	CQ097218 Sequence
c 996	6	20.0	446	6	CQ136045	CQ136045 Sequence
c 997	6	20.0	446	6	CQ219343	CQ219343 Sequence
c 998	6	20.0	446	6	CQ257850	CQ257850 Sequence
c 999	6	20.0	446	6	CQ295150	CQ295150 Sequence
c1000	6	20.0	446	6	CQ331773	CQ331773 Sequence

ALIGNMENTS

```
RESULT 1
AY437531
LOCUS       AY437531               1085 bp    mRNA    linear   PLN 20-JAN-2005
DEFINITION  Bougainvillea spectabilis antiviral protein (Ap1) mRNA, complete
            cds.
ACCESSION   AY437531
VERSION     AY437531.1  GI:40890052
KEYWORDS    .
SOURCE      Bougainvillea spectabilis
  ORGANISM  Bougainvillea spectabilis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE   1  (bases 1 to 1085)
  AUTHORS   Balasaraswathi,R., Suguna Rani,K. and Bansal,V.
  TITLE     A full length antiviral cDNA sequence from Bougainvillea
            spectabilis Willd.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1085)
  AUTHORS   Balasaraswathi,R., Suguna Rani,K. and Bansal,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-OCT-2003) Centre For Plant Molecular Biology, Tamil
            Nadu Agricultural University, Lawley Road, Coimbatore, Tamil Nadu
            641003, India
FEATURES             Location/Qualifiers
     source          1. .1085
                     /organism="Bougainvillea spectabilis"
                     /mol_type="mRNA"
                     /db_xref="taxon:146096"
                     /ecotype="Coimbatore region"
                     /country="India"
                     /note="biotype: red flower trait; authority: Bougainvillea
                     spectabilis Willd."
     gene            1. .1085
                     /gene="Ap1"
     5'UTR           1. .25
                     /gene="Ap1"
     CDS             26. .943
                     /gene="Ap1"
                     /note="crop antiviral and ribosome-inactivating protein;
                     BAP; BAP1; antiviral activity against tospo group of crop
                     viruses"
                     /codon_start=1
                     /product="antiviral protein"
                     /protein_id="AAR97371.1"
                     /db_xref="GI:40890053"
                     /translation="MGWWAIIVEPMLVMPSIVNKETTSLGYNTVSFNLGEAYEYPTFI
                     QDLRNELAKGTPVCQLPVTLQTIADAKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQD
                     KWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYK
                     LEFSIEAIHGKTINGQEIAKFFLITIQMVSEAARFKYIETEVVDRGLYGSFKPNFKVL
                     NLENNWGDISDAIHKSSPQCTTINPALQLISPSNDPWVVNKVSQISPDMGILKFKSSK
                     LTQFATMIRSAIAEDLDGDELEILEPNIA"
     3'UTR           944. .1085
                     /gene="Ap1"
     polyA_signal    984. .989
                     /gene="Ap1"
ORIGIN

Alignment Scores:
Pred. No.:                1.97e-24        Length:         1085
Score:                    30.00           Matches:        30
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       15              Gaps:           0

US-10-758-902-1 (1-30) x AY437531 (1-1085)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 TACAACACTGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 163

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        164 TTGCGCAATGAATTGGCTAAGGGCACACCA 193

RESULT 2
AF445416
LOCUS       AF445416               1387 bp    mRNA    linear   PLN 29-NOV-2001
DEFINITION  Bougainvillea spectabilis bouganin mRNA, complete cds.
ACCESSION   AF445416
VERSION     AF445416.1  GI:17149253
KEYWORDS    .
SOURCE      Bougainvillea spectabilis
  ORGANISM  Bougainvillea spectabilis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE   1  (bases 1 to 1387)
  AUTHORS   den Hartog,M.T., Lubelli,C., Boon,L., Heerkens,S., Ortiz
            Buijsse,A.P., de Boer,M. and Stirpe,F.
  TITLE     Cloning and expression of cDNA coding for bouganin: A type I
            ribosome-inactivating protein from Bougainvillea spectabilis Willd
  JOURNAL   Unpublished
```

```
REFERENCE   2  (bases 1 to 1387)
  AUTHORS   den Hartog,M.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-NOV-2001) Meibergdreef 45, Amsterdam 1105 BA, The
            Netherlands
FEATURES             Location/Qualifiers
     source          1. .1387
                     /organism="Bougainvillea spectabilis"
                     /mol_type="mRNA"
                     /db_xref="taxon:146096"
                     /note="authority: Bougainvillea spectabilis Willd"
     CDS             238. .1155
                     /note="ribosome-inactivating protein"
                     /codon_start=1
                     /product="bouganin"
                     /protein_id="AAL35962.1"
                     /db_xref="GI:17149254"
                     /translation="MGWWAIIVEPMLVMPSIVNKETTSLGYNTVSFNLGEAYEYPTPI
                     QDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQD
                     KWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYK
                     LEFSIEAIHGKTINGQEIAKFFLIVIQMVSEAARFKYIETEVVDRGLYGSFKPNFKVL
                     NLENNWGDISDAIHKSSPQCTTINPALQLISPSNDPWVVNKVSQISPDMGILKFKSSK
                     LTQFATMIRSAIVEDLDGDELEILEPNIA"
ORIGIN

Alignment Scores:
Pred. No.:              2.41e-24        Length:         1387
Score:                  30.00           Matches:        30
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     15              Gaps:           0

US-10-758-902-1 (1-30) x AF445416 (1-1387)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 375

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||||||||||||||||||||||||||||
Db        376 TTGCGCAACGAATTGGCTAAGGGCACACCA 405

RESULT 3
A82770
LOCUS       A82770                   65 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 5 from Patent WO9855623.
ACCESSION   A82770
VERSION     A82770.1  GI:6732460
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     TYPE-1 RIBOSOME-INACTIVATING PROTEIN
  JOURNAL   Patent: WO 9855623-A 5 10-DEC-1998;
            STIRPE FIORENZO (IT); BOLOGNESI ANDREA (IT)
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              3.15e-15        Length:         65
Score:                  21.00           Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            70.0%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x A82770 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 4
AR454120
LOCUS       AR454120                 65 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 5 from patent US 6680296.
ACCESSION   AR454120
VERSION     AR454120.1  GI:42687049
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     Type-1 ribosome-inactivating protein
  JOURNAL   Patent: US 6680296-A 5 20-JAN-2004;
            Tanox Pharma B.V.; Amsterdam;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.15e-15        Length:         65
Score:                  21.00           Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            70.0%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x AR454120 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 5
A82773
LOCUS       A82773                  363 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 8 from Patent WO9855623.
ACCESSION   A82773
VERSION     A82773.1  GI:6732463
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     TYPE-1 RIBOSOME-INACTIVATING PROTEIN
  JOURNAL   Patent: WO 9855623-A 8 10-DEC-1998;
            STIRPE FIORENZO (IT); BOLOGNESI ANDREA (IT)
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
```

```
Pred. No.:              1.13e-06       Length:         363
Score:                  14.00          Matches:        14
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            46.7%          Indels:         0
DB:                     6              Gaps:           0

US-10-758-902-1 (1-30) x A82773 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 6
AR454123
LOCUS       AR454123                363 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 8 from patent US 6680296.
ACCESSION   AR454123
VERSION     AR454123.1  GI:42687052
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     Type-1 ribosome-inactivating protein
  JOURNAL   Patent: US 6680296-A 8 20-JAN-2004;
            Tanox Pharma B.V.; Amsterdam;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.13e-06       Length:         363
Score:                  14.00          Matches:        14
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            46.7%          Indels:         0
DB:                     6              Gaps:           0

US-10-758-902-1 (1-30) x AR454123 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 7
BC086634/c
LOCUS       BC086634                1637 bp    mRNA    linear   VRT 01-FEB-2005
DEFINITION  Xenopus laevis hypothetical LOC495842, mRNA (cDNA clone MGC:98789
            IMAGE:3396392), complete cds.
ACCESSION   BC086634
VERSION     BC086634.1  GI:55991536
KEYWORDS    MGC.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 1637)
  AUTHORS   Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W.
            and Richardson,P.
  TITLE     Genetic and genomic tools for Xenopus research: The NIH Xenopus
            initiative
  JOURNAL   Dev. Dyn. 225 (4), 384-391 (2002)
   PUBMED   12454917
REFERENCE   2  (bases 1 to 1637)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   3  (bases 1 to 1637)
  AUTHORS   Klein,S. and Gerhard,D.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-NOV-2004) National Institutes of Health, Xenopus Gene
            Collection (XGC), National Institute of Child Health and Human
            Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
            20892-7510, USA
  REMARK    NIH-MGC Project
COMMENT     Contact: XGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 187 Row: a Column: 4
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis.
FEATURES             Location/Qualifiers
     source          1. .1637
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="MGC:98789 IMAGE:3396392"
                     /tissue_type="Liver"
                     /clone_lib="NICHD_XGC_Li1"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     gene            1. .1637
                     /gene="LOC495842"
                     /db_xref="GeneID:495842"
     CDS             306. .590
                     /gene="LOC495842"
                     /codon_start=1
                     /product="LOC495842 protein"
                     /protein_id="AAH86634.1"
                     /db_xref="GI:55991537"
                     /db_xref="GeneID:495842"
                     /translation="MVVQENENVVFCLECALRHVEKQKSSRGLKLMYRYDEEQIKSLV
```

NQICGKASFKNSNENCPMNCTPKRGPRKRATLEMPSSRVSSSTLSKSASS"
ORIGIN

Alignment Scores:

Pred. No.:	1.84	Length:	1637
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	30.0%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-1 (1-30) x BC086634 (1-1637)

```
Qy         18 IleGlnAspLeuArgAsnGluLeuAla 26
              |||||||||||||||||||||||||||
Db        620 ATTCAGGATTTGAGAAATGAGTTGGCA 594
```

RESULT 8
AC000119/c
LOCUS AC000119 191191 bp DNA linear PRI 15-OCT-2003
DEFINITION Homo sapiens BAC clone CTB-104I4 from 7, complete sequence.
ACCESSION AC000119
VERSION AC000119.1 GI:1809226
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 191191)
AUTHORS Sulston,J.E. and Wilson,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 9847074
REFERENCE 2 (bases 1 to 191191)
AUTHORS Gibson,A. and Wamsley,P.
TITLE The sequence of Homo sapiens BAC clone CTB-104I4
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 191191)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1997)
REFERENCE 4 (bases 1 to 191191)
AUTHORS Wilson,R.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT ---------- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
---------- Summary Statistics
Center project name: H_RG104I04
----------.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or mailto:egreen@nhgri.nih.gov

SOURCE INFORMATION:
Clone CTB-104I4 is from the first release of the human BAC library CITB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. (http://www.resgen.com).
VECTOR: pBeloBAC11
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of CTB-104I4 actual end is at 191191 of CTB-104I4. The orientation of this clone is unknown.

FEATURES	Location/Qualifiers
source	1. .191191
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="7"
	/map="7"
	/clone="CTB-104I4"
	/clone_lib="CITB-978SK-B"
repeat_region	1655. .1726
	/rpt_family="AcHobo"
repeat_region	1752. .1870
	/rpt_family="Alu"
repeat_region	1872. .1960
	/rpt_family="AcHobo"
repeat_region	4418. .4465
	/rpt_family="CT-rich"
repeat_region	5384. .5471
	/rpt_family="MIR"
repeat_region	6010. .6439
	/rpt_family="MaLR"
repeat_region	7812. .7895
	/rpt_family="MER1_type"
repeat_region	7931. .9288
	/rpt_family="L1"
repeat_region	11003. .11945
	/rpt_family="ERV1"
repeat_region	12538. .12710
	/rpt_family="MIR"
repeat_region	13031. .13142
	/rpt_family="L2"
repeat_region	13982. .14096
	/rpt_family="MIR"
repeat_region	14993. .15226
	/rpt_family="MIR"
repeat_region	16169. .16205
	/rpt_family="AT_rich"
repeat_region	16229. .16266
	/rpt_family="AT_rich"
repeat_region	16354. .16452
	/rpt_family="L2"
repeat_region	16509. .16797
	/rpt_family="Alu"
repeat_region	16798. .16870
	/rpt_family="(TA)n"
repeat_region	16901. .17789
	/rpt_family="L1"
repeat_region	17802. .18188
	/rpt_family="ERVL"
repeat_region	18189. .18219
	/rpt_family="(TCTG)n"
repeat_region	19807. .20062
	/rpt_family="Alu"
repeat_region	24317. .24420
	/rpt_family="(TA)n"

```
repeat_region   26099. .26146
                /rpt_family="L2"
repeat_region   26468. .26588
                /rpt_family="T2_type"
repeat_region   26589. .26784
                /rpt_family="Alu"
repeat_region   26792. .26841
                /rpt_family="T2_type"
repeat_region   26845. .27684
                /rpt_family="T2_type"
repeat_region   27689. .29178
                /rpt_family="ERV1"
repeat_region   29183. .29603
                /rpt_family="T2_type"
repeat_region   30200. .30243
                /rpt_family="(CAAAAA)n"
repeat_region   30249. .30273
                /rpt_family="AT_rich"
repeat_region   30274. .30416
                /rpt_family="L1"
repeat_region   30521. .30622
                /rpt_family="(TATATG)n"
repeat_region   30840. .30970
                /rpt_family="Alu"
repeat_region   31658. .31711
                /rpt_family="(CA)n"
misc_feature    31884. .32110
                /note="CpG_island (%GC=72.2, o/e=0.56, #CpGs=22)"
repeat_region   34694. .34782
                /rpt_family="MIR"
repeat_region   35891. .36437
                /rpt_family="L1"
repeat_region   36645. .37229
                /rpt_family="L1"
repeat_region   37230. .37275
                /rpt_family="(CAAAA)n"
repeat_region   37276. .38427
                /rpt_family="L1"
repeat_region   38428. .38699
                /rpt_family="Alu"
repeat_region   38700. .39084
                /rpt_family="L1"
repeat_region   39085. .39362
                /rpt_family="Alu"
repeat_region   39363. .39600
                /rpt_family="L1"
repeat_region   39601. .39885
                /rpt_family="L1"
repeat_region   39886. .40005
                /rpt_family="L1"
repeat_region   40006. .40343
                /rpt_family="MER1_type"
repeat_region   40344. .40364
                /rpt_family="L1"
repeat_region   40381. .40537
                /rpt_family="L1"
repeat_region   40564. .40976
                /rpt_family="L1"
repeat_region   41007. .41120
                /rpt_family="L1"
repeat_region   41355. .41630
                /rpt_family="L1"
repeat_region   41965. .42126
                /rpt_family="Alu"
repeat_region   42148. .42293
                /rpt_family="GA-rich"
repeat_region   42425. .42532
                /rpt_family="CR1"
repeat_region   42669. .42699
                /rpt_family="AT_rich"
repeat_region   42751. .42939
                /rpt_family="MIR"
repeat_region   42979. .43272
```

```
Alignment Scores:
Pred. No.:              93              Length:         191191
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            30.0%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x AC000119 (1-191191)

Qy          1 TyrAsnThrValSerPheAsnLeuGly 9
              |||||||||||||||||||||||||||
Db     186265 TACAACACAGTCAGTTTTAACTTGGGC 186239

RESULT 9
AC024117
LOCUS       AC024117              198134 bp    DNA     linear   HTG 03-MAR-2000
DEFINITION  Homo sapiens chromosome 3p clone RP11-327i12, WORKING DRAFT
            SEQUENCE, 30 unordered pieces.
ACCESSION   AC024117
VERSION     AC024117.1  GI:7025690
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 198134)
  AUTHORS   Tu,Y., Zhao,Y., Lin,W., Dong,H., Wan,M., Xu,S., Gu,W., Zhang,C.,
            Jia,J., Wu,C., Lu,G., Zhong,M., Zhou,Y., Ren,S., Fu,G., Chen,Z. and
            Huang,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-2000) Genomic Dept., Chinese National Human
            Genome Center at Shanghai, 315 Guo Shou Jing Road, Shanghai,
            Shanghai 201203, P. R. China
COMMENT     ----------Genome Center Informations----------
            Center: Chinese National Human Genome Center at Shanghai
            Center Code: CHGC
            Web site: http://www.chgc.sh.cn
            Email: mhuang@chgc.sh.cn or fugang@chgc.sh.cn
             ----------End Genome Center Informations----------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 30 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2466: contig of 2466 bp in length
            *                   gap of unknown length
            *     2467     5597: contig of 3131 bp in length
            *                   gap of unknown length
            *     5598     7794: contig of 2197 bp in length
            *                   gap of unknown length
            *     7795    10770: contig of 2976 bp in length
            *                   gap of unknown length
            *    10771    14382: contig of 3612 bp in length
            *                   gap of unknown length
            *    14383    17264: contig of 2882 bp in length
            *                   gap of unknown length
            *    17265    22426: contig of 5162 bp in length
            *                   gap of unknown length
            *    22427    24914: contig of 2488 bp in length
            *                   gap of unknown length
            *    24915    27774: contig of 2860 bp in length
            *                   gap of unknown length
            *    27775    33263: contig of 5489 bp in length
            *                   gap of unknown length
            *    33264    38487: contig of 5224 bp in length
            *                   gap of unknown length
            *    38488    43890: contig of 5403 bp in length
```

```
            *                    gap of unknown length
            *    43891    49788: contig of 5898 bp in length
            *                    gap of unknown length
            *    49789    55574: contig of 5786 bp in length
            *                    gap of unknown length
            *    55575    60049: contig of 4475 bp in length
            *                    gap of unknown length
            *    60050    65641: contig of 5592 bp in length
            *                    gap of unknown length
            *    65642    72478: contig of 6837 bp in length
            *                    gap of unknown length
            *    72479    78441: contig of 5963 bp in length
            *                    gap of unknown length
            *    78442    85088: contig of 6647 bp in length
            *                    gap of unknown length
            *    85089    93621: contig of 8533 bp in length
            *                    gap of unknown length
            *    93622   102041: contig of 8420 bp in length
            *                    gap of unknown length
            *   102042   109859: contig of 7818 bp in length
            *                    gap of unknown length
            *   109860   119036: contig of 9177 bp in length
            *                    gap of unknown length
            *   119037   126228: contig of 7192 bp in length
            *                    gap of unknown length
            *   126229   134394: contig of 8166 bp in length
            *                    gap of unknown length
            *   134395   141786: contig of 7392 bp in length
            *                    gap of unknown length
            *   141787   151483: contig of 9697 bp in length
            *                    gap of unknown length
            *   151484   160283: contig of 8800 bp in length
            *                    gap of unknown length
            *   160284   173523: contig of 13240 bp in length
            *                    gap of unknown length
            *   173524   198134: contig of 24611 bp in length.
FEATURES             Location/Qualifiers
     source          1. .198134
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3p"
                     /clone="RP11-327i12"
ORIGIN

Alignment Scores:
Pred. No.:                95.8          Length:         198134
Score:                    9.00          Matches:        9
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              30.0%         Indels:         0
DB:                       14            Gaps:           0

US-10-758-902-1 (1-30) x AC024117 (1-198134)

Qy          17 PheIleGlnAspLeuArgAsnGluLeu 25
               |||||||||||||||||||||||||||
Db       17166 TTTATCCAAGACCTTCGAAATGAACTT 17192

RESULT 10
AX069004
LOCUS       AX069004               1238 bp    DNA     linear   PAT 25-JAN-2001
DEFINITION  Sequence 12 from Patent WO0102569.
ACCESSION   AX069004
VERSION     AX069004.1  GI:12578824
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tang,Y.T., Yue,H., Yang,J., Azimzai,Y., Baughn,M.R. and Lu,D.A.
  TITLE     Human immune response molecules
  JOURNAL   Patent: WO 0102569-A 12 11-JAN-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1238
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                20            Length:         1238
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              26.7%         Indels:         0
DB:                       6             Gaps:           0

US-10-758-902-1 (1-30) x AX069004 (1-1238)

Qy           3 ThrValSerPheAsnLeuGlyGlu 10
               |||||||||||||||||||||||||
Db         994 ACAGTGTCATTTAATTTGGGAGAG 1017

RESULT 11
BC069192
LOCUS       BC069192               2108 bp    mRNA    linear   PRI 30-JUN-2004
DEFINITION  Homo sapiens Wilms tumor 1 associated protein, transcript variant
            1, mRNA (cDNA clone MGC:78409 IMAGE:4653831), complete cds.
ACCESSION   BC069192
VERSION     BC069192.1  GI:46623319
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2108)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2108)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 54 Row: d Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23199975.

```
FEATURES             Location/Qualifiers
     source          1. .2108
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:78409 IMAGE:4653831"
                     /tissue_type="Placenta, choriocarcinoma"
                     /clone_lib="NIH_MGC_21"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     gene            1. .2108
                     /gene="WTAP"
                     /note="synonyms: KIAA0105, MGC3925"
                     /db_xref="GeneID:9589"
                     /db_xref="MIM:605442"
     CDS             181. .1371
                     /gene="WTAP"
                     /codon_start=1
                     /product="Wilms' tumour 1-associating protein, isoform 1"
                     /protein_id="AAH69192.1"
                     /db_xref="GI:46623320"
                     /db_xref="GeneID:9589"
                     /db_xref="MIM:605442"
                     /translation="MTNEEPLPKKVRLSETDFKVMARDELILRWKQYEAYVQALEGKY
                     TDLNSNDVTGLRESEEKLKQQQQESARRENILVMRLATKEQEMQECTTQIQYLKQVQQ
                     PSVAQLRSTMVDPAINLFFLKMKGELEQTKDKLEQAQNELSAWKFTPDSQTGKKLMAK
                     CRMLIQENQELGRQLSQGRIAQLEAELALQKKYSEELKSSQDELNDFIIQLDEEVEGM
                     QSTILVLQQQLKETRQQLAQYQQQQSQASAPSTSRTTASEPVEQSEATSKDCSRLTNG
                     PSNGSSSRQRTSGSGFHREGNTTEDDFPSSPGNGNKSSNSSEERTGRGGSGYVNQLSA
                     GYESVDSPTGSENSLTHQSNDTDSSHDPQEEKAVSGKGNRTVGSRHVQNGLDSSVNVQ
                     GSVL"
ORIGIN
```

Alignment Scores:

Pred. No.:	30.9	Length:	2108
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x BC069192 (1-2108)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db       1394 ACAGTGTCATTTAATTTGGGAGAG 1417
```

```
RESULT 12
AF374416
LOCUS       AF374416               2134 bp    mRNA    linear   PRI 21-MAY-2001
DEFINITION  Homo sapiens putative pre-mRNA splicing regulator female-lethal(2D)
            mRNA, complete cds.
ACCESSION   AF374416
VERSION     AF374416.1  GI:14161494
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2134)
  AUTHORS   Ortega,A., Penalva,L. and Valcarcel,J.
  TITLE     cDNA of human homolog of the drosophila putative pre-mRNA splicing
            regulator female-lethal(2D) [FL(2)D]
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2134)
  AUTHORS   Ortega,A., Penalva,L. and Valcarcel,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-2001) Gene Expression Programme, European
            Molecular Biology Laboratory, Meyerhofstrasse 1, Heidelberg,
            Baden-Wuttenberg 69117, Germany
FEATURES             Location/Qualifiers
     source          1. .2134
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
     CDS             226. .1416
                     /note="FL(2)D; similar to Homo sapiens WTAP protein
                     encoded by GenBank Accession Number AJ276706"
                     /codon_start=1
                     /product="putative pre-mRNA splicing regulator
                     female-lethal(2D)"
                     /protein_id="AAK54764.1"
                     /db_xref="GI:14161495"
                     /translation="MTNEEPLPKKVRLSETDFKVMARDELILRWKQYEAYVQALEGKY
                     TDLNSNDVTGLRESEEKLKQQQQESARRENILVMRLATKEQEMQECTTQIQYLKQVQQ
                     PSVAQLRSTMVDPAINLFFLKMKGELEQTKDKLEQAQNELSAWKFTPDSQTGKKLMAK
                     CRMLIQENQELGRQLSQGRIAQLEAELALQKKYSEELKSSQDELNDFIIQLDEEVEGM
                     QSTILVLQQQLKETRQQLAQYQQQQSQASAPSTSRTTASEPVEQSEATSKDCSRLTNG
                     PSNGSSSRQRTSGSGFHREGNTTEDDFPSSPGNGNKSSNSSEERTGRGGSGYVNQLSA
                     GYESVDSPTGSENSLTHQSNDTDSSHDPQEEKAVSGKGNRTVGSRHVQNGLDSSVNVQ
                     GSVL"
ORIGIN
```

Alignment Scores:

Pred. No.:	31.3	Length:	2134
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x AF374416 (1-2134)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db       1439 ACAGTGTCATTTAATTTGGGAGAG 1462
```

```
RESULT 13
CQ845798
LOCUS       CQ845798               2291 bp    DNA     linear   PAT 02-AUG-2004
DEFINITION  Sequence 4445 from Patent EP1440981.
ACCESSION   CQ845798
VERSION     CQ845798.1  GI:50895397
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J., Isono,Y., Nagai,K. and Irie,R.
  TITLE     Full-length human cdna
  JOURNAL   Patent: EP 1440981-A 4445 28-JUL-2004;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1. .2291
```

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.: 33.1 Length: 2291
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.7% Indels: 0
DB: 6 Gaps: 0

US-10-758-902-1 (1-30) x CQ845798 (1-2291)

Qy 3 ThrValSerPheAsnLeuGlyGlu 10
||||||||||||||||||||||||||
Db 1604 ACAGTGTCATTTAATTTGGGAGAG 1627

RESULT 14
AK131393
LOCUS AK131393 2291 bp mRNA linear PRI 07-MAY-2004
DEFINITION Homo sapiens cDNA FLJ16480 fis, clone BRTHA2016318, highly similar to WTAP protein.
ACCESSION AK131393
VERSION AK131393.1 GI:47077246
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T., Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2291)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2004) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
FEATURES Location/Qualifiers
source 1. .2291
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRTHA2016318"
/tissue_type="thalamus"
/clone_lib="BRTHA2"
/note="cloning vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.: 33.1 Length: 2291
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.7% Indels: 0
DB: 8 Gaps: 0

US-10-758-902-1 (1-30) x AK131393 (1-2291)

Qy 3 ThrValSerPheAsnLeuGlyGlu 10
||||||||||||||||||||||||||
Db 1604 ACAGTGTCATTTAATTTGGGAGAG 1627

RESULT 15
BC084217/c
LOCUS BC084217 7046 bp mRNA linear VRT 01-FEB-2005
DEFINITION Xenopus laevis hypothetical LOC495062, mRNA (cDNA clone MGC:80650 IMAGE:5506840), complete cds.
ACCESSION BC084217
VERSION BC084217.1 GI:54037983
KEYWORDS MGC.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 7046)
AUTHORS Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W. and Richardson,P.
TITLE Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative
JOURNAL Dev. Dyn. 225 (4), 384-391 (2002)
PUBMED 12454917
REFERENCE 2 (bases 1 to 7046)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 3 (bases 1 to 7046)
AUTHORS Klein,S. and Gerhard,D.S.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20892-7510, USA
REMARK NIH-MGC Project
COMMENT Contact: XGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,

```
          Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
          Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
          Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
          Schein, Asim Siddiqui, Rob Holt, Marco Marra.

          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAK Plate: 154 Row: i Column: 6
          This clone was selected for full length sequencing because it
          passed the following selection criteria: Hexamer frequency ORF
          analysis, Similarity but not identity to protein.
FEATURES             Location/Qualifiers
     source          1. .7046
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="MGC:80650 IMAGE:5506840"
                     /tissue_type="Spleen, adult Xenopus"
                     /clone_lib="NICHD_XGC_Sp1"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     gene            1. .7046
                     /gene="LOC495062"
                     /db_xref="GeneID:495062"
     CDS             461. .3685
                     /gene="LOC495062"
                     /codon_start=1
                     /product="LOC495062 protein"
                     /protein_id="AAH84217.1"
                     /db_xref="GI:54037984"
                     /db_xref="GeneID:495062"
                     /translation="MSKERPKRNIIQKRYDDSDGIPWSEERVVRKVLYLSLKEFKTAR
                     KRQSDDCINGSFKTPNGLLLNRKTKGSVQSSENEKDDTSQGSSHTNSVTSSDSEDGPV
                     RKRPRLQAQRKFAQSQPNSPSTTPIKIVEPLLHPPVTQMSDLSKRKPKTEDFLTFLCL
                     RGSPALPSKMVYFGTSQDEEEIEDDDDAGFEDTKTTNTSSSCHSTPRKKKMRKHVTNG
                     HVFNGSCKSSKEKETPQRHKSKEATPGKERNSEQKAESRRESAAANHQPASNMGSSAK
                     GLTANNHHSHLRSAQVLRKQVSKVNGVTRLSSLGSNAVGAKKTREVRPTPSKTVKYTA
                     RVTKGTVTYTKAKKELDKAAKQNHNKTSSSVHHKISGTTESSNAKTRKQVLSLSTSRA
                     NCAAVLNCVKVNGKLNKRTCSREEGRQLREGLRNSKRRLEEANLPAKAQPLLKKIKVS
                     ACLPEVRSKRLAVEKQVLNGHLKKEVPEKMLERNRPKRASAARSSPVPQPGGKAEDTG
                     CENRSTSPSDSPPKSLDSAKLEKNVGRARCTAMCEIPVLRPSVKEFHDPLIYIESIRA
                     RVEKYGMCTVIPPADWRPECKLNDEMRFVTQIQHIHKLGRRWGPNVRRLACIKKHLKY
                     QGITLDELPLIGGCELDLAQFFQLINEMGGMQQVTDLKKWNKLADMLRIPKTAQDRLA
                     KLQEAYCQYLLSYDSLSPEEHKNLEKDVLREKENLEKKKGPLESHSDNAYKLHLLPRY
                     EPKNGLINGVVQRNGLRGKLKEMDVQVKNGRRRLFTQEKESAEEEPEDKSLFGELHKC
                     IYKGRSVSLTTFYRTARNVMNMCFNKEPTVSEVEQEYWHIVEQKNCHVAVHCGKVDTK
                     THGSGFPVGKAEPFSRHGWNLNVLPNNSGSILRHLGAVPGVTIPWLNIGMVFSTSCWS
                     RDQNHLPYIDYLHTGADCIWYCIPAEEERKLEKVVHTLLQANGTPGLQMLESNVMISP
                     EMLCKEGIKVHRTVQKSGQFVVCFPGSFVSKVCCGYSVSETVHFATTQWTSMGFKTAM
                     EMKRRHIAKPFSMEKLLYQIATVEAKKENSPTLSVISTLLRELR"
ORIGIN

Alignment Scores:
Pred. No.:              83.6            Length:         7046
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     5               Gaps:           0

US-10-758-902-1 (1-30) x BC084217 (1-7046)

Qy         18 IleGlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||||
Db       6488 ATTCAGGATTTGAGAAATGAGTTG 6465

RESULT 16
AF507073
LOCUS       AF507073               15626 bp    DNA     linear   INV 29-MAR-2004
DEFINITION  Trypanosoma brucei vacuolar-type Ca2+-ATPase gene, complete cds.
ACCESSION   AF507073
VERSION     AF507073.2  GI:30525172
KEYWORDS    .
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 15626)
  AUTHORS   Luo,S., Rohloff,P., Cox,J., Uyemura,S.A. and Docampo,R.
  TITLE     Trypanosoma brucei plasma membrane-type Ca2+-ATPase 1 (TbPMC1) and
            2 (TbPMC2) genes encode functional Ca2+-ATPases localized to the
            acidocalcisomes and plasma membrane, and essential for Ca2+
            homeostasis and growth
  JOURNAL   J. Biol. Chem. 279 (14), 14427-14439 (2004)
   PUBMED   14724285
REFERENCE   2  (bases 1 to 15626)
  AUTHORS   Luo,S., Uyemura,S.A., Moreno,S.N.J. and Docampo,R.
  TITLE     Trypanasoma brucei (strain IL TAR I) vacuolar-type Ca2+-ATPase
            (TbA2)
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 15626)
  AUTHORS   Luo,S., Uyemura,S.A., Moreno,S.N.J. and Docampo,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-APR-2002) Pathobiology, University of Illinois at
            Urbana-Champaign, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA
REFERENCE   4  (bases 1 to 15626)
  AUTHORS   Luo,S., Uyemura,S.A., Moreno,S.N.J. and Docampo,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-2003) Pathobiology, University of Illinois at
            Urbana-Champaign, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA
  REMARK    Sequence update by submitter
COMMENT     On May 12, 2003 this sequence version replaced gi:30315294.
FEATURES             Location/Qualifiers
     source          1. .15626
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="IL TAR I"
                     /db_xref="taxon:5691"
     mRNA            <12223. .>15465
                     /product="vacuolar-type Ca2+-ATPase"
     CDS             12223. .15465
                     /note="TbA2"
                     /codon_start=1
                     /product="vacuolar-type Ca2+-ATPase"
                     /protein_id="AAP30858.1"
                     /db_xref="GI:30315295"
                     /translation="MHPLESPQEHKTQVSPENNGNETKSVLQKLFTCNEDPKPLYEEL
                     GGVEGIAERLGTSITDGIDSFSVENRRAVYGRNELPEEAPLTFWKILKAAWSDRMIIL
                     LTLAACVSLILGLTVPEPGHEKVDYKTGWIEGTAILMAVIAVTSASSIQDYRKELKFR
                     ALVEENSAQPISVIRDGHKVTVDVTEIVVGDLVSLSPGLVIPVDGLYVRGLSVVVDES
                     SVTGENDLKKKGAEHPILLSGTVVSTAEDAYILACAVGESSFGGKLLMESRLDGEPRA
                     TPLQERLDELAAFIGRVAIISAVLLFIVLCIIEIERIATNKQQFYPKKFLNFLLLCVT
                     IVVVAVPEGLPLAVTIALAYSQNQMQKDNNQVRRLCACETMGNATQICSDKTGTLTQN
                     RMTVVQGYIGMRRFRVSNPGDPSSTVNLEGVSSDAQSLLMLGLALNSSSEKELLPGNV
                     GAESDLLSRWTWRTDKGNKTDQAILDFVDRVLISVPGSCNDKELPHQKLRMTNRSRGF
                     AIFPFTSERKFMTAVVAGADGVVMQYVKGGSDRVLGMCNRYLSSEGREEPLTEEVTEM
                     ITEQIRSIAGDANRTIGVAYGRIGTDGAVPEEEPEGPFVWLALLGIQDPLRPEVVDAV
                     RMCQRAGVTVRMCTGDNLDTAVAISRQCGIYNRLRGDLALTGKDFRNLVYDTYGDEAN
                     MEKFWPVLDRMMVMGRSQPLDKQLLVLMLMLRGEVVAVTGDGTNDAPALRLANVGFVM
                     RSGTDIAVKSGDIVLLDDNFRSVQRAVVWGRTVNDNIRKFLQLQLTVNVVSFLVTVVG
                     TLVREGKSSPLTTVQLLWVNLLMDTLAALALATEQPTEDCLNRGPSSPRAPLVSRRMW
                     FTIFSVATVQLTAFFSVLTFGGKYFGEDENGKHLHRTFLFNVFVFGTIFHMLNCRKLY
                     RELNVFEGMGRSVFFIVVVGSCIAFQVLAICTFNDFMGVRPLSIKQWGVSIGIAAISL
                     VVGILSRVVSIREPVFALIPDSRNVDGSASRLIKDVSVAAEQRQRETDGTSDASSLLA
                     GRLRAQSRWRRLQAEHVKKPRVVNAFRRAWTDRDMKRGSTRQLYDTLRMV"
ORIGIN

Alignment Scores:
Pred. No.:              161             Length:         15626
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-1 (1-30) x AF507073 (1-15626)
```

```
Qy         18 IleGlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||||
Db      10278 ATTCAGGATCTGCGGAATGAACTT 10301

RESULT 17
AC153364_5
WPCOMMENT
  Sequence split into 6 fragments  LOCUS AC153364 Accession AC153364
     Fragment Name      Begin     End
     AC153364_0             1     110000
     AC153364_1        100001     210000
     AC153364_2        200001     310000
     AC153364_3        300001     410000
     AC153364_4        400001     510000
     AC153364_5        500001     517981
Continuation (6 of 6) of AC153364 from base 500001 (AC153364 Mus musculus chromosome 10

Alignment Scores:
Pred. No.:              181             Length:         17981
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC153364_5 (1-17981)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db       6863 ACTGTTAGTTTTAATTTGGGGGAA 6886

RESULT 18
CEC08H9/c
LOCUS       CEC08H9                 42282 bp    DNA     linear   INV 09-AUG-2005
DEFINITION  Caenorhabditis elegans Cosmid C08H9, complete sequence.
ACCESSION   Z54342
VERSION     Z54342.1  GI:1015446
KEYWORDS    HTG; Chitinase; Glucosyltransferase; High density
            lipoprotein-binding protein; Serine carboxypeptidase;
            Tyrosine-protein kinase precursor.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 42282)
  AUTHORS   .
  CONSRTM   C. elegans Sequencing Consortium
  TITLE     Genome sequence of the nematode C. elegans: a platform for
            investigating biology
  JOURNAL   Science 282 (5396), 2012-2018 (1998)
   PUBMED   9851916
REFERENCE   2  (bases 1 to 42282)
  AUTHORS   Lloyd,C.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-1995) Nematode Sequencing Project, Sanger
            Institute, Hinxton, Cambridge CB10 1SA, England and Department of
            Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
            worm@sanger.ac.uk
COMMENT     Coding sequences below are predicted from computer analysis, using
            predictions from Genefinder (P. Green, U. Washington), and other
            available information.
            Current sequence finishing criteria for the C. elegans genome
            sequencing consortium are that all bases are either sequenced
            unambiguously on both strands, or on a single strand with both a
            dye primer and dye terminator reaction, from distinct subclones.
            Exceptions are indicated by an explicit note.
            IMPORTANT:  This sequence is NOT necessarily the entire insert of
            the specified clone.  It may be shorter because we only sequence
            overlapping sections once, or longer because we arrange for a small
            overlap between neighbouring submissions.
            For a graphical representation of this sequence and its analysis
            see:- http://www.wormbase.org/perl/ace/elegans/seq/sequence?
            name=C08H9;class=Sequence
            IMPORTANT: This sequence is not the entire insert of clone C08H9.
            It may be shorter because we only sequence overlapping sections
            once, or longer because we arrange for a small overlap between
            neighbouring submissions.
            The true left end of clone C08H9 is at 1 in this sequence. The true
            right end of clone C08H9 is at 1052 in
            sequence Z47072.
            The true left end of clone F26C11 is at 42179 in this sequence. The
            true right end of clone ZK938 is at 17445 in this sequence. The
            start of this sequence (1. .101) overlaps with the end of sequence
            Z49913.
            The end of this sequence (42179. .42282) overlaps with the start of
            sequence Z47072.
FEATURES            Location/Qualifiers
     source         1. .42282
                    /organism="Caenorhabditis elegans"
                    /mol_type="genomic DNA"
                    /strain="Bristol N2"
                    /db_xref="taxon:6239"
                    /chromosome="II"
                    /clone="C08H9"
     gene           join(complement(976. .1058),complement(713. .924),
                    complement(550. .670),complement(273. .501),
                    complement(Z49913.1:21813. .21886),
                    complement(Z49913.1:21484. .21726),
                    complement(Z49913.1:21294. .21429))
                    /locus_tag="C08H9.8"
     CDS            join(complement(976. .1058),complement(713. .924),
                    complement(550. .670),complement(273. .501),
                    complement(Z49913.1:21813. .21886),
                    complement(Z49913.1:21484. .21726),
                    complement(Z49913.1:21294. .21429))
                    /locus_tag="C08H9.8"
                    /standard_name="C08H9.8"
                    /note="contains similarity to Pfam domain PF00069
                    (Eukaryotic protein kinase domain)"
                    /codon_start=1
                    /product="Hypothetical protein C08H9.8"
                    /protein_id="CAA91155.2"
                    /db_xref="GI:50507481"
                    /db_xref="GOA:Q17842"
                    /db_xref="HSSP:1JPA"
                    /db_xref="InterPro:IPR000719"
                    /db_xref="InterPro:IPR001245"
                    /db_xref="InterPro:IPR008266"
                    /db_xref="UniProt/TrEMBL:Q17842"
                    /translation="MSILTCLLWVLCKSKKNCRSSENRQVVVNPMLELQSVPIDLNYV
                    EDLDTNCYEIKLENLEIVSGSLILSESVAVSKGLLHIRNPSGEEHGCLEVAVKSSAAN
                    NRSCSDYTIYKELMLMCAIGKHSDVLTLIGAVTSLGKHKTMIVSEHVECGDLLNYLRQ
                    NRERFQAKQPIWSNEDNSGYLIPKSKPIENSLYTSGLLSFAYQIANGMKHLASVLCVH
                    RDLALRNILVKRNKIIRISDFEVLSGYDVPLPFFWLAPECFEEYKFSEKTDVWAFGIC
                    LYELFSLGETLYKDIPASGNTVDAIIEFLKVGNRLPQPEHCSFRIYEFMKLCWSTDPI
                    KRPTFDECKNFFADELKDLSPQVICYICQYF"
     gene           complement(join(1848. .2932,3165. .3254,3299. .3441,
                    3490. .3545))
                    /locus_tag="C08H9.10"
     CDS            complement(join(1848. .2932,3165. .3254,3299. .3441,
                    3490. .3545))
                    /locus_tag="C08H9.10"
                    /standard_name="C08H9.10"
                    /note="contains similarity to Pfam domain PF00704
                    (Glycosyl hydrolases family 18)"
                    /codon_start=1
                    /product="Hypothetical protein C08H9.10"
                    /protein_id="CAA91147.1"
                    /db_xref="GI:3874126"
                    /db_xref="GOA:Q17834"
                    /db_xref="HSSP:1HJX"
                    /db_xref="InterPro:IPR001223"
                    /db_xref="InterPro:IPR011583"
                    /db_xref="UniProt/TrEMBL:Q17834"
                    /translation="MNPADLNSTSVPLLRNQNITQKNNRQWKNFIKHCYILITILVLS
```

```
                     APIAFSLSKLIMVARHKSPTVSNLIRVFIPSSKKLKTTTEKNLPTTKQLFKYSTETIF
                     PPAALCGKRIVGYFAEFENTALTRKQLQMLTHIIYLFAIPKNGNMTFGGERSRRKFEE
                     MKNEARKANSTLKVMISIGGQSNSRSFSRLVSNETSRNVFVNSIVSFVQKYDIDGIEI
                     FWTWPKYEDANNYLIFIQELRYAFIELQKKLNRKEDYVISIIVNCYDNQLSNLMGFSK
                     FVDFFNIYSIHYQSRQVGPSSPLYGGGSRNIDETMKYYICRTGQPSKFNMMVLFHGTF
                     WKGAELPLRNDSDDIFKDQNSAKGGFAVRWRELLQQKWDMSNIKFHNLTKTSYMWIPG
                     SSLFLTLEDEQSLRVKNRYVADHNIGGITMWTIDQDDGDHTLLKVVSSAELCTGDEKN
                     TIKFKCE"
gene                 complement(join(3791. .4878,5326. .5415,5460. .5608,
                     5657. .5712))
                     /locus_tag="C08H9.12"
CDS                  complement(join(3791. .4878,5326. .5415,5460. .5608,
                     5657. .5712))
                     /locus_tag="C08H9.12"
                     /standard_name="C08H9.12"
                     /note="contains similarity to Pfam domain PF00704
                     (Glycosyl hydrolases family 18)"
                     /codon_start=1
                     /product="Hypothetical protein C08H9.12"
                     /protein_id="CAA91149.1"
                     /db_xref="GI:3874128"
                     /db_xref="GOA:Q17836"
                     /db_xref="InterPro:IPR001223"
                     /db_xref="InterPro:IPR011583"
                     /db_xref="UniProt/TrEMBL:Q17836"
                     /translation="MNRADLNSTSIPLLRIQNITRKTNRFAQWKNLINPCLILIAILV
                     ISAPVAFSLSELIMVARHKSETVSNLINMLIPSSQTSRTTMKTNNSPTTKLVQKSNEK
                     VSPPAASCGKRIVGYFAEFENSPLSKKQLQMLTHIIYLFAIPKNGSLTFRDESSRRKF
                     VAMKNEARKESSTLKVMISIGGQYSSGEFSGLVSKETSRNLFTNSIVSFVQNYDIDGV
                     DIFWTWPKYSDENNYLMFIRELRYAFTELQKKLNRKETFVISLVISRNVNHLSNLVEF
                     SNFVDFLNIYLFNSFLNQIGPDSPLYGGGSRIVDENMKYYICKSGQPSKFNIIVSFHA
                     TYWNGAELPLRDDSDDIWKDNNSGRLPIALPRRQLRQYNWNLTDIKFHNLTKTSYIWI
                     PGPPTRFMTLEEERSLREKNRYVADHNIGGITMWTIDQDDDDHTLLKVVSSAELCTGD
                     EKNTIKYKCE"
gene                 complement(join(5965. .7052,7103. .7189,7234. .7382,
                     7431. .7486))
                     /locus_tag="C08H9.11"
CDS                  complement(join(5965. .7052,7103. .7189,7234. .7382,
                     7431. .7486))
                     /locus_tag="C08H9.11"
                     /standard_name="C08H9.11"
                     /note="contains similarity to Pfam domain PF00704
                     (Glycosyl hydrolases family 18)"
                     /codon_start=1
                     /product="Hypothetical protein C08H9.11"
                     /protein_id="CAA91148.1"
                     /db_xref="GI:3874127"
                     /db_xref="GOA:Q17835"
                     /db_xref="InterPro:IPR001223"
                     /db_xref="InterPro:IPR011583"
                     /db_xref="UniProt/TrEMBL:Q17835"
                     /translation="MNPVPSNSTNAPLLENQQITRRISCLIQWKHLIKPCLILIAILV
                     FSAPVAYSLSELIMVARHKSETVSNLIKIFIPSSKKLSTTTKTNSPPKHLIQESHQTI
                     SPPAAFCGKRIVGYFAEFENAGLSRKQLHMLTHIIYLFARPTNGVITLDGEQTRRKFE
                     EMKSKAREASSTLKVMISVGGHDYYKEYSRLVSNETSRNVFVKSIVSFFKKNDIDGIE
                     IFWTRPKYEDIKSYSSFIQELRSAFTELQKRWNRKNEYIISLIVPKEKHWSFDLKDFS
                     KFVDFFNIYSTQFREKQVGPDSPLYGGEGRNIDETMKYYICKTGQPSKFNIMVSFHGT
                     FWEGAELPLRDYSDDIWKEKNVARGPFAVRWRHLRQRNWNLTDIKFHNLTKTSYIWIP
                     GPPTWFLTLEDEKSLREKNRYVADHNIGGITMWTIDQDDDDHTLLKVVSSAELCTGDE
                     KNTIKYTCE"
gene                 complement(join(7723. .8810,8950. .9006,9070. .9218,
                     9273. .9322))
                     /locus_tag="C08H9.7"
CDS                  complement(join(7723. .8810,8950. .9006,9070. .9218,
                     9273. .9322))
                     /locus_tag="C08H9.7"
                     /standard_name="C08H9.7"
                     /note="contains similarity to Pfam domain PF00704
                     (Glycosyl hydrolases family 18)"
                     /codon_start=1
                     /product="Hypothetical protein C08H9.7"
                     /protein_id="CAA91150.1"
                     /db_xref="GI:3874129"
                     /db_xref="GOA:Q17837"
                     /db_xref="InterPro:IPR001223"
                     /db_xref="InterPro:IPR011583"
                     /db_xref="UniProt/TrEMBL:Q17837"
                     /translation="MNSLNTTYNPLLKYHKLSLKTRALTQGENIVKPCVILVAIILIS
                     TPFVFVFSKLIILACCKCQTVSTSINALMLNNSTTSQHALKSNETISPPAALCGKRIV
                     GYFAEFENSGLTRRHLQMVTHIIYLFARPTNGVMTLDGERTRRKFQEMRSKAREVSST
                     VKVMISVGGHDHSGAFSAIMSNEASRSVFIKSIVSFVKNEDIDGIEIFWMWPKHRDVN
                     NYSIFIQDLRNEPTELQKRTNRKNEYIISLLVPKKSYWSFDFEDFLKFVDFFNIYSTQ
                     FREKQVGPDSPLYGGEGRNIDETMKYYTCKTGQPSKFNIFVSFHGTFWKDAELPLRND
                     FDDIFKDKNLTKGAFAVRWRELLQQKWNLEDIKFHNLTKTSYIWIPGPPTWFMTLEDK
                     RSLREKTKYVADYNIGGITMWTIDQDDDDHTLLKVVSSAELCTGKEKNEINYKCD"
     gene            complement(join(11367. .11380,11824. .11937,11983. .12131,
                     12180. .12226))
                     /locus_tag="C08H9.4"

Alignment Scores:
Pred. No.:              366             Length:         42282
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-1 (1-30) x CEC08H9 (1-42282)

Qy         17 PheIleGlnAspLeuArgAsnGlu 24
              ||||||||||||||||||||||||
Db       8400 TTTATTCAAGACCTCCGAAACGAA 8377

RESULT 19
AC106844
LOCUS       AC106844               47872 bp    DNA     linear   HTG 12-JAN-2002
DEFINITION  Mus musculus clone RP24-142O2, LOW-PASS SEQUENCE SAMPLING.
ACCESSION   AC106844
VERSION     AC106844.1  GI:18139478
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 47872)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus, clone RP24-142O2
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 47872)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
            Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
            Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JAN-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     All repeats were identified using RepeatMasker:
```

```
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
---------- Genome Center
    Center: Whitehead Institute/ MIT Center for Genome Research
    Center code: WIBR
    Web site: http://www-seq.wi.mit.edu
    Contact: sequence_submissions@genome.wi.mit.edu
-------------- Project Information
    Center project name: L20255
    Center clone name: 142_O_2
--------------.
* NOTE: This record contains 60 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*        1      699: contig of 699 bp in length
*      700      799: gap of 100 bp
*      800     1474: contig of 675 bp in length
*     1475     1574: gap of 100 bp
*     1575     2291: contig of 717 bp in length
*     2292     2391: gap of 100 bp
*     2392     3051: contig of 660 bp in length
*     3052     3151: gap of 100 bp
*     3152     3785: contig of 634 bp in length
*     3786     3885: gap of 100 bp
*     3886     4596: contig of 711 bp in length
*     4597     4696: gap of 100 bp
*     4697     5406: contig of 710 bp in length
*     5407     5506: gap of 100 bp
*     5507     6195: contig of 689 bp in length
*     6196     6295: gap of 100 bp
*     6296     7008: contig of 713 bp in length
*     7009     7108: gap of 100 bp
*     7109     7799: contig of 691 bp in length
*     7800     7899: gap of 100 bp
*     7900     8616: contig of 717 bp in length
*     8617     8716: gap of 100 bp
*     8717     9383: contig of 667 bp in length
*     9384     9483: gap of 100 bp
*     9484    10134: contig of 651 bp in length
*    10135    10234: gap of 100 bp
*    10235    10912: contig of 678 bp in length
*    10913    11012: gap of 100 bp
*    11013    11685: contig of 673 bp in length
*    11686    11785: gap of 100 bp
*    11786    12499: contig of 714 bp in length
*    12500    12599: gap of 100 bp
*    12600    13281: contig of 682 bp in length
*    13282    13381: gap of 100 bp
*    13382    14096: contig of 715 bp in length
*    14097    14196: gap of 100 bp
*    14197    14916: contig of 720 bp in length
*    14917    15016: gap of 100 bp
*    15017    15670: contig of 654 bp in length
*    15671    15770: gap of 100 bp
*    15771    16485: contig of 715 bp in length
*    16486    16585: gap of 100 bp
*    16586    17304: contig of 719 bp in length
*    17305    17404: gap of 100 bp
*    17405    18168: contig of 764 bp in length
*    18169    18268: gap of 100 bp
*    18269    18958: contig of 690 bp in length
*    18959    19058: gap of 100 bp
*    19059    19748: contig of 690 bp in length
*    19749    19848: gap of 100 bp
*    19849    20555: contig of 707 bp in length
*    20556    20655: gap of 100 bp
*    20656    21376: contig of 721 bp in length
*    21377    21476: gap of 100 bp
*    21477    22195: contig of 719 bp in length
*    22196    22295: gap of 100 bp
*    22296    23010: contig of 715 bp in length
*    23011    23110: gap of 100 bp
*    23111    23808: contig of 698 bp in length
*    23809    23908: gap of 100 bp
*    23909    24635: contig of 727 bp in length
*    24636    24735: gap of 100 bp
*    24736    25432: contig of 697 bp in length
*    25433    25532: gap of 100 bp
*    25533    26239: contig of 707 bp in length
*    26240    26339: gap of 100 bp
*    26340    27055: contig of 716 bp in length
*    27056    27155: gap of 100 bp
*    27156    27807: contig of 652 bp in length
*    27808    27907: gap of 100 bp
*    27908    28636: contig of 729 bp in length
*    28637    28736: gap of 100 bp
*    28737    29450: contig of 714 bp in length
*    29451    29550: gap of 100 bp
*    29551    30221: contig of 671 bp in length
*    30222    30321: gap of 100 bp
*    30322    31021: contig of 700 bp in length
*    31022    31121: gap of 100 bp
*    31122    31840: contig of 719 bp in length
*    31841    31940: gap of 100 bp
*    31941    32622: contig of 682 bp in length
*    32623    32722: gap of 100 bp
*    32723    33439: contig of 717 bp in length
*    33440    33539: gap of 100 bp
*    33540    34231: contig of 692 bp in length
*    34232    34331: gap of 100 bp
*    34332    35056: contig of 725 bp in length
*    35057    35156: gap of 100 bp
*    35157    35841: contig of 685 bp in length
*    35842    35941: gap of 100 bp
*    35942    36639: contig of 698 bp in length
*    36640    36739: gap of 100 bp
*    36740    37443: contig of 704 bp in length
*    37444    37543: gap of 100 bp
*    37544    38261: contig of 718 bp in length
*    38262    38361: gap of 100 bp
*    38362    39093: contig of 732 bp in length
*    39094    39193: gap of 100 bp
*    39194    39912: contig of 719 bp in length
*    39913    40012: gap of 100 bp
*    40013    40712: contig of 700 bp in length
*    40713    40812: gap of 100 bp
*    40813    41495: contig of 683 bp in length
*    41496    41595: gap of 100 bp
*    41596    42283: contig of 688 bp in length
*    42284    42383: gap of 100 bp
*    42384    43094: contig of 711 bp in length
*    43095    43194: gap of 100 bp
*    43195    43910: contig of 716 bp in length
*    43911    44010: gap of 100 bp
*    44011    44729: contig of 719 bp in length
*    44730    44829: gap of 100 bp
*    44830    45549: contig of 720 bp in length
*    45550    45649: gap of 100 bp
*    45650    46329: contig of 680 bp in length
*    46330    46429: gap of 100 bp
*    46430    47131: contig of 702 bp in length
*    47132    47231: gap of 100 bp
*    47232    47872: contig of 641 bp in length.
FEATURES             Location/Qualifiers
     source          1. .47872
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
```

```
                  /clone="RP24-142O2"
                  /clone_lib="RPCI-24 Male Mouse BAC"
     gap          700. .799
                  /estimated_length=100
     gap          1475. .1574
                  /estimated_length=100
     gap          2292. .2391
                  /estimated_length=100
     gap          3052. .3151
                  /estimated_length=100
     gap          3786. .3885
                  /estimated_length=100
     gap          4597. .4696

Alignment Scores:
Pred. No.:              405           Length:        47872
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     14            Gaps:          0

US-10-758-902-1 (1-30) x AC106844 (1-47872)

Qy         20 AspLeuArgAsnGluLeuAlaLys 27
              ||||||||||||||||||||||||
Db      32441 GATTTAAGGAATGAATTAGCAAAA 32464

RESULT 20
AC010228/c
LOCUS       AC010228               78680 bp    DNA     linear   PRI 16-JUL-2002
DEFINITION  Homo sapiens chromosome 5 clone CTC-298B17, complete sequence.
ACCESSION   AC010228
VERSION     AC010228.8  GI:21844555
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 78680)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 78680)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 78680)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 78680)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   5  (bases 1 to 78680)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jul 16, 2002 this sequence version replaced gi:21637453.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.9% of Sequence;
            Estimated Total Number of Errors is 0.
            NOTE:  This insert is not the entire sequence of the clone (entire
            sequence is 145.4kb). It is clipped at the overlap with AC008955.
            The number of bases overlapped is 9996.
FEATURES             Location/Qualifiers
     source          1. .78680
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTC-298B17"
ORIGIN

Alignment Scores:
Pred. No.:              610           Length:        78680
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x AC010228 (1-78680)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db       6121 ACAGTAAGTTTCAATTTGGGAGAA 6098

RESULT 21
AC153364_4
WPCOMMENT
  Sequence split into 6 fragments  LOCUS AC153364 Accession AC153364
     Fragment Name      Begin     End
     AC153364_0             1     110000
     AC153364_1         100001    210000
     AC153364_2         200001    310000
     AC153364_3         300001    410000
     AC153364_4         400001    510000
     AC153364_5         500001    517981
Continuation (5 of 6) of AC153364 from base 400001 (AC153364 Mus musculus chromosome 10

Alignment Scores:
Pred. No.:              804           Length:        110000
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     14            Gaps:          0

US-10-758-902-1 (1-30) x AC153364_4 (1-110000)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db     106863 ACTGTTAGTTTTAATTTGGGGGAA 106886

RESULT 22
TANN3_10/c
WPCOMMENT
  Sequence split into 19 fragments  LOCUS TANN3 Accession CR940352
     Fragment Name      Begin     End
     TANN3_00               1     110000
     TANN3_01           100001    210000
     TANN3_02           200001    310000
     TANN3_03           300001    410000
     TANN3_04           400001    510000
     TANN3_05           500001    610000
     TANN3_06           600001    710000
     TANN3_07           700001    810000
     TANN3_08           800001    910000
     TANN3_09           900001   1010000
     TANN3_10          1000001   1110000
     TANN3_11          1100001   1210000
     TANN3_12          1200001   1310000
     TANN3_13          1300001   1410000
     TANN3_14          1400001   1510000
     TANN3_15          1500001   1610000
     TANN3_16          1600001   1710000
```

```
     TANN3_17          1700001   1810000
     TANN3_18          1800001   1898942
Continuation (11 of 19) of TANN3 from base 1000001 (CR940352 Theileria annulata strain A

Alignment Scores:
Pred. No.:              804           Length:        110000
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     14            Gaps:          0

US-10-758-902-1 (1-30) x TANN3_10 (1-110000)

Qy         23 AsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||
Db      65502 AATGAACTAGCCAAAGGTACTCCT 65479

RESULT 23
CR380954_08
WPCOMMENT
  Sequence split into 11 fragments  LOCUS CR380954 Accession CR380954
     Fragment Name     Begin     End
     CR380954_00           1    110000
     CR380954_01      100001    210000
     CR380954_02      200001    310000
     CR380954_03      300001    410000
     CR380954_04      400001    510000
     CR380954_05      500001    610000
     CR380954_06      600001    710000
     CR380954_07      700001    810000
     CR380954_08      800001    910000
     CR380954_09      900001   1010000
     CR380954_10     1000001   1050361
Continuation (9 of 11) of CR380954 from base 800001 (CR380954 Candida glabrata strain CE

Alignment Scores:
Pred. No.:              804           Length:        110000
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     15            Gaps:          0

US-10-758-902-1 (1-30) x CR380954_08 (1-110000)

Qy         17 PheIleGlnAspLeuArgAsnGlu 24
              ||||||||||||||||||||||||
Db      39115 TTCATTCAAGATTTGCGCAATGAA 39138

RESULT 24
AC159438/c
LOCUS       AC159438              138187 bp    DNA     linear   INV 02-APR-2005
DEFINITION  Trypanosoma brucei chromosome 8 clone RPCI93-29O4, complete
            sequence.
ACCESSION   AC159438
VERSION     AC159438.1  GI:62176198
KEYWORDS    HTG.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 138187)
  AUTHORS   Ghedin,E., Blandin,G., Bartholomeu,D., Caler,E., Haas,B.,
            Hannick,L., Shallom,J., Hou,L., Djikeng,A., Feldblyum,T.,
            Hostetler,J., Johnson,J., Jones,K., Koo,H.L., Larkin,C., Pai,G.,
            Peterson,J., Khalak,H.G., Salzberg,S., Simpson,A.J., Tallon,L., Van
            Aken,S., Wanless,D., White,O., Wortman,J., Fraser,C.M. and
            El-Sayed,N.M.A.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 138187)
  AUTHORS   Haas,B., Blandin,G. and El-Sayed,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-2005) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, nelsayed@tigr.org
COMMENT     BAC clone RPCI93-29O4 from Trypanosoma brucei chromosome 8.
            Putative protein coding regions (>30 codons) were predicted by
            combining the output of the gene finding algorithm GLIMMER with
            similarity data and manual annotation of open reading frames.
            Further refinement of gene models (additions, deletions and
            alterations to boundary coordinates) were done manually based on
            detailed comparisons with the T. cruzi and L. major genomes. Genes
            on BACs were assigned a systematic name based on the chromosome and
            the BAC from which they originated (e.g. Tb03.27F10.410). Gene
            products were assigned a putative function when they shared
            significant similarity with experimentally characterized gene
            products or when they contained functionally known protein domains.
            Gene products were labelled either 'hypothetical protein', or
            'hypothetical protein, conserved' in the case of products showing
            significant similarity with proteins or domains of unknown function
            from other organisms. Gene products of unknown function with
            predicted orthologs in Trypanosoma cruzi and Leishmania major
            genomes were automatically classified as conserved proteins. Short
            predicted coding sequences (less than 150 codons) with no
            additional evidence of coding potential were labelled 'hypothetical
            protein, unlikely'.
FEATURES             Location/Qualifiers
     source          1. .138187
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /isolate="GUTat10.1"
                     /db_xref="taxon:5691"
                     /chromosome="8"
                     /clone="RPCI93-29O4"
     misc_feature    1. .1429
                     /note="annotation for this sequence region can be found on
                     overlapping clone 25L8."
     gene            complement(<1876. .>2649)
                     /locus_tag="Tb927.8.1000"
                     /note="synonym: Tb08.29O4.30; hypothetical protein,
                     conserved"
     mRNA            complement(<1876. .>2649)
                     /locus_tag="Tb927.8.1000"
                     /product="hypothetical protein, conserved"
     CDS             complement(1876. .2649)
                     /locus_tag="Tb927.8.1000"
                     /codon_start=1
                     /product="hypothetical protein, conserved"
                     /protein_id="AAX70342.1"
                     /db_xref="GI:62176226"
                     /translation="MRQRQLQGESAMKRPSWSMSCRSPAFDTIKDRISWVGQQIASPT
                     RVVTAASKNFTAGSPMISNDADFSGAADETPAECCGRLKIDAMEEDFFLDVGWGPCRS
                     LTVSPVVSNPEDSNDETDEMWARRYVCERRPLKKRASERAREHHLNSSAMGVLFCHPI
                     AMKRFHTGVRDIQPNGSSYAGGASNGKCDHSFEEEADAEGSDCGSFSEAKVQFGSGTA
                     FSFTSGDVSAGRAIALEMMEEDEKIRSCVNSQQPNRGRR"
     gene            complement(<3404. .>4876)
                     /locus_tag="Tb927.8.1010"
                     /note="synonym: Tb08.29O4.50; chaperone protein DNAJ,
                     putative"
     mRNA            complement(<3404. .>4876)
                     /locus_tag="Tb927.8.1010"
                     /product="chaperone protein DNAJ, putative"
     CDS             complement(3404. .4876)
                     /locus_tag="Tb927.8.1010"
                     /note="go_component: integral to membrane [goid 0016021];
                     go_function: protein binding [goid 0005515];
                     go_process: protein folding [goid 0006457]"
                     /codon_start=1
                     /product="chaperone protein DNAJ, putative"
                     /protein_id="AAX70343.1"
                     /db_xref="GI:62176227"
                     /translation="MSYGKWAGVYSPHFLMSHVTMCRRVAHILWRRPSCSPQRSRSDT
                     ESPFGYVETLVSRPRAYARSTPLMTSAALLRSGLTARTGIRFATLPPAWPQVTARRFA
                     SAGQRAPTYDEVRDACSVLGVDVDSDPKHLKKIYRGLVQKHHPDAGGDAAAMSRITVA
                     YNRLKDLSKLEREQFKAQQATYRGGSYHYSSRAGSSGNGTPSYDTSGRYAAQGSHDAG
                     TSYDYRGASNADYFKQTANPRRGFYTYKQSDRSFTDNPFSTSNPFSMHAQVRRAWNMP
```

```
                MSSILLRAIVAYLGICVLFLLAYRRYRDWMHDDGWKMAESFARHERLAELQRLRQEMN
                DRIQSSREAAAAERLDAQRYSLARGFGGQSGTDYNVVTTSKERELRALERARRQRIEN
                NTIARGWPFIPEEKGRLVVRAHHPPGVVFPEPSRREEQLRQLTNMQRGRAWSDANQSL
                AEGAAVNPQSVVSDELNAVRAIRTILNGIHDGGQAENRVL"
repeat_region   5859. .5880
                /note="microsatellite"
                /rpt_type=tandem
                /rpt_unit="ta"
gene            complement(<6069. .>8177)
                /locus_tag="Tb927.8.1020"
                /note="synonym: Tb08.29O4.60;
                6-phosphofructo-2-kinase/fructose-2,6-biphosphatase,
                putative"
mRNA            complement(<6069. .>8177)
                /locus_tag="Tb927.8.1020"
                /product="6-phosphofructo-2-kinase/fructose-2,
                6-biphosphatase, putative"
CDS             complement(6069. .8177)
                /locus_tag="Tb927.8.1020"
                /EC_number="2.7.1.105"
                /note="go_function: carbohydrate phosphatase activity
                [goid 0019203];
                go_process: glycolysis [goid 0006096]"
                /codon_start=1
                /product="6-phosphofructo-2-kinase/fructose-2,
                6-biphosphatase, putative"
                /protein_id="AAX70344.1"
                /db_xref="GI:62176228"
                /translation="MTEAPKPQTTSEAEVLMELSERNAMNKGNRYSRGGCCSEVDASC
                PLDASQRMLVVKKLLHGPIRPFHKWKWRKINLQRRAEIAKTSAHTVVGVSGEQNGEEP
                GVDRGDADTVSKSIASLNSPAVDFQNDVDLCVGEGSHVAGASQVSSTPLYSPAVSASP
                PLDNYTGPLSYQGPVHFDDKTHSYTTTLCVIMVGLPARGKTFLAHKVCRLLGWHGHRA
                KVLNVQVAWRRLLMNYYNGQGDESRSERSRLKEKDPVYVRAEHFHALVSDSNSVERRL
                YRCVLQQYAHDAQNFYAEGGEVLVLNDDFPTEELRDEAEGLFSPLCTQTFFVEVVRSN
                KFNKTFDEFKVRDVMEYHSSVKLNDAKRDFERRVDYLKSVYTSVGAASCCANQSNSKT
                GDNSACTMLEEKVAKQRGTKRYVRVNNFHEVEVCGVMGYIASRIVSFVMNVTQLKVQH
                PIYFVRNGMSVYHCEDRIGGDSPLSPEGEQDTIELLEFVASLTQYVEQERNDTDSCVC
                ETAHTAGDGDGRVREGSGTCASTDTHSAYGFPDSPQRVVIWTSQLYRAIQTVEKCEQL
                LGIKTTRCHSLNELYAGVCENLTHAELREQCPLMQELRNCNKFSFRYPKGESYKDLVQ
                RLEPVIMELENTDRVVVVIVAHRAVLRALLTYFGSISAESCMWLDVPYRTVWKCTYDSK
                GMTSLEELRFDEQDEAAPVE"
repeat_region   9080. .9119
                /note="microsatellite"
                /rpt_type=tandem
                /rpt_unit="tatatg"
gene            complement(<9416. .>10297)
                /locus_tag="Tb927.8.1030"
                /note="synonym: Tb08.29O4.70; chaperone protein DNAJ,
                putative"
mRNA            complement(<9416. .>10297)
                /locus_tag="Tb927.8.1030"
                /product="chaperone protein DNAJ, putative"
CDS             complement(9416. .10297)
                /locus_tag="Tb927.8.1030"
                /note="go_component: integral to membrane [goid 0016021];
                go_function: protein binding [goid 0005515];
                go_process: protein folding [goid 0006457]"
                /codon_start=1
                /product="chaperone protein DNAJ, putative"
                /protein_id="AAX70345.1"
                /db_xref="GI:62176229"
                /translation="MRTEGLRRALISDVAARWYVFQRRFLSTSTAHLVEEIRQALRVL
                SLSDSASDAEVRDRFQSLAKSNHPDVLQGGTEESSVAEDKMRRGVEAYKLLRRFTEAE
                RHALLKQRVQQEEETERGRRVYEGVAGRKGEGSRATFEFNKFEQRRREMRNEAPPWKV
                DNHPPRNQRRSFLFYVLGGAATDARVSAAEILREYRRTGHLAGGRFRDCCAGSFGSRA
                PSGLFGANADEWARTRQRAERAQIVSAAFGRHIVAGVFAVTVFLLICMIFVAVKKHYA
                ARGLYTNSESFSKRELR"
gene            complement(<11087. .>11521)
                /locus_tag="Tb927.8.1040"
                /note="synonym: Tb08.29O4.90; hypothetical protein,
                conserved"
mRNA            complement(<11087. .>11521)
                /locus_tag="Tb927.8.1040"
                /product="hypothetical protein, conserved"
CDS             complement(11087. .11521)
                /locus_tag="Tb927.8.1040"
                /codon_start=1
                /product="hypothetical protein, conserved"
                /protein_id="AAX70346.1"
                /db_xref="GI:62176230"
                /translation="MSSSQQLGTHQAEGIQQTQVAFIPRREVTLHLRPAPSSASRDRH
                ISWEANVKDNQNQRVSKSCCIFHKKKLFGESSSDDDSTSSSCSDQDDSCHGCANNNEA
                KQNGEACGDGEGGAGAQGSCGSRRKKRPPCTREHCYCGTRFH"
repeat_region   12492. .12531
                /note="microsatellite"
                /rpt_type=tandem
                /rpt_unit="ca"
gene            complement(<13374. .>21335)
                /locus_tag="Tb927.8.1050"
                /note="synonym: Tb08.29O4.100; hypothetical protein,
                conserved"
mRNA            complement(<13374. .>21335)
                /locus_tag="Tb927.8.1050"
                /product="hypothetical protein, conserved"
CDS             complement(13374. .21335)
                /locus_tag="Tb927.8.1050"
                /codon_start=1
                /product="hypothetical protein, conserved"
                /protein_id="AAX70347.1"
                /db_xref="GI:62176231"
                /translation="MSTLTGSVGPNSAHGSTVGVSLDFEVNAAASHGDDEAETKSCFA
                EFSSPAADTKLAEEGESISRAPASPSGSHAVRNRSVSVPFVSFTDADEQPKDGLWSSK
                SLVPPLKRRPKQSRITRKSFRSLGAYRNPSTLSVLDLATTDLDKLKLSFVAHAAILNH
                GDLNDMQKLVNHVEREMRYGEQHLDRSHRGRQGSKAPSYQASVRSEDDGANADGGTDR
                AWQSLDDQSSSDVSVEESVKSMMDVPSQTKAMLCTWIYDRYVQQRIFELRAKRKARPN
                DTFTAVVSRQFPDAGTKELMVNLRNAPKPRNMRDLDLHDGIGSCLNEAGEKVGHTHLV

Alignment Scores:
Pred. No.:              970             Length:         138187
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-1 (1-30) x AC159438 (1-138187)

Qy         18 IleGlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||||
Db      69707 ATTCAGGATCTGCGGAATGAACTT 69684

RESULT 25
AL844588
LOCUS       AL844588              142422 bp    DNA     linear   ROD 13-JUN-2003
DEFINITION  Mouse DNA sequence from clone RP23-244N6 on chromosome 2, complete
            sequence.
ACCESSION   AL844588
VERSION     AL844588.17  GI:31746489
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 142422)
  AUTHORS   Martin,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Jun 14, 2003 this sequence version replaced gi:30348844.
            Sequence from the Mouse Genome Sequencing Consortium whole genome
            shotgun may have been used to confirm this sequence.  Sequence data
            from the whole genome shotgun alone has only been used where it has
            a phred quality of at least 30.
            -------------- Genome Center
```

```
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest, except on the rare
            occasion of the clone being a YAC.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-244N6 is
            from the RPCI-23 Mouse BAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .142422
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="2"
                     /clone="RP23-244N6"
                     /clone_lib="RPCI-23"
ORIGIN

Alignment Scores:
Pred. No.:              995          Length:        142422
Score:                  8.00         Matches:       8
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            26.7%        Indels:        0
DB:                     9            Gaps:          0

US-10-758-902-1 (1-30) x AL844588 (1-142422)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db     127851 ACTGTATCTTTTAATTTAGGGGAA 127874

RESULT 26
AC130471/c
LOCUS       AC130471              148008 bp    DNA     linear   HTG 10-AUG-2002
DEFINITION  Homo sapiens chromosome 5 clone RP11-420M3, WORKING DRAFT SEQUENCE,
            3 unordered pieces.
ACCESSION   AC130471
VERSION     AC130471.1  GI:22203244
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 148008)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Human Chromosome 5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 148008)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2002) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     -------Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -------
            Project Information
            Center Project Name: 567936
            Center clone name: RPCI-11_420M3
            -------
            Summary Statistics
            Consensus quality: 146731 bases at least Q40
            Consensus quality: 146937 bases at least Q30
            Consensus quality: 147107 bases at least Q20
            Estimated insert size: 0; null estimation
            Estimated insert size: 147808; sum-of-contigs estimation
            Quality coverage:  2.1474836E7 in Q20 bases; null estimation
            Quality coverage:  30.25 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     1000: contig of 1000 bp in length
            *    1001     1100: gap of unknown length
            *    1101     2353: contig of 1253 bp in length
            *    2354     2453: gap of unknown length
            *    2454   148008: contig of 145555 bp in length.
FEATURES             Location/Qualifiers
     source          1. .148008
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="RP11-420M3"
                     /clone_lib="RPCI human BAC library 11"
     gap             1001. .1100
                     /estimated_length=unknown
     gap             2354. .2453
                     /estimated_length=unknown
ORIGIN

Alignment Scores:
Pred. No.:              1.03e+03     Length:        148008
Score:                  8.00         Matches:       8
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            26.7%        Indels:        0
DB:                     14           Gaps:          0

US-10-758-902-1 (1-30) x AC130471 (1-148008)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db      47374 ACAGTAAGTTTCAATTTGGGAGAA 47351

RESULT 27
AC011421/c
LOCUS       AC011421              148142 bp    DNA     linear   PRI 18-APR-2000
DEFINITION  Homo sapiens chromosome 5 clone CTD-2303O5, complete sequence.
ACCESSION   AC011421
VERSION     AC011421.2  GI:6102634
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 148142)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
```

```
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 148142)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 148142)
  AUTHORS   DOE Joint Genome Center and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-1999) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 148142)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   5  (bases 1 to 148142)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   6  (bases 1 to 148142)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-APR-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Oct 23, 1999 this sequence version replaced gi:6013521.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.9% of Sequence;
            Estimated Total Number of Errors is 0.1.
            STS Content:
            WI-6744 G05721
            WI-6988 G06342.
FEATURES             Location/Qualifiers
     source          1. .148142
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-2303O5"
ORIGIN

Alignment Scores:
Pred. No.:              1.03e+03        Length:         148142
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x AC011421 (1-148142)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db      93308 ACAGTAAGTTTCAATTTGGGAGAA 93285

RESULT 28
AC108196/c
LOCUS       AC108196              155629 bp    DNA     linear   HTG 22-OCT-2002
DEFINITION  Felis catus clone RP86-591N22, WORKING DRAFT SEQUENCE, 2 ordered
            pieces.
ACCESSION   AC108196
VERSION     AC108196.2  GI:24211121
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 155629)
  AUTHORS   Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
            Cariaga,K., Coleman,B., Dietrich,N.L., Engle,J., Granite,S.,
            Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L.,
            Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R.,
            Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B.,
            Mastrian,S.D., McCloskey,J.C., McDowell,J., Paguirigan,C.,
            Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schandler,K.,
            Schueler,M.G., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J.,
            Touchman,J.W., Vogt,J.L., Walker,M., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 155629)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JAN-2002) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
REFERENCE   3  (bases 1 to 155629)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2002) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     On Oct 22, 2002 this sequence version replaced gi:18376895.
            ------------- Genome Center
                 Center: NIH Intramural Sequencing Center
                 Center code: NISC
                 Web site: http://www.nisc.nih.gov
                 Contact: nisc_zoo@nhgri.nih.gov
            ------------- Project Information
                 Center project name: coc
                 Center clone name: 591N22

            The sequence data in this record represents an 'enhanced'
            version of a Phase 2 submission. Specifically, the indicated
            order and orientation of each sequence contig has been
            established using one or more of the following: read-pair
            data from individual subclones, overlaps with neighboring
            clones, alignment with available reference sequence (e.g.,
            human), and/or confirmation by PCR testing. In addition,
            the sequence assembly is based on at least 8X average
            coverage in Q20 bases and has been reviewed to rule out
            gross misassemblies, the low-quality ends of sequence
            contigs have been trimmed away, and each base is associated
            with a Phrap-derived quality score.
            ------------- Summary Statistics
                 Sequencing vector: plasmid; n/a; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990319
                 Consensus quality: 155508 bases at least Q40
                 Consensus quality: 155520 bases at least Q30
                 Consensus quality: 155528 bases at least Q20
                 Insert size: 149000; agarose-fp
                 Insert size: 155529; sum-of-contigs
                 Quality coverage: 11.64x in Q20 bases; agarose-fp
                 Quality coverage: 11.15x in Q20 bases; sum-of-contigs
            -------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    26785: contig of 26785 bp in length
            *    26786    26885: gap of unknown length
            *    26886   155629: contig of 128744 bp in length.
FEATURES             Location/Qualifiers
     source          1. .155629
                     /organism="Felis catus"
```

```
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9685"
                     /clone="RP86-591N22"
                     /clone_lib="RP86"
     misc_feature    1. .31488
                     /note="clone overlaps with GenBank Accession Number
                     AC108192 clone RP86-459K24 (center project name cob)"
     misc_feature    1. .26785
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:left"
     gap             26786. .26885
                     /estimated_length=unknown
     misc_feature    26886. .155629
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:right"
     misc_feature    85307. .155629
                     /note="clone overlaps with GenBank Accession Number
                     AC108190 clone RP86-443I2 (center project name cod)"
ORIGIN

Alignment Scores:
Pred. No.:          1.07e+03        Length:         155629
Score:              8.00            Matches:        8
Percent Similarity: 100.0%          Conservative:   0
Best Local Similarity: 100.0%       Mismatches:     0
Query Match:        26.7%           Indels:         0
DB:                 14              Gaps:           0

US-10-758-902-1 (1-30) x AC108196 (1-155629)

Qy         23 AsnGluLeuAlaLysGlyThrPro 30
              |||||||||||||||||||||||
Db      82980 AATGAATTGGCCAAAGGGACACCT 82957

RESULT 29
AL135914
LOCUS       AL135914               165802 bp    DNA     linear   PRI 18-MAY-2005
DEFINITION  Human DNA sequence from clone RP1-56L9 on chromosome 6 Contains a
            novel gene, the SOD2 gene for superoxide dismutase 2,
            mitochondrial, a pseudogene similar to heterogenous nuclear
            ribonucleoprotein H, the gene for Wilms' tumor 1-associating
            protein (KIAA0105) (WTAP), the ACAT2 gene for acetyl-Coenzyme A
            acetyltransferase 2 (acetoacetyl Coenzyme A thiolase), the TCP1
            gene for t-complex 1 (CCT1, Ccta, D6S230E), the 5' end of the
            MRPL18 gene for mitochondrial ribosomal protein L18, and 4 CpG
            islands, complete sequence.
ACCESSION   AL135914
VERSION     AL135914.25  GI:15020718
KEYWORDS    HTG; ACAT2; acetoacetyl Coenzyme A thiolase; CCT1; Ccta; D6S230E;
            KIAA105; MRPL18; ribonucleoprotein; SOD2; TCP1; WTAP.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 165802)
  AUTHORS   Williams,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Jul 25, 2001 this sequence version replaced gi:14970777.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr6
            RP1-56L9 is from the library RPCI-1 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pCYPAC2
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            --------------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one subclone; and the assembly was confirmed by restriction digest,
            except on the rare occasion of the clone being a YAC.
FEATURES             Location/Qualifiers
     source          1. .165802
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="RZPD:RPCIP704L0956"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /clone="RP1-56L9"
                     /clone_lib="RPCI-1"
     misc_feature    1
                     /note="Clone_left_end: RP1-56L9"
     gene            complement(join(10990. .11029,11084. .11784))
                     /locus_tag="RP1-56L9.7-001"
     mRNA            complement(join(10990. .11029,11084. .11784))
                     /locus_tag="RP1-56L9.7-001"
                     /note="match: ESTs: AV647011"
     misc_feature    24081. .24105
                     /note="Tandem repeat. Single clone region. Assembly
                     confirmed by restriction digest data"
     gene            complement(join(50799. .50981,54157. .54321,56537. .56716,
                     59809. .59925,64344. .64546,64828. .65003))
                     /gene="SOD2"
                     /locus_tag="RP1-56L9.2-002"
     mRNA            complement(join(50799. .50981,54157. .54321,56537. .56716,
                     59809. .59925,64344. .64546,64828. .65003))
                     /gene="SOD2"
                     /locus_tag="RP1-56L9.2-002"
                     /product="superoxide dismutase 2, mitochondrial"
                     /note="match: cDNAs: BC012423 D17152 Y00472"
     polyA_site      complement(50799)
                     /gene="SOD2"
                     /locus_tag="RP1-56L9.2-002"
     polyA_signal    complement(50819. .50824)
                     /gene="SOD2"
                     /locus_tag="RP1-56L9.2-002"
     gene            complement(join(53823. .54321,56537. .56716,59809. .59925,
                     64344. .64546,64828. .64854))
                     /gene="SOD2"
                     /locus_tag="RP1-56L9.2-001"
     mRNA            complement(join(53823. .54321,56537. .56716,59809. .59925,
                     64344. .64546,64828. .64854))
                     /gene="SOD2"
                     /locus_tag="RP1-56L9.2-001"
                     /product="superoxide dismutase 2, mitochondrial"
                     /note="match: ESTs: BG699596
                     match: cDNAs: X07834"
     CDS             complement(join(54176. .54321,56537. .56716,59809. .59925,
                     64344. .64546,64828. .64850))
                     /gene="SOD2"
                     /locus_tag="RP1-56L9.2-001"
                     /standard_name="OTTHUMP00000017530"
                     /codon_start=1
                     /product="superoxide dismutase 2, mitochondrial"
                     /protein_id="CAI21845.1"
                     /db_xref="GI:56204992"
                     /translation="MLSRAVCGTSRQLAPVLGYLGSRQKHSLPDLPYDYGALEPHINA
```

```
                QIMQLHHSKHHAAYVNNLNVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFW
                TNLSPNGGGEPKGELLEAIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKERGHLQ
                IAACPNQDPLQGTTGLIPLLGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYM
                ACKK"
gene            complement(join(62678. .64546,64828. .>64913))
                /gene="SOD2"
                /locus_tag="RP1-56L9.2-003"
mRNA            complement(join(62678. .64546,64828. .>64913))
                /gene="SOD2"
                /locus_tag="RP1-56L9.2-003"
                /product="superoxide dismutase 2, mitochondrial"
                /note="match: ESTs: BF338920 BI906790
                match: cDNAs: AL050388 BC016934"
CDS             complement(join(64147. .64546,64828. .>64913))
                /gene="SOD2"
                /locus_tag="RP1-56L9.2-003"
                /standard_name="OTTHUMP00000017532"
                /codon_start=1
                /product="superoxide dismutase 2, mitochondrial"
                /protein_id="CAI21846.1"
                /db_xref="GI:56204993"
                /db_xref="GOA:Q5TCM0"
                /db_xref="InterPro:IPR001189"
                /db_xref="UniProt/TrEMBL:Q5TCM0"
                /translation="WWLRQRLQQIGGISGSTSTSSMLSRAVCGTSRQLAPVLGYLGSR
                QKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVTEEKYQEALAKGRFQAE
                RREAVPGRGDPREPGPIRTGLSVEENSLRICTGSEFSRHDSLSFKHMVYLIVEGVPRW
                V"
gene            complement(84484. .85668)
                /locus_tag="RP1-56L9.3-001"
                /pseudo
CDS             complement(84484. .85668)
                /locus_tag="RP1-56L9.3-001"
                /note="match: proteins: AAL90203 CAB55879 P55795 P70333
                Q12849 Q9NP96 Q9NPA7 Q9VGH5 Q9Y4J5"
                /pseudo
                /codon_start=1
gene            join(97268. .99016,107941. .107978,110673. .110728,
                113771. .113829,115348. .115475,119874. .120052,
                125143. .125297,126711. .128002)
                /gene="WTAP"
                /locus_tag="RP1-56L9.4-001"
mRNA            join(97268. .99016,107941. .107978,110673. .110728,
                113771. .113829,115348. .115475,119874. .120052,
                125143. .125297,126711. .128002)
                /gene="WTAP"
                /locus_tag="RP1-56L9.4-001"
                /product="Wilms tumor 1 associated protein"
                /note="match: ESTs: AA460837 AJ397868 AU119665 AU121632
                AW936415 AW936487 BE397592 BE652088 BE882897 BF060664
                BF920995 BF930039 BF930054 BG260600 BG388508 BG389986
                BG704031 BG924897 BM706948 BM875371 BM983785 BM983973
                N72123
                match: cDNAs: AF374416 AJ276706 AJ276707 AL583911"
gene            join(99213. .99386,107941. .108401)
                /gene="WTAP"
                /locus_tag="RP1-56L9.4-004"
mRNA            join(99213. .99386,107941. .108401)
                /gene="WTAP"
                /locus_tag="RP1-56L9.4-004"
                /product="Wilms tumor 1 associated protein"
                /note="match: ESTs: AV708967"
gene            join(99271. .99386,107941. .107978,110673. .110728,
                113771. .113829,115348. .115475,119874. .121098)
                /gene="WTAP"
                /locus_tag="RP1-56L9.4-002"
mRNA            join(99271. .99386,107941. .107978,110673. .110728,
                113771. .113829,115348. .115475,119874. .121098)
                /gene="WTAP"
                /locus_tag="RP1-56L9.4-002"
                /product="Wilms tumor 1 associated protein"
                /note="match: ESTs: AL531094 AL532682 AL564272 AL575461
                AL577327 BE872907 BM453486 BM472081 BM805127
                match: cDNAs: AF277190 BC000383 BC004432 D14661"
CDS             join(107949. .107978,110673. .110728,113771. .113829,
                115348. .115475,119874. .120052,125143. .125297,
                126711. .127294)
                /gene="WTAP"
                /locus_tag="RP1-56L9.4-001"
                /standard_name="OTTHUMP00000017522"
                /note="match: proteins: Q15007 Q96T28 Q9BYJ7 Q9H4E2
                Q9Y091"
                /codon_start=1
                /product="Wilms tumor 1 associated protein"
                /protein_id="CAI21849.1"
                /db_xref="GI:56204995"
                /translation="MTNEEPLPKKVRLSETDFKVMARDELILRWKQYEAYVQALEGKY
                TDLNSNDVTGLRESEEKLKQQQQESARRENILVMRLATKEQEMQECTTQIQYLKQVQQ
                PSVAQLRSTMVDPAINLFFLKMKGELEQTKDKLEQAQNELSAWKFTPDSQTGKKLMAK
                CRMLIQENQELGRQLSQGRIAQLEAELALQKKYSEELKSSQDELNDFIIQLDEEVEGM
                QSTILVLQQQLKETRQQLAQYQQQQSQASAPSTSRTTASEPVEQSEATSKDCSRLTNG
                PSNGSSSRQRTSGSGFHREGNTTEDDFPSSPGNGNKSSNSSEERTGRGGSGYVNQLSA
```

```
Alignment Scores:
Pred. No.:              1.13e+03        Length:         165802
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x AL135914 (1-165802)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db     127317 ACAGTGTCATTTAATTTGGGAGAG 127340

RESULT 30
AC112269/c
LOCUS       AC112269              172714 bp    DNA     linear   ROD 05-NOV-2003
DEFINITION  Mus musculus BAC clone RP24-115O19 from 2, complete sequence.
ACCESSION   AC112269
VERSION     AC112269.3  GI:21844653
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 172714)
  AUTHORS   Tomlinson,C., Meyer,R. and Boyer,E.
  TITLE     The sequence of Mus musculus BAC clone RP24-115O19
  JOURNAL   Unpublished (2001)
REFERENCE   2  (bases 1 to 172714)
  AUTHORS   Wilson,R.
  TITLE     Sequencing of Mus musculus
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 172714)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
REFERENCE   4  (bases 1 to 172714)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
REFERENCE   5  (bases 1 to 172714)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
REFERENCE   6  (bases 1 to 172714)
  AUTHORS   Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2003) Department of Genetics, Washington
```

```
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Jul 16, 2002 this sequence version replaced gi:21039975.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu
                Contact: submissions@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: M_BB0115O19
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. Wes Warren,
            Department of Genetics, Washington University, St. Louis MO. For
            additional information about the map position of this sequence, see
            http://genome.wustl.edu

            SOURCE INFORMATION:
            The RPCI-24 BAC Library has been constructed by Pieter de Jong and
            coworkers (http://www.chori.org) from male C57BL/6J mouse spleen
            and/or brain genomic DNA. The clone and detailed information can be
            obtained from Pieter de Jong and coworkers at http://www.chori.org

            NEIGHBORING SEQUENCE INFORMATION:
            This sequence is the entire insert of the clone.
FEATURES                    Location/Qualifiers
     source                 1. .172714
                            /organism="Mus musculus"
                            /mol_type="genomic DNA"
                            /db_xref="taxon:10090"
                            /chromosome="2"
                            /map="2"
                            /clone="RP24-115O19"
                            /clone_lib="RPCI-24"
     repeat_region          1996. .2391
                            /rpt_family="MaLR"
     repeat_region          5658. .5691
                            /rpt_family="Alu"
     repeat_region          6868. .6998
                            /rpt_family="Alu"
     repeat_region          6999. .7030
                            /rpt_family="B4"
     repeat_region          7156. .7343
                            /rpt_family="B2"
     misc_feature           8002. .8774
                            /note="CpG_island (%GC=66.5, o/e=1.11, #CpGs=84)"
     repeat_region          9531. .9574
                            /rpt_family="Alu"
     repeat_region          9575. .9798
                            /rpt_family="B2"
     repeat_region          9799. .9909
                            /rpt_family="Alu"
     repeat_region          9805. .9912
                            /rpt_family="B4"
     repeat_region          9944. .10121
                            /rpt_family="B2"
     repeat_region          10138. .10201
                            /rpt_family="Alu"
     repeat_region          10256. .10463
                            /rpt_family="B2"
     repeat_region          10503. .10598
                            /rpt_family="Alu"
     repeat_region          10602. .10790
                            /rpt_family="B2"
     repeat_region          10994. .11203
                            /rpt_family="ERVK"
     repeat_region          11196. .11396
                            /rpt_family="ERVK"
     repeat_region          11415. .11553
                            /rpt_family="Alu"
     repeat_region          11582. .11719
                            /rpt_family="Alu"
     repeat_region          11904. .12094
                            /rpt_family="B2"
     repeat_region          12113. .12311
                            /rpt_family="B2"
     repeat_region          12464. .12616
                            /rpt_family="B2"
     repeat_region          12622. .12815
                            /rpt_family="B2"
     repeat_region          12849. .12998
                            /rpt_family="Alu"
     repeat_region          12999. .13036
                            /rpt_family="B2"
     repeat_region          13284. .13607
                            /rpt_family="B4"
     repeat_region          13719. .13789
                            /rpt_family="ID"
     repeat_region          13836. .14035
                            /rpt_family="B2"
     repeat_region          14052. .14206
                            /rpt_family="Alu"
     repeat_region          14237. .14314
                            /rpt_family="ID"
     repeat_region          14318. .14416
                            /rpt_family="B4"
     repeat_region          14477. .14589
                            /rpt_family="Alu"
     repeat_region          14810. .14976
                            /rpt_family="B2"
     repeat_region          14977. .15197
                            /rpt_family="L1"
     repeat_region          15199. .15265
                            /rpt_family="Alu"
     repeat_region          15307. .15467
                            /rpt_family="B2"
     repeat_region          15511. .15574
                            /rpt_family="ID"
     repeat_region          15551. .15673
                            /rpt_family="ERVK"
     repeat_region          15915. .16015
                            /rpt_family="Alu"
     repeat_region          16140. .16271
                            /rpt_family="Alu"
     repeat_region          16336. .16469
                            /rpt_family="Alu"
     repeat_region          16672. .16788
                            /rpt_family="Alu"
     repeat_region          17565. .17669
                            /rpt_family="Alu"
     repeat_region          17577. .17690
                            /rpt_family="MaLR"
     repeat_region          17673. .17884
                            /rpt_family="B4"
     repeat_region          18408. .18482
                            /rpt_family="ID"
     repeat_region          19404. .19532
                            /rpt_family="Alu"
     repeat_region          20150. .20236
                            /rpt_family="L1"
     repeat_region          20665. .20760
                            /rpt_family="Alu"
     repeat_region          20803. .21294
```

```
                 /rpt_family="L1"
     repeat_region   21302. .21446
                 /rpt_family="B4"
     repeat_region   21473. .21522
                 /rpt_family="RMER15"
     repeat_region   21524. .21848
                 /rpt_family="L1"
     repeat_region   22146. .22296
                 /rpt_family="B2"
     repeat_region   22341. .22486
                 /rpt_family="Alu"
     repeat_region   22742. .22833
                 /rpt_family="Alu"
     repeat_region   22877. .22919
                 /rpt_family="L1"
     repeat_region   22981. .23089
                 /rpt_family="Alu"

Alignment Scores:
Pred. No.:              1.17e+03        Length:         172714
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     9               Gaps:           0

US-10-758-902-1 (1-30) x AC112269 (1-172714)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db     166611 ACTGTATCTTTTAATTTAGGGGAA 166588

RESULT 31
AC011783
LOCUS       AC011783               175178 bp    DNA     linear   HTG 13-JUL-2000
DEFINITION  Homo sapiens clone RP11-16L10, LOW-PASS SEQUENCE SAMPLING.
ACCESSION   AC011783
VERSION     AC011783.3  GI:7144945
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 175178)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-16L10
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 175178)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 3, 2000 this sequence version replaced gi:6446867.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L3568
                Center clone name: 16_L_10
            --------------.
            * NOTE: This record contains 185 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *        1      916: contig of 916 bp in length
            *      917     1016: gap of 100 bp
            *     1017     1893: contig of 877 bp in length
            *     1894     1993: gap of 100 bp
            *     1994     2899: contig of 906 bp in length
            *     2900     2999: gap of 100 bp
            *     3000     3975: contig of 976 bp in length
            *     3976     4075: gap of 100 bp
            *     4076     5009: contig of 934 bp in length
            *     5010     5109: gap of 100 bp
            *     5110     6049: contig of 940 bp in length
            *     6050     6149: gap of 100 bp
            *     6150     7075: contig of 926 bp in length
            *     7076     7175: gap of 100 bp
            *     7176     8110: contig of 935 bp in length
            *     8111     8210: gap of 100 bp
            *     8211     9126: contig of 916 bp in length
            *     9127     9226: gap of 100 bp
            *     9227    10157: contig of 931 bp in length
            *    10158    10257: gap of 100 bp
            *    10258    11178: contig of 921 bp in length
            *    11179    11278: gap of 100 bp
            *    11279    12202: contig of 924 bp in length
            *    12203    12302: gap of 100 bp
            *    12303    13218: contig of 916 bp in length
            *    13219    13318: gap of 100 bp
            *    13319    14252: contig of 934 bp in length
            *    14253    14352: gap of 100 bp
            *    14353    15290: contig of 938 bp in length
            *    15291    15390: gap of 100 bp
            *    15391    16319: contig of 929 bp in length
            *    16320    16419: gap of 100 bp
            *    16420    17356: contig of 937 bp in length
            *    17357    17456: gap of 100 bp
            *    17457    18374: contig of 918 bp in length
            *    18375    18474: gap of 100 bp
            *    18475    19399: contig of 925 bp in length
            *    19400    19499: gap of 100 bp
            *    19500    20434: contig of 935 bp in length
            *    20435    20534: gap of 100 bp
            *    20535    21209: contig of 675 bp in length
            *    21210    21309: gap of 100 bp
            *    21310    22235: contig of 926 bp in length
            *    22236    22335: gap of 100 bp
            *    22336    23293: contig of 958 bp in length
            *    23294    23393: gap of 100 bp
            *    23394    24333: contig of 940 bp in length
            *    24334    24433: gap of 100 bp
            *    24434    25365: contig of 932 bp in length
            *    25366    25465: gap of 100 bp
            *    25466    26394: contig of 929 bp in length
            *    26395    26494: gap of 100 bp
            *    26495    27441: contig of 947 bp in length
            *    27442    27541: gap of 100 bp
            *    27542    28440: contig of 899 bp in length
            *    28441    28540: gap of 100 bp
```

```
*    28541    29468: contig of 928 bp in length
*    29469    29568: gap of 100 bp
*    29569    30504: contig of 936 bp in length
*    30505    30604: gap of 100 bp
*    30605    31513: contig of 909 bp in length
*    31514    31613: gap of 100 bp
*    31614    32552: contig of 939 bp in length
*    32553    32652: gap of 100 bp
*    32653    33586: contig of 934 bp in length
*    33587    33686: gap of 100 bp
*    33687    34615: contig of 929 bp in length
*    34616    34715: gap of 100 bp
*    34716    35640: contig of 925 bp in length
*    35641    35740: gap of 100 bp
*    35741    36676: contig of 936 bp in length
*    36677    36776: gap of 100 bp
*    36777    37684: contig of 908 bp in length
*    37685    37784: gap of 100 bp
*    37785    38781: contig of 997 bp in length
*    38782    38881: gap of 100 bp
*    38882    39829: contig of 948 bp in length
*    39830    39929: gap of 100 bp
*    39930    40857: contig of 928 bp in length
*    40858    40957: gap of 100 bp
*    40958    41882: contig of 925 bp in length
*    41883    41982: gap of 100 bp
*    41983    42918: contig of 936 bp in length
*    42919    43018: gap of 100 bp
*    43019    43943: contig of 925 bp in length
*    43944    44043: gap of 100 bp
*    44044    44994: contig of 951 bp in length
*    44995    45094: gap of 100 bp
*    45095    46032: contig of 938 bp in length
*    46033    46132: gap of 100 bp
*    46133    47063: contig of 931 bp in length
*    47064    47163: gap of 100 bp
*    47164    48113: contig of 950 bp in length
*    48114    48213: gap of 100 bp
*    48214    49162: contig of 949 bp in length
*    49163    49262: gap of 100 bp
*    49263    50166: contig of 904 bp in length
*    50167    50266: gap of 100 bp
*    50267    51189: contig of 923 bp in length
*    51190    51289: gap of 100 bp
*    51290    52212: contig of 923 bp in length
*    52213    52312: gap of 100 bp
*    52313    53209: contig of 897 bp in length
*    53210    53309: gap of 100 bp
*    53310    54254: contig of 945 bp in length
*    54255    54354: gap of 100 bp
*    54355    55298: contig of 944 bp in length
*    55299    55398: gap of 100 bp
*    55399    56307: contig of 909 bp in length
*    56308    56407: gap of 100 bp
*    56408    57325: contig of 918 bp in length
*    57326    57425: gap of 100 bp
*    57426    58366: contig of 941 bp in length
*    58367    58466: gap of 100 bp
*    58467    59390: contig of 924 bp in length
*    59391    59490: gap of 100 bp
*    59491    60416: contig of 926 bp in length
*    60417    60516: gap of 100 bp
*    60517    61462: contig of 946 bp in length
*    61463    61562: gap of 100 bp
*    61563    62510: contig of 948 bp in length
*    62511    62610: gap of 100 bp
*    62611    63538: contig of 928 bp in length
*    63539    63638: gap of 100 bp
*    63639    64574: contig of 936 bp in length
*    64575    64674: gap of 100 bp
*    64675    65613: contig of 939 bp in length
*    65614    65713: gap of 100 bp
*    65714    66625: contig of 912 bp in length
*    66626    66725: gap of 100 bp
*    66726    67636: contig of 911 bp in length
*    67637    67736: gap of 100 bp
*    67737    68689: contig of 953 bp in length
*    68690    68789: gap of 100 bp
*    68790    69734: contig of 945 bp in length
*    69735    69834: gap of 100 bp
*    69835    70735: contig of 901 bp in length
*    70736    70835: gap of 100 bp
*    70836    71771: contig of 936 bp in length
*    71772    71871: gap of 100 bp
*    71872    72819: contig of 948 bp in length
*    72820    72919: gap of 100 bp
*    72920    73902: contig of 983 bp in length
*    73903    74002: gap of 100 bp

Alignment Scores:
Pred. No.:              1.18e+03        Length:         175178
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC011783 (1-175178)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db      25971 ACAGTAAGTTTCAATTTGGGAGAA 25994

RESULT 32
AL606919/c
LOCUS       AL606919              187816 bp    DNA     linear   ROD 24-JUL-2002
DEFINITION  Mouse DNA sequence from clone RP23-264F10 on chromosome 4, complete
            sequence.
ACCESSION   AL606919
VERSION     AL606919.12  GI:21732059
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 187816)
  AUTHORS   Kimberley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Jul 11, 2002 this sequence version replaced gi:21694380.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
```

```
           http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-264F10 is
           from the RPCI-23 Mouse PAC Library
           constructed by the group of Pieter de Jong.
           For further details see http://www.chori.org/bacpac/home.htm
           VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .187816
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="4"
                     /clone="RP23-264F10"
                     /clone_lib="RPCI-23"
ORIGIN

Alignment Scores:
Pred. No.:              1.25e+03        Length:         187816
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     9               Gaps:           0

US-10-758-902-1 (1-30) x AL606919 (1-187816)

Qy          9 GlyGluAlaTyrGluTyrProThr 16
              |||||||||||||||||||||||
Db     112126 GGAGAGGCCTATGAATATCCTACA 112103

RESULT 33
AC147190/c
LOCUS       AC147190              189341 bp    DNA     linear   HTG 06-NOV-2003
DEFINITION  Otolemur garnettii clone CH256-377C7, WORKING DRAFT SEQUENCE, 11
           unordered pieces.
ACCESSION   AC147190
VERSION     AC147190.1  GI:38194237
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Otolemur garnettii (small-eared galago)
  ORGANISM  Otolemur garnettii
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirhini;
           Galagonidae; Otolemur.
REFERENCE   1  (bases 1 to 189341)
  AUTHORS   Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W.,
           Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,B.,
           Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
           Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R.,
           Karlins,E., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,
           Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C.,
           Maskeri,B., McDowell,J., Mullikin,J.C., Paguirigan,C., Pearson,R.,
           Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schandler,K.,
           Schueler,M.G., Shah,K., Sison,C., Stantripop,S., Thomas,J.W.,
           Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Young,A. and
           Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 189341)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-NOV-2003) NIH Intramural Sequencing Center, 8717
           Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     -------------- Genome Center
               Center: NIH Intramural Sequencing Center
               Center code: NISC
               Web site: http://www.nisc.nih.gov
               Contact: nisc_zoo@nhgri.nih.gov
            -------------- Project Information
               Center project name: foi
               Center clone name: 377C07
            -------------- Summary Statistics
               Sequencing vector: plasmid; n/a; 100% of reads
               Chemistry: Dye-terminator Big Dye; 100% of reads
               Assembly program: Phrap; version 0.990319
               Consensus quality: 184548 bases at least Q40
               Consensus quality: 185704 bases at least Q30
               Consensus quality: 186398 bases at least Q20
               Insert size: 193000; agarose-fp
               Insert size: 188341; sum-of-contigs
               Quality coverage: 12.42x in Q20 bases; agarose-fp
               Quality coverage: 12.73x in Q20 bases; sum-of-contigs
            --------------.
           * NOTE: This is a 'working draft' sequence. It currently
           * consists of 11 contigs. The true order of the pieces
           * is not known and their order in this sequence record is
           * arbitrary. Gaps between the contigs are represented as
           * runs of N, but the exact sizes of the gaps are unknown.
           * This record will be updated with the finished sequence
           * as soon as it is available and the accession number will
           * be preserved.
           *        1     2871: contig of 2871 bp in length
           *     2872     2971: gap of unknown length
           *     2972     7216: contig of 4245 bp in length
           *     7217     7316: gap of unknown length
           *     7317    14840: contig of 7524 bp in length
           *    14841    14940: gap of unknown length
           *    14941    23859: contig of 8919 bp in length
           *    23860    23959: gap of unknown length
           *    23960    34086: contig of 10127 bp in length
           *    34087    34186: gap of unknown length
           *    34187    46613: contig of 12427 bp in length
           *    46614    46713: gap of unknown length
           *    46714    56962: contig of 10249 bp in length
           *    56963    57062: gap of unknown length
           *    57063    82049: contig of 24987 bp in length
           *    82050    82149: gap of unknown length
           *    82150   119736: contig of 37587 bp in length
           *   119737   119836: gap of unknown length
           *   119837   153645: contig of 33809 bp in length
           *   153646   153745: gap of unknown length
           *   153746   189341: contig of 35596 bp in length.
FEATURES             Location/Qualifiers
     source          1. .189341
                     /organism="Otolemur garnettii"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:30611"
                     /clone="CH256-377C7"
                     /clone_lib="CH256"
     misc_feature    1. .2871
                     /note="assembly_fragment"
     gap             2872. .2971
                     /estimated_length=unknown
     misc_feature    2972. .7216
                     /note="assembly_fragment"
     gap             7217. .7316
                     /estimated_length=unknown
     misc_feature    7317. .14840
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:right"
     gap             14841. .14940
                     /estimated_length=unknown
     misc_feature    14941. .23859
                     /note="assembly_fragment"
     gap             23860. .23959
                     /estimated_length=unknown
     misc_feature    23960. .34086
                     /note="assembly_fragment"
     gap             34087. .34186
                     /estimated_length=unknown
     misc_feature    34187. .46613
                     /note="assembly_fragment"
     gap             46614. .46713
                     /estimated_length=unknown
     misc_feature    46714. .56962
                     /note="assembly_fragment"
     gap             56963. .57062
```

```
                     /estimated_length=unknown
     misc_feature    57063. .82049
                     /note="assembly_fragment"
     gap             82050. .82149
                     /estimated_length=unknown
     misc_feature    82150. .119736
                     /note="assembly_fragment"
     gap             119737. .119836
                     /estimated_length=unknown
     misc_feature    119837. .153645
                     /note="assembly_fragment"
     gap             153646. .153745
                     /estimated_length=unknown
     misc_feature    153746. .189341
                     /note="assembly_fragment"
ORIGIN

Alignment Scores:
Pred. No.:              1.26e+03        Length:         189341
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC147190 (1-189341)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db      91657 ACAGTTTCTTTCAACTTGGGGGAA 91634

RESULT 34
AL691424
LOCUS       AL691424               194520 bp    DNA     linear   ROD 26-JUL-2002
DEFINITION  Mouse DNA sequence from clone RP23-219K12 on chromosome X, complete
            sequence.
ACCESSION   AL691424
VERSION     AL691424.7  GI:22002699
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 194520)
  AUTHORS   Wray,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Jul 29, 2002 this sequence version replaced gi:21912679.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            --------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-219K12 is
            from the RPCI-23 Mouse PAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .194520
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="X"
                     /clone="RP23-219K12"
                     /clone_lib="RPCI-23"
ORIGIN

Alignment Scores:
Pred. No.:              1.29e+03        Length:         194520
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     9               Gaps:           0

US-10-758-902-1 (1-30) x AL691424 (1-194520)

Qy         20 AspLeuArgAsnGluLeuAlaLys 27
              |||||||||||||||||||||||
Db      83174 GATTTAAGGAATGAATTAGCAAAA 83197

RESULT 35
AC108508/c
LOCUS       AC108508               196162 bp    DNA     linear   ROD 04-SEP-2002
DEFINITION  Genomic sequence for Mus musculus, clone RP23-437O14, complete
            sequence.
ACCESSION   AC108508
VERSION     AC108508.2  GI:22711548
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 196162)
  AUTHORS   McCombie,W.R., de la Bastide,M., Spiegel,L., Preston,R.,
            Nascimento,L., Zutavern,T., Balija,V., Bell,M., Miller,B.,
            Katzenberger,F., Muller,S., Sullivan,P., Yang,C., Dike,S.,
            Palmer,L., O'Shaughnessy,A. and Dedhia,N.
  TITLE     Genomic sequence for Mus musculus, clone RP23-437O14, complete
            sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 196162)
  AUTHORS   McCombie,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-2002) Lita Annenberg Hazen Genome Sequencing
            Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
            Harbor, NY 11724, USA
REFERENCE   3  (bases 1 to 196162)
  AUTHORS   McCombie,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-SEP-2002) Lita Annenberg Hazen Genome Sequencing
            Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
            Harbor, NY 11724, USA
COMMENT     On Sep 4, 2002 this sequence version replaced gi:18425264.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest.
FEATURES             Location/Qualifiers
     source          1. .196162
```

```
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="RP23-437O14"
                     /clone_lib="RPCI-23"
     misc_feature    52396. .52410
                     /note="The sequence is covered by a single high quality
                     subclone which was sequenced with dye terminator
                     chemistry."
     misc_feature    61550. .61757
                     /note="The sequence is a polynucleotide repeat (TCTGCC) in
                     which the exact number of repeat copies is unknown.  The
                     assembly shows one fewer repeat copy than subclones in the
                     overlapping assembly of clone RP23-17D4 (AC108507)."
     misc_feature    77974. .77997
                     /note="The sequence is a polynucleotide repeat (CCCAGT) in
                     which the exact number of repeat copies is unknown.  One
                     subclone in the region shows one fewer repeat copy than
                     that represented by the assembly."
     misc_feature    100488. .100600
                     /note="We believe the assembly to be correct.  The
                     sequence is covered solely by a PCR product which was
                     generated with  a high fidelity polymerase.  The PCR
                     product was subcloned before sequencing.  The sequence is
                     high quality."
     misc_feature    complement(100756)
                     /note="We believe the assembly to be correct.  The base at
                     this position is called as a G, however, there is a strong
                     A peak underneath the G in both the sequence from a
                     subclone and sequences generated by PCR.  Further
                     sequencing is underway to resolve this ambiguity."
     misc_feature    complement(124655. .124699)
                     /note="The sequence is covered by a single high quality
                     subclone which was sequenced with dye terminator
                     chemistry."
ORIGIN

Alignment Scores:
Pred. No.:              1.29e+03        Length:         196162
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     9               Gaps:           0

US-10-758-902-1 (1-30) x AC108508 (1-196162)

Qy          9 GlyGluAlaTyrGluTyrProThr 16
              |||||||||||||||||||||||
Db      47791 GGAGAGGCCTATGAATATCCTACA 47768

RESULT 36
AC147189
LOCUS       AC147189               206806 bp    DNA     linear   HTG 06-NOV-2003
DEFINITION  Otolemur garnettii clone CH256-218O12, WORKING DRAFT SEQUENCE, 9
            unordered pieces.
ACCESSION   AC147189
VERSION     AC147189.1  GI:38194236
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Otolemur garnettii (small-eared galago)
  ORGANISM  Otolemur garnettii
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirhini;
            Galagonidae; Otolemur.
REFERENCE   1  (bases 1 to 206806)
  AUTHORS   Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W.,
            Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,B.,
            Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R.,
            Karlins,E., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,
            Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C.,
            Maskeri,B., McDowell,J., Mullikin,J.C., Paguirigan,C., Pearson,R.,
            Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schandler,K.,
            Schueler,M.G., Shah,K., Sison,C., Stantripop,S., Thomas,J.W.,
            Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Young,A. and
            Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 206806)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-NOV-2003) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     -------------- Genome Center
                Center: NIH Intramural Sequencing Center
                Center code: NISC
                Web site: http://www.nisc.nih.gov
                Contact: nisc_zoo@nhgri.nih.gov
            -------------- Project Information
                Center project name: foh
                Center clone name: 218O12
            -------------- Summary Statistics
                Sequencing vector: plasmid; n/a; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.990319
                Consensus quality: 202414 bases at least Q40
                Consensus quality: 203175 bases at least Q30
                Consensus quality: 203746 bases at least Q20
                Insert size: 238000; agarose-fp
                Insert size: 206006; sum-of-contigs
                Quality coverage: 14.34x in Q20 bases; agarose-fp
                Quality coverage: 16.57x in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 9 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    12387: contig of 12387 bp in length
            *    12388    12487: gap of unknown length
            *    12488    23839: contig of 11352 bp in length
            *    23840    23939: gap of unknown length
            *    23940    33203: contig of 9264 bp in length
            *    33204    33303: gap of unknown length
            *    33304    55864: contig of 22561 bp in length
            *    55865    55964: gap of unknown length
            *    55965    83581: contig of 27617 bp in length
            *    83582    83681: gap of unknown length
            *    83682   114622: contig of 30941 bp in length
            *   114623   114722: gap of unknown length
            *   114723   143060: contig of 28338 bp in length
            *   143061   143160: gap of unknown length
            *   143161   172331: contig of 29171 bp in length
            *   172332   172431: gap of unknown length
            *   172432   206806: contig of 34375 bp in length.
FEATURES             Location/Qualifiers
     source          1. .206806
                     /organism="Otolemur garnettii"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:30611"
                     /clone="CH256-218O12"
                     /clone_lib="CH256"
     misc_feature    1. .12387
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
     gap             12388. .12487
                     /estimated_length=unknown
     misc_feature    12488. .23839
                     /note="assembly_fragment"
     gap             23840. .23939
                     /estimated_length=unknown
     misc_feature    23940. .33203
```

```
                     /note="assembly_fragment"
     gap             33204. .33303
                     /estimated_length=unknown
     misc_feature    33304. .55864
                     /note="assembly_fragment"
     gap             55865. .55964
                     /estimated_length=unknown
     misc_feature    55965. .83581
                     /note="assembly_fragment"
     gap             83582. .83681
                     /estimated_length=unknown
     misc_feature    83682. .114622
                     /note="assembly_fragment"
     gap             114623. .114722
                     /estimated_length=unknown
     misc_feature    114723. .143060
                     /note="assembly_fragment"
     gap             143061. .143160
                     /estimated_length=unknown
     misc_feature    143161. .172331
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
     gap             172332. .172431
                     /estimated_length=unknown
     misc_feature    172432. .206806
                     /note="assembly_fragment"
ORIGIN

Alignment Scores:
Pred. No.:              1.35e+03        Length:         206806
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC147189 (1-206806)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db     152164 ACAGTTTCTTTCAACTTGGGGGAA 152187

RESULT 37
AC108507/c
LOCUS       AC108507               207845 bp    DNA     linear   HTG 30-JAN-2002
DEFINITION  Mus musculus clone RP23-17D4, WORKING DRAFT SEQUENCE, 10 unordered
            pieces.
ACCESSION   AC108507
VERSION     AC108507.1  GI:18425263
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 207845)
  AUTHORS   McCombie,W.R., Baker,J.P., Balija,V., Dedhia,N.N., de la
            Bastide,M., Katzenberger,F., Kuit,K., King,L., Kirchoff,K.A.,
            Miller,B., Muller,S., Nascimento,L.U., O'Shaughnessy,A.L.,
            Preston,R.R., Santos,L., Spiegel,L.A., Palmer,L., Yang,C. and
            Zutavern,T.
  TITLE     Mouse Genomic Sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 207845)
  AUTHORS   McCombie,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-2002) Lita Annenberg Hazen Genome Sequencing
            Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
            Harbor, NY 11724, USA
COMMENT     -------------- Genome Center -------------
            Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
            Laboratory
            Center code: CSHL
            Web site: http://www.cshl.org/genseq
            Contact:  mccombie@cshl.org
            ------------------ Project Information
            Project name: RP23-17D4
            Clone name: RP23-17D4
            Insert size: 0; agarose-fp
            Insert size: 218440; sum-of-contigs
            Quality coverage: 0.00 in Q20 bases; agarose-fp
            Quality coverage: 7.30 in Q20 bases; sum-of-contigs
            ----------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 10 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    44789: contig of 44789 bp in length
            *    44790    45521: gap of unknown length
            *    45522    85357: contig of 39836 bp in length
            *    85358    86089: gap of unknown length
            *    86090   118131: contig of 32042 bp in length
            *   118132   118863: gap of unknown length
            *   118864   142049: contig of 23186 bp in length
            *   142050   142781: gap of unknown length
            *   142782   162938: contig of 20157 bp in length
            *   162939   163670: gap of unknown length
            *   163671   178962: contig of 15292 bp in length
            *   178963   179694: gap of unknown length
            *   179695   194610: contig of 14916 bp in length
            *   194611   195342: gap of unknown length
            *   195343   201829: contig of 6487 bp in length
            *   201830   202560: gap of unknown length
            *   202561   206954: contig of 4394 bp in length
            *   206955   207685: gap of unknown length
            *   207686   207845: contig of 160 bp in length.
FEATURES             Location/Qualifiers
     source          1. .207845
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="RP23-17D4"
     gap             44790. .45521
                     /estimated_length=unknown
     gap             85358. .86089
                     /estimated_length=unknown
     gap             118132. .118863
                     /estimated_length=unknown
     gap             142050. .142781
                     /estimated_length=unknown
     gap             162939. .163670
                     /estimated_length=unknown
     gap             178963. .179694
                     /estimated_length=unknown
     gap             194611. .195342
                     /estimated_length=unknown
     gap             201830. .202560
                     /estimated_length=unknown
     gap             206955. .207685
                     /estimated_length=unknown
ORIGIN

Alignment Scores:
Pred. No.:              1.36e+03        Length:         207845
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC108507 (1-207845)
```

```
Qy          9 GlyGluAlaTyrGluTyrProThr 16
              ||||||||||||||||||||||||
Db      93188 GGAGAGGCCTATGAATATCCTACA 93165

RESULT 38
AC134261
LOCUS       AC134261               230706 bp    DNA     linear   HTG 13-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-2B20, *** SEQUENCING IN PROGRESS ***.
ACCESSION   AC134261
VERSION     AC134261.2  GI:24941385
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 230706)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
            Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
            Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
            Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
            Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
            Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
            Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
            Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
            Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
            Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
            Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
            Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
            Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
            Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
            Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
            Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
            Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
            Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
            Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
            Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
            Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
            Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
            Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
            Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
            Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
            Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
            Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
            Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
            Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
            Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
            Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
            Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
            Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
            Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
            Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 230706)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-SEP-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 230706)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 13, 2002 this sequence version replaced gi:23307915.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: TUPV
                Center clone name: CH230-2B20
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 225288 bases at least Q40
                Consensus quality: 226863 bases at least Q30
                Consensus quality: 227872 bases at least Q20
                Estimated insert size: 232162; sum-of-contigs estimation
                Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1   230706: contig of 230706 bp in length.
FEATURES             Location/Qualifiers
     source          1. .230706
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-2B20"
     misc_feature    1. .2209
                     /note="wgs_contig"
     misc_feature    complement(226600. .227492)
                     /note="clone_boundary
                     clone_end:T7
                     site:
                     end_sequence:BH262081"
ORIGIN

Alignment Scores:
Pred. No.:              1.48e+03        Length:         230706
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC134261 (1-230706)

Qy          2 AsnThrValSerPheAsnLeuGly 9
              |||||||||||||||||||||||
Db     130017 AACACTGTTAGCTTCAATTTGGGA 130040

RESULT 39
AC131516
LOCUS       AC131516               258088 bp    DNA     linear   HTG 13-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-2B8, WORKING DRAFT SEQUENCE, 8
```

```
          unordered pieces.
ACCESSION AC131516
VERSION   AC131516.3  GI:24941472
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE    Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1  (bases 1 to 258088)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
            Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
            Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
            Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
            Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
            Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
            Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
            Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
            Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
            Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
            Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
            Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
            Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
            Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
            Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
            Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
            Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
            Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
            Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
            Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
            Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
            Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
            Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
            Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
            Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
            Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
            Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
            Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
            Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
            Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
            Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
            Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
            Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
            Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
            Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE 2  (bases 1 to 258088)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3  (bases 1 to 258088)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT   On Nov 13, 2002 this sequence version replaced gi:23195704.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: TUMY
                Center clone name: CH230-2B8
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 206635 bases at least Q40
                Consensus quality: 210014 bases at least Q30
                Consensus quality: 212312 bases at least Q20
                Estimated insert size: 209596; sum-of-contigs estimation
                Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *         1     5175: contig of 5175 bp in length
            *      5176     5275: gap of unknown length
            *      5276   104600: contig of 99325 bp in length
            *    104601   104700: gap of unknown length
            *    104701   167710: contig of 63010 bp in length
            *    167711   167810: gap of unknown length
            *    167811   175267: contig of 7457 bp in length
            *    175268   175367: gap of unknown length
            *    175368   254058: contig of 78691 bp in length
            *    254059   254158: gap of unknown length
            *    254159   255365: contig of 1207 bp in length
            *    255366   255465: gap of unknown length
            *    255466   256469: contig of 1004 bp in length
            *    256470   256569: gap of unknown length
            *    256570   258088: contig of 1519 bp in length.
FEATURES             Location/Qualifiers
     source          1. .258088
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-2B8"
     misc_feature    1. .1539
                     /note="wgs_contig"
     gap             5176. .5275
                     /estimated_length=unknown
     misc_feature    5276. .6357
                     /note="wgs_contig"
     gap             104601. .104700
                     /estimated_length=unknown
     misc_feature    116705. .117734
                     /note="wgs_contig"
     gap             167711. .167810
                     /estimated_length=unknown
     gap             175268. .175367
                     /estimated_length=unknown
     gap             254059. .254158
                     /estimated_length=unknown
     gap             255366. .255465
                     /estimated_length=unknown
     gap             256470. .256569
                     /estimated_length=unknown
ORIGIN
```

```
Alignment Scores:
Pred. No.:              1.62e+03        Length:         258088
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC131516 (1-258088)

Qy         22 ArgAsnGluLeuAlaLysGlyThr 29
              ||||||||||||||||||||||||
Db     249763 CGAAATGAGTTGGCGAAAGGAACG 249786

RESULT 40
AC129451
LOCUS       AC129451               265438 bp    DNA     linear   HTG 21-SEP-2002
DEFINITION  Rattus norvegicus clone CH230-10H11, *** SEQUENCING IN PROGRESS
            ***, 3 unordered pieces.
ACCESSION   AC129451
VERSION     AC129451.3  GI:23264589
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 265438)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 265438)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUL-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 265438)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-SEP-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Sep 21, 2002 this sequence version replaced gi:22038433.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequening reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/).  As a result, the
            sequence may extend beyond the ends of the clone and there may be
            contigs that consist entirely of whole genome shotgun sequence
            reads.  Both end sequences and whole genome shotgun sequence only
            contigs will be indicated in the feature table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GDLZ
                Center clone name: CH230-10H11
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 235205 bases at least Q40
                Consensus quality: 238457 bases at least Q30
                Consensus quality: 240684 bases at least Q20
                Estimated insert size: 262648; sum-of-contigs estimation
                Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
            * NOTE: This sequence may represent more than one clone.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1   262765: contig of 262765 bp in length
            *  262766   262865: gap of unknown length
            *  262866   264219: contig of 1354 bp in length
            *  264220   264319: gap of unknown length
            *  264320   265438: contig of 1119 bp in length.
FEATURES             Location/Qualifiers
     source          1. .265438
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-10H11"
     misc_feature    complement(1814. .85887)
                     /note="clone_boundary
                     clone_end:T7
                     site:EcoRI
                     end_sequence:BH305634"
     misc_feature    complement(258984. .259817)
                     /note="clone_boundary
                     clone_end:Sp6
                     site:EcoRI
```

```
                     end_sequence:BH305636"
     gap             262766. .262865
                     /estimated_length=unknown
     gap             264220. .264319
                     /estimated_length=unknown
ORIGIN

Alignment Scores:
Pred. No.:              1.66e+03        Length:         265438
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-1 (1-30) x AC129451 (1-265438)

Qy         14 TyrProThrPheIleGlnAspLeu 21
              |||||||||||||||||||||||
Db      73643 TACCCCACCTTCATCCAAGATCTC 73666


Search completed: February 20, 2006, 03:05:37
Job time : 1334.56 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:48:17 ; Search time 124.693 Seconds
(without alignments)
1603.468 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 30
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9989042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160831_4002/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US10758902_@CGN_1_1_1359_@runat_17022006_160831_4002 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	70.0	65	2	AAV81465	Aav81465 Ribosome-
2	14	46.7	363	2	AAV81468	Aav81468 Ribosome-
3	8	26.7	1238	4	AAF31245	Aaf31245 Human imm
4	8	26.7	2143	12	ADP07317	Adp07317 Human WT1
5	8	26.7	2291	12	ADQ67284	Adq67284 Novel hum
6	8	26.7	2772	10	ADE54051	Ade54051 Human pro
7	7	23.3	23	2	AAV81463	Aav81463 PCR prime
c 8	7	23.3	23	2	AAV81464	Aav81464 PCR prime
9	7	23.3	25	2	AAV81466	Aav81466 PCR prime
c 10	7	23.3	431	5	ABV18359	Abv18359 Human pro
11	7	23.3	439	3	ABQ62599	Abq62599 Mycobacte
c 12	7	23.3	471	12	ADP95365	Adp95365 Cotton ex
c 13	7	23.3	472	4	AAS35302	Aas35302 Human car
c 14	7	23.3	472	10	ADE45381	Ade45381 Human car
c 15	7	23.3	472	13	ADJ06799	Adj06799 Human car
c 16	7	23.3	484	13	ADT06364	Adt06364 Nicotiana
c 17	7	23.3	498	5	ABV48145	Abv48145 Human pro
c 18	7	23.3	543	6	ABQ92793	Abq92793 Triticum
c 19	7	23.3	555	9	ACH38914	Ach38914 Human foe
c 20	7	23.3	562	14	ACL61717	Acl61717 Human col
21	7	23.3	588	5	ABV55005	Abv55005 Human pro
22	7	23.3	588	6	ABK77612	Abk77612 Bacillus
23	7	23.3	651	10	ADH82120	Adh82120 Enterococ
24	7	23.3	693	6	ABK77619	Abk77619 Bacillus
25	7	23.3	731	3	AAA27409	Aaa27409 Soybean g
c 26	7	23.3	1024	10	ABZ83251	Abz83251 Toxicolog
c 27	7	23.3	1146	2	AAQ86989	Aaq86989 Creatine-
c 28	7	23.3	1167	8	ACA49107	Aca49107 Prokaryot
c 29	7	23.3	1355	13	ACN39756	Acn39756 Tumour-as
c 30	7	23.3	1360	6	ABL62370	Abl62370 Colon ade
c 31	7	23.3	1360	6	ABN95771	Abn95771 Gene #226
c 32	7	23.3	1376	2	AAQ51619	Aaq51619 Human cre
33	7	23.3	1390	6	ABQ54381	Abq54381 Human ova
c 34	7	23.3	1431	14	ADZ48855	Adz48855 Insulin s
c 35	7	23.3	1431	14	AEA81138	Aea81138 Human cre
c 36	7	23.3	1432	12	ADP10454	Adp10454 Reference
c 37	7	23.3	1432	13	ADR14270	Adr14270 Human NF-
c 38	7	23.3	1432	14	ADX07813	Adx07813 Cyclin-de
c 39	7	23.3	1432	14	ADZ22658	Adz22658 Creatine
c 40	7	23.3	1432	14	AEA04437	Aea04437 Human cDN
c 41	7	23.3	1539	8	ACA51659	Aca51659 Prokaryot
42	7	23.3	1554	6	ABQ70468	Abq70468 Listeria
c 43	7	23.3	1659	4	AAS56326	Aas56326 Salmonell
44	7	23.3	1818	13	ADT44156	Adt44156 Bacterial
45	7	23.3	1897	11	ADM76429	Adm76429 cDNA sequ
c 46	7	23.3	1912	3	AAA39806	Aaa39806 C. versic
c 47	7	23.3	1917	3	AAA39805	Aaa39805 C. versic
c 48	7	23.3	2169	3	AAA39804	Aaa39804 C. versic
c 49	7	23.3	2343	2	AAX99989	Aax99989 Creatine
50	7	23.3	2746	2	AAQ07044	Aaq07044 Gene enco
51	7	23.3	2777	14	ADY66017	Ady66017 S. manson
c 52	7	23.3	3016	11	ADI30933	Adi30933 Human cDN
c 53	7	23.3	3016	13	ADS83000	Ads83000 Human lym
c 54	7	23.3	3224	3	AAA39803	Aaa39803 C. versic
55	7	23.3	3225	2	AAT47238	Aat47238 FIV env g
56	7	23.3	3225	2	AAT49091	Aat49091 Feline im
57	7	23.3	3225	2	AAT78402	Aat78402 Feline im
58	7	23.3	3225	2	AAT62514	Aat62514 FIV envel
59	7	23.3	4962	4	ABL19052	Abl19052 Drosophil
60	7	23.3	4995	4	ABL19050	Abl19050 Drosophil
61	7	23.3	5862	4	AAL04675	Aal04675 Human rep
62	7	23.3	5862	4	ABL97582	Abl97582 Human tes
c 63	7	23.3	7893	2	AAX13165	Aax13165 Enterococ
c 64	7	23.3	7893	6	ABS98960	Abs98960 Enterococ
65	7	23.3	9471	2	AAV57356	Aav57356 FIV-NCSU1
66	7	23.3	9474	2	AAV57355	Aav57355 FIV-NCSU1
67	7	23.3	9804	4	ABL19048	Abl19048 Drosophil
c 68	7	23.3	10475	1	AAN80643	Aan80643 Sequence
c 69	7	23.3	10475	1	AAN80616	Aan80616 Genomic c
c 70	7	23.3	10476	6	ABL67518	Abl67518 Thyroid c
c 71	7	23.3	10476	6	ABL67064	Abl67064 Thyroid c
c 72	7	23.3	10968	2	AAV17789	Aav17789 Tomato Pr
73	7	23.3	32249	4	AAL04676	Aal04676 Human rep
74	7	23.3	32249	4	ABL97583	Abl97583 Human tes
c 75	7	23.3	35871	4	AAK84974	Aak84974 Human imm
c 76	7	23.3	38504	12	ADQ59185	Adq59185 MSI-H car
77	7	23.3	83432	14	AEA61124_3	Continuation (4 of

c 78	7	23.3	96596	10	ADC85287	Adc85287 Mouse Fis
c 79	7	23.3	96597	9	ADA02807	Ada02807 Mouse Fis
c 80	7	23.3	96597	10	ADB72545	Adb72545 Mouse Fis
c 81	7	23.3	96597	12	ADM74402	Adm74402 Murine ca
82	7	23.3	110000	6	ABA90521_01	Continuation (2 of
83	7	23.3	110000	14	AEB39174_07	Continuation (8 of
c 84	7	23.3	110000	14	AEB42737_11	Continuation (12 o
c 85	7	23.3	110000	14	AEB42737_12	Continuation (13 o
c 86	6	20.0	24	8	AAL54377	Aal54377 Neuronal
c 87	6	20.0	29	12	ADF77091	Adf77091 Insertion
c 88	6	20.0	34	9	ADA14256	Ada14256 Plasmodiu
89	6	20.0	50	6	ABZ07475	Abz07475 Human leu
c 90	6	20.0	55	10	ADL02062	Adl02062 ATFalpha
91	6	20.0	60	6	ABN42756	Abn42756 Human spl
92	6	20.0	60	6	ABN50358	Abn50358 Human spl
c 93	6	20.0	60	14	ADW19712	Adw19712 Pinus rad
94	6	20.0	70	5	AAC92421	Aac92421 Transcrip
95	6	20.0	70	5	AAC92408	Aac92408 Oligonucl
96	6	20.0	93	3	AAC14699	Aac14699 Human sec
97	6	20.0	96	10	ADL01976	Adl01976 ATFalpha
98	6	20.0	96	10	ADL02003	Adl02003 Coiled-co
c 99	6	20.0	105	2	AAT07015	Aat07015 Immunogen
c 100	6	20.0	105	6	ABA82868	Aba82868 Human pro
101	6	20.0	123	14	ADW83699	Adw83699 MAP3K9 ma
c 102	6	20.0	129	6	ABA82870	Aba82870 Human pro
c 103	6	20.0	138	11	ADL66779	Adl66779 Shg prote
104	6	20.0	139	3	AAC23679	Aac23679 Human sec
105	6	20.0	147	3	AAC09141	Aac09141 Human sec
c 106	6	20.0	183	4	AAI52710	Aai52710 Probe #21
c 107	6	20.0	183	4	AAK46872	Aak46872 Human bon
c 108	6	20.0	183	4	AAK20726	Aak20726 Human bra
c 109	6	20.0	183	4	ABS46641	Abs46641 Human liv
c 110	6	20.0	196	10	ABX61370	Abx61370 Arabidops
c 111	6	20.0	198	6	ABN22281	Abn22281 Human ORF
c 112	6	20.0	201	13	ADS36981	Ads36981 Human aut
113	6	20.0	210	8	ACA13098	Aca13098 Prokaryot
c 114	6	20.0	217	12	ADL88106	Adl88106 DNA up-re
c 115	6	20.0	217	12	ADL88105	Adl88105 DNA up-re
116	6	20.0	224	12	ADJ62827	Adj62827 Corn even
117	6	20.0	253	10	ADC75343	Adc75343 T harzian
118	6	20.0	256	12	ADH00302	Adh00302 Kidney di
c 119	6	20.0	258	3	AAC22129	Aac22129 Human sec
120	6	20.0	265	13	ADX29612	Adx29612 Plant ful
c 121	6	20.0	269	2	AAV87922	Aav87922 EST clone
c 122	6	20.0	270	4	AAK53464	Aak53464 Murine tr
c 123	6	20.0	285	6	ABL72594	Abl72594 Corn tass
c 124	6	20.0	286	4	ABA71138	Aba71138 Human foe
c 125	6	20.0	286	4	AAK45415	Aak45415 Human bon
c 126	6	20.0	286	4	AAK19429	Aak19429 Human bra
c 127	6	20.0	286	4	ABS45097	Abs45097 Human liv
c 128	6	20.0	286	6	ABS19679	Abs19679 Human gen
c 129	6	20.0	288	9	ADB06417	Adb06417 Alloiococ
130	6	20.0	291	5	AAF94405	Aaf94405 Haemophil
131	6	20.0	291	6	ABK64969	Abk64969 DNA encod
c 132	6	20.0	293	2	AAQ61122	Aaq61122 Human bra
c 133	6	20.0	293	12	ADJ10982	Adj10982 Recombina
c 134	6	20.0	297	14	ACL61260	Acl61260 Human col
c 135	6	20.0	306	12	ADJ10702	Adj10702 Recombina
136	6	20.0	308	3	AAC17859	Aac17859 Human sec
137	6	20.0	314	4	AAF92335	Aaf92335 Bovine ma
138	6	20.0	332	3	AAZ61688	Aaz61688 cDNA enco
139	6	20.0	332	4	AAC99621	Aac99621 Skin cell
140	6	20.0	332	6	ABL34773	Abl34773 Murine cD
c 141	6	20.0	333	4	AAL01392	Aal01392 Human rep
c 142	6	20.0	333	4	ABL96845	Abl96845 Human tes
143	6	20.0	347	6	ABZ15660	Abz15660 Arabidops
144	6	20.0	350	9	ACH23631	Ach23631 Human adu
145	6	20.0	355	5	ABV46957	Abv46957 Human pro
c 146	6	20.0	357	4	AAK59908	Aak59908 Human imm
c 147	6	20.0	360	9	ACH42906	Ach42906 Human foe
148	6	20.0	361	4	AAS37029	Aas37029 Novel hum
c 149	6	20.0	365	9	ACH42943	Ach42943 Human foe
c 150	6	20.0	367	4	AAI23117	Aai23117 Probe #13
c 151	6	20.0	367	4	ABA68209	Aba68209 Human foe
c 152	6	20.0	367	4	AAI48424	Aai48424 Probe #17
c 153	6	20.0	367	4	ABA50269	Aba50269 Human bre
c 154	6	20.0	367	4	ABA35221	Aba35221 Probe #13
c 155	6	20.0	367	4	AAK42345	Aak42345 Human bon
c 156	6	20.0	367	4	AAK16591	Aak16591 Human bra
c 157	6	20.0	367	4	ABS41954	Abs41954 Human liv
c 158	6	20.0	367	5	AAI08771	Aai08771 Probe #87
c 159	6	20.0	367	6	ABS16401	Abs16401 Human gen
c 160	6	20.0	371	4	AAI93359	Aai93359 Human pol
c 161	6	20.0	372	8	ABX53707	Abx53707 Bovine ES
162	6	20.0	376	13	ADX64911	Adx64911 Plant ful
163	6	20.0	377	4	AAL10485	Aal10485 Human bre
c 164	6	20.0	378	6	ABN16790	Abn16790 Human ORF
165	6	20.0	382	4	AAK66689	Aak66689 Human imm
166	6	20.0	384	5	ABV17162	Abv17162 Human pro
167	6	20.0	385	10	ADF81076	Adf81076 Leukaemia
168	6	20.0	389	5	AAF66881	Aaf66881 Novel hum
c 169	6	20.0	390	5	AAH65089	Aah65089 C glutami
c 170	6	20.0	394	6	ABV94324	Abv94324 Breast ca
171	6	20.0	402	8	ACF73130	Acf73130 Staphyloc
c 172	6	20.0	402	10	ACF69030	Acf69030 Photorhab
c 173	6	20.0	403	8	ABX46573	Abx46573 Bovine ES
174	6	20.0	404	4	AAI92518	Aai92518 Human pol
175	6	20.0	404	6	ABN22802	Abn22802 Human ORF
c 176	6	20.0	404	9	ACH18877	Ach18877 Human adu
c 177	6	20.0	408	5	AAS33882	Aas33882 Human cDN
c 178	6	20.0	412	8	ABX39490	Abx39490 Bovine ES
179	6	20.0	413	4	ABA53793	Aba53793 Human foe
180	6	20.0	413	4	AAI33427	Aai33427 Probe #21
181	6	20.0	413	4	ABA23541	Aba23541 Probe #20
182	6	20.0	413	4	AAK02056	Aak02056 Human bra
183	6	20.0	413	12	ADM66984	Adm66984 Human hom
c 184	6	20.0	414	8	ABX43794	Abx43794 Bovine ES
c 185	6	20.0	417	8	ABX36132	Abx36132 Bovine ES
186	6	20.0	419	6	ABN78874	Abn78874 Human ORF
c 187	6	20.0	424	8	ABX40445	Abx40445 Bovine ES
188	6	20.0	426	10	ADF80377	Adf80377 Leukaemia
189	6	20.0	428	5	ABV58931	Abv58931 Human pro
190	6	20.0	433	9	ACH29389	Ach29389 Human adu
191	6	20.0	440	8	ABX50288	Abx50288 Bovine ES
c 192	6	20.0	441	4	AAL00414	Aal00414 Human rep
c 193	6	20.0	441	4	ABA07492	Aba07492 Human ova
194	6	20.0	442	13	ADX31375	Adx31375 Plant ful
c 195	6	20.0	446	4	ABA57806	Aba57806 Human foe
c 196	6	20.0	446	4	AAI37391	Aai37391 Probe #60
c 197	6	20.0	446	4	AAK31510	Aak31510 Human bon
c 198	6	20.0	446	4	AAK05876	Aak05876 Human bra
c 199	6	20.0	446	4	ABS31192	Abs31192 Human liv
c 200	6	20.0	446	6	ABS06264	Abs06264 Human gen
201	6	20.0	446	12	ACH89183	Ach89183 Human gen
c 202	6	20.0	449	4	AAI38200	Aai38200 Probe #68
c 203	6	20.0	449	4	AAK32353	Aak32353 Human bon
c 204	6	20.0	449	4	AAK06657	Aak06657 Human bra
c 205	6	20.0	449	4	ABS32061	Abs32061 Human liv
c 206	6	20.0	449	6	ABS07136	Abs07136 Human gen
c 207	6	20.0	455	13	ADX35947	Adx35947 Plant ful
208	6	20.0	456	13	ACF82903	Acf82903 Human SIR
209	6	20.0	458	11	ADL22559	Adl22559 Human dis
210	6	20.0	462	9	ADB06413	Adb06413 Alloiococ
211	6	20.0	462	9	ADB06411	Adb06411 Alloiococ
212	6	20.0	464	10	ADC31908	Adc31908 Human nov
c 213	6	20.0	464	12	ADP94816	Adp94816 Cotton ex
c 214	6	20.0	465	4	AAI13900	Aai13900 Probe #38
c 215	6	20.0	465	4	ABA55611	Aba55611 Human foe
c 216	6	20.0	465	4	AAI35266	Aai35266 Probe #39
c 217	6	20.0	465	4	ABA45133	Aba45133 Human bre
c 218	6	20.0	465	4	ABA25309	Aba25309 Probe #37
c 219	6	20.0	465	4	AAK29306	Aak29306 Human bon
220	6	20.0	465	4	AAK28527	Aak28527 Human bon
221	6	20.0	465	4	AAK03075	Aak03075 Human bra
c 222	6	20.0	465	4	AAK03840	Aak03840 Human bra
c 223	6	20.0	465	4	ABS28926	Abs28926 Human liv

c 224	6	20.0	465	5	AAI03768	Aai03768 Probe #37
c 225	6	20.0	465	6	ABS03865	Abs03865 Human gen
c 226	6	20.0	466	4	ABA58550	Aba58550 Human foe
c 227	6	20.0	466	4	AAK32365	Aak32365 Human bon
c 228	6	20.0	466	4	AAK06669	Aak06669 Human bra
c 229	6	20.0	466	4	ABS32073	Abs32073 Human liv
c 230	6	20.0	466	6	ABS07148	Abs07148 Human gen
231	6	20.0	466	9	ACH25500	Ach25500 Human adu
c 232	6	20.0	468	12	ACH81881	Ach81881 Human gen
c 233	6	20.0	469	10	ADA20750	Ada20750 Soybean c
c 234	6	20.0	470	14	ACL56099	Acl56099 Human col
c 235	6	20.0	471	10	ADE58679	Ade58679 Rat gene
c 236	6	20.0	471	10	ADE58678	Ade58678 Rat gene
c 237	6	20.0	471	12	ADP28391	Adp28391 Human sec
c 238	6	20.0	472	10	ADG37705	Adg37705 Aspergill
239	6	20.0	475	12	ADL87889	Adl87889 DNA up-re
240	6	20.0	475	12	ADL87890	Adl87890 DNA up-re
241	6	20.0	476	10	ADD71041	Add71041 Human glu
242	6	20.0	480	12	ADJ62008	Adj62008 E. faecal
243	6	20.0	480	12	ADJ62006	Adj62006 E. faecal
c 244	6	20.0	483	4	ABL22561	Abl22561 Drosophil
c 245	6	20.0	483	6	ABL59087	Abl59087 Nucleotid
c 246	6	20.0	483	13	ADS96473	Ads96473 Drosophil
247	6	20.0	483	13	ADV39703	Adv39703 Rat cardi
c 248	6	20.0	484	8	ABZ53832	Abz53832 Aspergill
c 249	6	20.0	486	14	ACL56040	Acl56040 Human col
250	6	20.0	487	13	ADQ52469	Adq52469 Novel can
251	6	20.0	488	5	ADL44217	Adl44217 Human ova
c 252	6	20.0	488	10	ADL07496	Adl07496 Rice leaf
c 253	6	20.0	490	4	AAK65933	Aak65933 Human imm
c 254	6	20.0	490	4	AAL03581	Aal03581 Human rep
c 255	6	20.0	490	4	AAL03580	Aal03580 Human rep
c 256	6	20.0	490	4	AAL03579	Aal03579 Human rep
c 257	6	20.0	490	4	ABA07790	Aba07790 Human ova
c 258	6	20.0	490	4	ABA07789	Aba07789 Human ova
c 259	6	20.0	490	4	ABA07788	Aba07788 Human ova
c 260	6	20.0	492	9	ACH21822	Ach21822 Human adu
261	6	20.0	492	10	ADH83486	Adh83486 Enterococ
262	6	20.0	495	5	ABV14582	Abv14582 Human pro
c 263	6	20.0	496	4	AAH11509	Aah11509 Human cDN
c 264	6	20.0	500	8	ABX05335	Abx05335 Human nov
c 265	6	20.0	500	9	ACC73100	Acc73100 Cat flea
c 266	6	20.0	500	12	ADL09745	Adl09745 Cat flea
267	6	20.0	505	10	ADB58721	Adb58721 Toxicity-
268	6	20.0	505	10	ADB53415	Adb53415 Primary r
269	6	20.0	505	10	ABT42279	Abt42279 Toxicity
c 270	6	20.0	508	4	AAI18015	Aai18015 Probe #79
c 271	6	20.0	508	4	ABA62982	Aba62982 Human foe
c 272	6	20.0	508	4	AAI43009	Aai43009 Probe #11
c 273	6	20.0	508	4	AAK37180	Aak37180 Human bon
c 274	6	20.0	508	4	AAK11395	Aak11395 Human bra
c 275	6	20.0	508	4	ABS36854	Abs36854 Human liv
c 276	6	20.0	509	6	ABN63252	Abn63252 Human can
c 277	6	20.0	510	4	AAI17893	Aai17893 Probe #78
c 278	6	20.0	510	4	ABA62852	Aba62852 Human foe
c 279	6	20.0	510	4	AAI42869	Aai42869 Probe #11
c 280	6	20.0	510	4	ABA30132	Aba30132 Probe #85
c 281	6	20.0	510	4	AAK37050	Aak37050 Human bon
c 282	6	20.0	510	4	AAK11255	Aak11255 Human bra
c 283	6	20.0	510	4	ABS36733	Abs36733 Human liv
c 284	6	20.0	510	6	ABS11056	Abs11056 Human gen
c 285	6	20.0	511	13	ADQ57425	Adq57425 Novel can
c 286	6	20.0	513	4	AAF71672	Aaf71672 Corynebac
287	6	20.0	514	2	AAV29561	Aav29561 Protein i
c 288	6	20.0	514	8	ABZ56244	Abz56244 Aspergill
289	6	20.0	515	6	ABN60841	Abn60841 Human can
c 290	6	20.0	515	6	ABV88107	Abv88107 Human col
c 291	6	20.0	516	6	ABN65117	Abn65117 Human can
c 292	6	20.0	516	6	ABV87765	Abv87765 Human col
c 293	6	20.0	517	4	AAL22208	Aal22208 Human bre
c 294	6	20.0	517	6	AAD42844	Aad42844 Human DNA
c 295	6	20.0	517	10	ADH62575	Adh62575 Human tel
296	6	20.0	524	5	ABV43929	Abv43929 Human pro
297	6	20.0	524	5	ABV44465	Abv44465 Human pro
298	6	20.0	524	5	ABV35660	Abv35660 Human pro
299	6	20.0	525	12	ADP28795	Adp28795 Human sec
c 300	6	20.0	527	6	ABQ99594	Abq99594 Human cod
c 301	6	20.0	527	12	ACH77119	Ach77119 Human gen
c 302	6	20.0	528	6	ABN65919	Abn65919 Human can
303	6	20.0	532	6	ABQ31638	Abq31638 Oligonucl
c 304	6	20.0	532	6	ABQ31639	Abq31639 Oligonucl
c 305	6	20.0	532	10	ADB55926	Adb55926 Toxicity-
c 306	6	20.0	532	10	ADB50496	Adb50496 Primary r
307	6	20.0	537	12	ACH75455	Ach75455 Human gen
c 308	6	20.0	537	12	ACH68179	Ach68179 Human gen
c 309	6	20.0	538	6	ABQ75282	Abq75282 Human lun
c 310	6	20.0	539	3	AAC75145	Aac75145 Human ORF
c 311	6	20.0	539	5	ADL44006	Adl44006 Human ova
312	6	20.0	543	2	AAX57358	Aax57358 Human p-4
c 313	6	20.0	545	8	ABZ52741	Abz52741 Aspergill
314	6	20.0	546	4	AAK41584	Aak41584 Human bon
315	6	20.0	546	4	AAK15841	Aak15841 Human bra
c 316	6	20.0	546	6	AAI67812	Aai67812 Wheat alp
c 317	6	20.0	547	5	ABV55719	Abv55719 Human pro
318	6	20.0	549	3	AAA05849	Aaa05849 Group B S
c 319	6	20.0	549	8	ABX64583	Abx64583 Human gen
c 320	6	20.0	549	9	ACC72937	Acc72937 Cat flea
c 321	6	20.0	549	12	ADL09579	Adl09579 Cat flea
c 322	6	20.0	549	12	ADP28392	Adp28392 Human sec
c 323	6	20.0	552	3	AAZ38987	Aaz38987 Escherich
324	6	20.0	554	9	ACH26959	Ach26959 Human adu
c 325	6	20.0	555	10	ADH85485	Adh85485 Enterococ
c 326	6	20.0	555	13	ADT48255	Adt48255 Bacterial
c 327	6	20.0	557	3	AAC95043	Aac95043 Cat flea
c 328	6	20.0	559	12	ACH78037	Ach78037 Human gen
329	6	20.0	559	13	ACN48165	Acn48165 Cotton pr
c 330	6	20.0	564	11	ABD06756	Abd06756 Pseudomon
331	6	20.0	569	6	ABN60445	Abn60445 Human can
332	6	20.0	572	11	ACN89900	Acn89900 Breast ca
c 333	6	20.0	577	12	ADO61614	Ado61614 Transcrip
334	6	20.0	578	3	AAF09047	Aaf09047 Fusarium
335	6	20.0	578	4	AAL17561	Aal17561 Human bre
336	6	20.0	578	13	ADU53088	Adu53088 Fusarium
337	6	20.0	578	14	ADZ91091	Adz91091 Fusarium
c 338	6	20.0	581	9	ACL22362	Acl22362 DNA clone
c 339	6	20.0	581	10	ACF56874	Acf56874 Rice leaf
340	6	20.0	584	12	ADJ62825	Adj62825 Corn even
c 341	6	20.0	585	3	AAC69688	Aac69688 Novel hum
c 342	6	20.0	586	5	AAS86390	Aas86390 DNA encod
c 343	6	20.0	586	13	ACN60723	Acn60723 Cotton gy
c 344	6	20.0	589	4	AAK11875	Aak11875 Human bra
c 345	6	20.0	589	4	ABS37239	Abs37239 Human liv
346	6	20.0	589	13	ADR59995	Adr59995 Cotton cD
c 347	6	20.0	590	12	ACH72664	Ach72664 Human gen
348	6	20.0	591	6	ABQ31724	Abq31724 Oligonucl
c 349	6	20.0	591	6	ABQ31725	Abq31725 Oligonucl
350	6	20.0	591	12	ACH68593	Ach68593 Human gen
351	6	20.0	591	13	ACN54454	Acn54454 Cotton an
352	6	20.0	592	5	ABA12038	Aba12038 Human ner
353	6	20.0	596	3	AAA81784	Aaa81784 N. mening
c 354	6	20.0	597	6	ABQ66421	Abq66421 Arabidops
c 355	6	20.0	600	4	AAI39628	Aai39628 Probe #83
c 356	6	20.0	600	4	AAK33903	Aak33903 Human bon
c 357	6	20.0	600	4	AAK08031	Aak08031 Human bra
c 358	6	20.0	600	4	ABS33710	Abs33710 Human liv
c 359	6	20.0	601	11	ADW22038	Adw22038 Rat hepat
c 360	6	20.0	601	12	ADP71955	Adp71955 Renal tox
361	6	20.0	602	4	AAS28885	Aas28885 Human imm
362	6	20.0	602	4	AAS28898	Aas28898 Human imm
363	6	20.0	602	4	ABA06805	Aba06805 Human gen
364	6	20.0	602	4	ABA06848	Aba06848 Human gen
365	6	20.0	602	6	ABV84185	Abv84185 Human pol
366	6	20.0	602	6	ABV84142	Abv84142 Human pol
367	6	20.0	602	10	ADB31726	Adb31726 Human nov
368	6	20.0	602	10	ADB31739	Adb31739 Human nov
c 369	6	20.0	605	5	ABV39240	Abv39240 Human pro

	370	6	20.0	606	5	ABV43916 Abv43916 Human pro
	371	6	20.0	609	5	ABV35070 Abv35070 Human pro
	372	6	20.0	609	11	ACL33813 Acl33813 Rice abio
	373	6	20.0	610	6	AAI72335 Aai72335 Dog ECMRP
	374	6	20.0	612	10	ACC61494 Acc61494 Gene sequ
	375	6	20.0	612	10	ADK64621 Adk64621 Disease t
c	376	6	20.0	617	5	ABV59145 Abv59145 Human pro
c	377	6	20.0	619	13	ADR64210 Adr64210 Cotton cD
	378	6	20.0	621	5	ABV05578 Abv05578 Human pro
c	379	6	20.0	621	10	ACC61364 Acc61364 Gene sequ
c	380	6	20.0	621	10	ADK63479 Adk63479 Disease t
	381	6	20.0	623	5	ABA16747 Aba16747 Human ner
c	382	6	20.0	624	6	ABQ43385 Abq43385 Oligonucl
	383	6	20.0	624	6	ABQ43384 Abq43384 Oligonucl
c	384	6	20.0	630	13	ACN46444 Acn46444 Cotton pr
c	385	6	20.0	635	4	AAL24147 Aal24147 Human bre
c	386	6	20.0	635	10	ADK54572 Adk54572 Plant DNA
c	387	6	20.0	639	12	ADJ39964 Adj39964 Plant cDN
c	388	6	20.0	641	10	ADD16366 Add16366 DNA (SeqI
	389	6	20.0	643	4	AAS28789 Aas28789 Human imm
	390	6	20.0	643	4	ABA06577 Aba06577 Human cDN
	391	6	20.0	643	6	ABV83914 Abv83914 Human pol
	392	6	20.0	643	10	ADB31514 Adb31514 Human cDN
c	393	6	20.0	644	11	ACN86742 Acn86742 Breast ca
c	394	6	20.0	648	3	AAF11974 Aaf11974 Aspergill
c	395	6	20.0	648	13	ADU56015 Adu56015 Aspergill
c	396	6	20.0	648	14	ADZ94018 Adz94018 Aspergill
c	397	6	20.0	650	3	AAC95122 Aac95122 Cat flea
	398	6	20.0	655	14	ADZ62577 Adz62577 Murine Dn
c	399	6	20.0	665	4	AAI98825 Aai98825 Human exc
c	400	6	20.0	665	5	AAI63221 Aai63221 Human kid
	401	6	20.0	666	8	ACA05041 Aca05041 Flea ecdy
c	402	6	20.0	666	8	ACA05042 Aca05042 Flea ecdy
	403	6	20.0	666	13	ADU48260 Adu48260 Ctenoceph
c	404	6	20.0	666	13	ADU48261 Adu48261 Ctenoceph
c	405	6	20.0	667	6	ABK77672 Abk77672 Bacillus
c	406	6	20.0	668	6	ABK77679 Abk77679 Bacillus
	407	6	20.0	680	6	ABT09426 Abt09426 Phase-1 R
	408	6	20.0	680	12	ADH22767 Adh22767 Partial D
	409	6	20.0	680	13	ADR91118 Adr91118 Spleen ne
	410	6	20.0	684	3	AAF15007 Aaf15007 Trichoder
	411	6	20.0	684	13	ADU59048 Adu59048 Trichoder
	412	6	20.0	684	14	ADZ97051 Adz97051 Trichoder
	413	6	20.0	686	12	ADJ43379 Adj43379 Plant cDN
	414	6	20.0	689	10	ADC75945 Adc75945 DNA homol
c	415	6	20.0	690	6	ABN91941 Abn91941 Staphyloc
c	416	6	20.0	690	13	ADS00813 Ads00813 Staphyloc
	417	6	20.0	693	8	ACA41356 Aca41356 Prokaryot
	418	6	20.0	693	10	ABZ41679 Abz41679 N. gonorr
c	419	6	20.0	693	10	ABZ41203 Abz41203 N. gonorr
c	420	6	20.0	694	6	ABZ78012 Abz78012 Human bre
	421	6	20.0	696	8	ACA41582 Aca41582 Prokaryot
	422	6	20.0	713	8	ACA21865 Aca21865 Prokaryot
c	423	6	20.0	714	13	ADX12488 Adx12488 Plant ful
c	424	6	20.0	722	4	AAI99403 Aai99403 Human exc
c	425	6	20.0	722	5	AAI63753 Aai63753 Human kid
c	426	6	20.0	732	6	AAI67813 Aai67813 Wheat alp
	427	6	20.0	739	3	AAA78572 Aaa78572 Plant SDF
	428	6	20.0	741	3	AAA78507 Aaa78507 Plant SDF
	429	6	20.0	746	12	ACH87244 Ach87244 Human gen
	430	6	20.0	749	4	AAH07650 Aah07650 Human cDN
c	431	6	20.0	752	3	AAC47794 Aac47794 Arabidops
	432	6	20.0	754	9	ACF06313 Acf06313 Corn geno
c	433	6	20.0	755	6	ABX66546 Abx66546 Helicobac
c	434	6	20.0	756	13	ADT43341 Adt43341 Bacterial
c	435	6	20.0	758	11	ADT94587 Adt94587 Colon can
c	436	6	20.0	758	11	ADX41069 Adx41069 Human cDN
	437	6	20.0	759	4	AAL22953 Aal22953 Human bre
	438	6	20.0	760	3	AAF15254 Aaf15254 Trichoder
	439	6	20.0	760	13	ADU59295 Adu59295 Trichoder
	440	6	20.0	760	14	ADZ97298 Adz97298 Trichoder
c	441	6	20.0	768	5	AAH67853 Aah67853 C glutami
c	442	6	20.0	768	11	ADM07017 Adm07017 Aspergill
c	443	6	20.0	769	3	AAC34868 Aac34868 Arabidops
c	444	6	20.0	771	11	ADM07138 Adm07138 Aspergill
c	445	6	20.0	779	10	ADD35057 Add35057 Mouse mit
c	446	6	20.0	780	3	AAC40347 Aac40347 Arabidops
c	447	6	20.0	780	5	ABV03994 Abv03994 Human pro
	448	6	20.0	780	13	ADS50405 Ads50405 Bacterial
	449	6	20.0	780	13	ADS50406 Ads50406 Bacterial
c	450	6	20.0	787	6	ABX92103 Abx92103 Lung spec
c	451	6	20.0	789	6	ABK30344 Abk30344 Human G-p
c	452	6	20.0	789	14	ACL66493 Acl66493 M. xanthu
	453	6	20.0	793	4	AAI96184 Aai96184 Human neu
c	454	6	20.0	795	14	AEB66163 Aeb66163 Rice geno
	455	6	20.0	801	13	ADS57957 Ads57957 Bacterial
	456	6	20.0	802	2	AAZ15507 Aaz15507 Human gen
	457	6	20.0	810	5	AAH52245 Aah52245 Human AFP
c	458	6	20.0	822	4	AAI97511 Aai97511 Human neu
c	459	6	20.0	826	13	ADX63182 Adx63182 Plant ful
	460	6	20.0	834	13	ADS50646 Ads50646 Bacterial
	461	6	20.0	839	13	ADX60030 Adx60030 Plant ful
c	462	6	20.0	849	13	ADX34175 Adx34175 Plant ful
c	463	6	20.0	850	3	AAC45162 Aac45162 Arabidops
c	464	6	20.0	850	6	ABX65534 Abx65534 Helicobac
	465	6	20.0	853	3	AAC32789 Aac32789 Arabidops
c	466	6	20.0	855	5	AAS91600 Aas91600 DNA encod
c	467	6	20.0	855	13	ADX46377 Adx46377 Plant ful
	468	6	20.0	861	8	ACA53347 Aca53347 Prokaryot
c	469	6	20.0	868	13	ADX48920 Adx48920 Plant ful
c	470	6	20.0	868	13	ADX34544 Adx34544 Plant ful
	471	6	20.0	870	5	ABV13962 Abv13962 Human pro
	472	6	20.0	872	4	AAH26845 Aah26845 Human pro
c	473	6	20.0	876	13	ADO84200 Ado84200 Plant ful
	474	6	20.0	878	11	ACN80683 Acn80683 Breast ca
	475	6	20.0	884	12	ADJ39173 Adj39173 Plant cDN
c	476	6	20.0	888	13	ADX46663 Adx46663 Plant ful
c	477	6	20.0	891	4	AAF72322 Aaf72322 Corynebac
c	478	6	20.0	891	6	ABS65357 Abs65357 DNA encod
	479	6	20.0	893	13	ADO83291 Ado83291 Plant ful
c	480	6	20.0	896	13	ADX36666 Adx36666 Plant ful
c	481	6	20.0	896	13	ADX46814 Adx46814 Plant ful
c	482	6	20.0	897	13	ADO81849 Ado81849 Plant ful
c	483	6	20.0	897	13	ADO83669 Ado83669 Plant ful
	484	6	20.0	899	12	ADK99494 Adk99494 Streptoco
c	485	6	20.0	899	13	ADX31014 Adx31014 Plant ful
c	486	6	20.0	899	13	ADX60473 Adx60473 Plant ful
c	487	6	20.0	900	13	ADX36618 Adx36618 Plant ful
c	488	6	20.0	901	12	ACH91753 Ach91753 Human gen
c	489	6	20.0	903	6	ABK74033 Abk74033 Bacillus
c	490	6	20.0	909	2	AAT11233 Aat11233 Coding re
	491	6	20.0	909	11	ABD03499 Abd03499 Pseudomon
c	492	6	20.0	909	13	ADX52079 Adx52079 Plant ful
c	493	6	20.0	911	13	ADO81439 Ado81439 Plant ful
c	494	6	20.0	913	3	AAC44054 Aac44054 Zea mays
c	495	6	20.0	920	13	ADX10483 Adx10483 Plant ful
	496	6	20.0	923	7	ADS31139 Ads31139 Human gen
	497	6	20.0	923	7	ADY36527 Ady36527 HIRA geno
	498	6	20.0	927	6	ABZ13759 Abz13759 Arabidops
	499	6	20.0	927	6	ADG87913 Adg87913 A. thalia
	500	6	20.0	927	6	ADG88072 Adg88072 A. thalia
	501	6	20.0	930	13	ADS49951 Ads49951 Bacterial
	502	6	20.0	933	8	ACA47067 Aca47067 Prokaryot
	503	6	20.0	933	10	ADF00319 Adf00319 Bacterial
c	504	6	20.0	936	2	AAQ73666 Aaq73666 Maize QM
	505	6	20.0	936	6	ABN91935 Abn91935 Staphyloc
	506	6	20.0	936	13	ADS00805 Ads00805 Staphyloc
c	507	6	20.0	939	13	ADX29875 Adx29875 Plant ful
	508	6	20.0	948	12	ADK99492 Adk99492 Streptoco
	509	6	20.0	948	12	ADK99491 Adk99491 Streptoco
	510	6	20.0	948	12	ADK99495 Adk99495 Streptoco
	511	6	20.0	948	12	ADK99486 Adk99486 Streptoco
	512	6	20.0	948	12	ADK99490 Adk99490 Streptoco
	513	6	20.0	948	12	ADK99493 Adk99493 Streptoco
	514	6	20.0	948	12	ADK99487 Adk99487 Streptoco
	515	6	20.0	948	12	ADK99489 Adk99489 Streptoco

c 516	6	20.0	963	13	ADX52627	Adx52627 Plant ful
c 517	6	20.0	972	10	ADK58588	Adk58588 Plant DNA
518	6	20.0	981	14	ACL69774	Acl69774 M. xanthu
c 519	6	20.0	982	2	AAQ04258	Aaq04258 Sequence
c 520	6	20.0	982	2	AAQ45592	Aaq45592 Sequence
c 521	6	20.0	982	2	AAZ23960	Aaz23960 Human VH
c 522	6	20.0	982	2	AAZ39423	Aaz39423 Nucleotid
c 523	6	20.0	982	3	AAZ40701	Aaz40701 VHalphaTA
c 524	6	20.0	982	3	AAA29682	Aaa29682 VHalphaTA
c 525	6	20.0	982	4	AAS02621	Aas02621 Mouse DNA
c 526	6	20.0	982	9	ADB17792	Adb17792 DNA encod
c 527	6	20.0	982	10	ADG46914	Adg46914 Mouse VHa
c 528	6	20.0	982	10	ADK66813	Adk66813 Mouse VH
c 529	6	20.0	987	6	AAD38074	Aad38074 Grape chl
530	6	20.0	987	8	ACA25646	Aca25646 Prokaryot
c 531	6	20.0	990	13	ADX15347	Adx15347 Plant ful
532	6	20.0	994	6	ABQ99071	Abq99071 Human ORF
c 533	6	20.0	995	6	ABX66323	Abx66323 Helicobac
534	6	20.0	997	13	ADX27899	Adx27899 Plant ful
535	6	20.0	999	13	ADT42393	Adt42393 Bacterial
c 536	6	20.0	1000	4	AAS30805	Aas30805 Human cDN
537	6	20.0	1002	11	ABD03410	Abd03410 Pseudomon
538	6	20.0	1003	3	AAC42373	Aac42373 Arabidops
c 539	6	20.0	1009	13	ADX64530	Adx64530 Plant ful
540	6	20.0	1013	13	ADR62495	Adr62495 Cotton cD
541	6	20.0	1017	7	ADS31144	Ads31144 Human gen
542	6	20.0	1017	7	ADY36532	Ady36532 HIRA geno
c 543	6	20.0	1018	4	AAH21493	Aah21493 Tobacco a
c 544	6	20.0	1024	6	ABX66337	Abx66337 Helicobac
c 545	6	20.0	1024	6	ABX66066	Abx66066 Helicobac
c 546	6	20.0	1028	2	AAX34304	Aax34304 Hybrid sh
547	6	20.0	1035	6	ABN66851	Abn66851 Streptoco
c 548	6	20.0	1035	11	ADM07016	Adm07016 Aspergill
549	6	20.0	1035	12	ADK99485	Adk99485 Streptoco
c 550	6	20.0	1037	11	ADM07137	Adm07137 Aspergill
551	6	20.0	1038	13	ADT46721	Adt46721 Bacterial
552	6	20.0	1038	13	ADV85186	Adv85186 Streptoco
553	6	20.0	1040	8	ADA68165	Ada68165 Arabidops
554	6	20.0	1041	12	ADN72434	Adn72434 Thale cre
555	6	20.0	1045	4	AAS36783	Aas36783 Human car
556	6	20.0	1045	4	AAS36784	Aas36784 Human car
557	6	20.0	1045	4	AAK61872	Aak61872 Human imm
558	6	20.0	1045	10	ADE47477	Ade47477 Human car
559	6	20.0	1045	10	ADE47478	Ade47478 Human car
560	6	20.0	1045	13	ADJ08895	Adj08895 Human car
561	6	20.0	1045	13	ADJ08896	Adj08896 Human car
562	6	20.0	1047	4	AAS35654	Aas35654 Human car
563	6	20.0	1047	10	ADE45733	Ade45733 Human car
564	6	20.0	1047	13	ADJ07151	Adj07151 Human car
c 565	6	20.0	1064	13	ADX11902	Adx11902 Plant ful
566	6	20.0	1065	9	ADA32412	Ada32412 DNA encod
567	6	20.0	1089	13	ADX31199	Adx31199 Plant ful
c 568	6	20.0	1110	4	ABL06661	Abl06661 Drosophil
569	6	20.0	1110	8	ADA69351	Ada69351 Rice gene
570	6	20.0	1110	11	ACL27122	Acl27122 Rice abio
c 571	6	20.0	1122	4	AAH01654	Aah01654 Candida n
c 572	6	20.0	1125	12	ADJ39707	Adj39707 Plant cDN
573	6	20.0	1154	3	AAC47424	Aac47424 Arabidops
574	6	20.0	1155	6	ABK35055	Abk35055 Human cDN
c 575	6	20.0	1161	6	ABQ16360	Abq16360 Oligonucl
576	6	20.0	1161	6	ABQ16361	Abq16361 Oligonucl
c 577	6	20.0	1162	3	AAA08588	Aaa08588 Human cyt
578	6	20.0	1171	3	AAC41131	Aac41131 Arabidops
c 579	6	20.0	1173	8	ACA20601	Aca20601 Prokaryot
580	6	20.0	1176	12	ADN98421	Adn98421 Novel hum
581	6	20.0	1176	12	ADN99989	Adn99989 Novel hum
582	6	20.0	1188	12	ADL02914	Adl02914 DNA encod
583	6	20.0	1203	8	ADA71043	Ada71043 Rice gene
c 584	6	20.0	1203	8	ADA70977	Ada70977 Rice gene
c 585	6	20.0	1215	8	ACA37724	Aca37724 Prokaryot
586	6	20.0	1216	8	ACA24442	Aca24442 Prokaryot
587	6	20.0	1221	14	AEB67825	Aeb67825 Rice geno
c 588	6	20.0	1230	10	ABX06009	Abx06009 S. pneumo
c 589	6	20.0	1233	8	ACA49614	Aca49614 Prokaryot
c 590	6	20.0	1233	13	ADK44787	Adk44787 Streptoco
c 591	6	20.0	1236	12	ADP10522	Adp10522 Reference
c 592	6	20.0	1243	4	ABL11071	Abl11071 Drosophil
c 593	6	20.0	1260	8	ACA37049	Aca37049 Prokaryot
c 594	6	20.0	1275	6	AAD31863	Aad31863 Lactobaci
c 595	6	20.0	1275	13	ADR93964	Adr93964 Novel S.
c 596	6	20.0	1275	14	AEA57834	Aea57834 Streptoco
c 597	6	20.0	1290	13	ADT46928	Adt46928 Bacterial
598	6	20.0	1314	13	ADS60864	Ads60864 Bacterial
599	6	20.0	1320	9	ACF06308	Acf06308 5' genome
c 600	6	20.0	1323	8	ACA38436	Aca38436 Prokaryot
c 601	6	20.0	1326	8	ACA40391	Aca40391 Prokaryot
c 602	6	20.0	1327	6	ABS67104	Abs67104 Human col
c 603	6	20.0	1327	6	ABT07682	Abt07682 Human bre
c 604	6	20.0	1327	6	ABT05252	Abt05252 Human col
c 605	6	20.0	1327	8	ABT13412	Abt13412 Breast sp
606	6	20.0	1341	4	ABL02663	Abl02663 Drosophil
607	6	20.0	1341	11	ABD06644	Abd06644 Pseudomon
c 608	6	20.0	1352	10	ABX14300	Abx14300 Human bet
c 609	6	20.0	1356	5	ABV25852	Abv25852 Human pro
c 610	6	20.0	1365	2	AAQ87044	Aaq87044 Pig inter
c 611	6	20.0	1365	2	AAQ85772	Aaq85772 Porcine i
612	6	20.0	1371	6	ABN68017	Abn68017 Streptoco
613	6	20.0	1372	12	ADM66983	Adm66983 Murine ad
614	6	20.0	1374	13	ADV85289	Adv85289 Streptoco
c 615	6	20.0	1375	4	AAL06662	Aal06662 Human rep
c 616	6	20.0	1375	4	AAL06661	Aal06661 Human rep
c 617	6	20.0	1375	4	ABA08000	Aba08000 Human ova
c 618	6	20.0	1375	4	ABA08001	Aba08001 Human ova
619	6	20.0	1377	6	ABT11654	Abt11654 Yeast sel
620	6	20.0	1380	8	ACF74047	Acf74047 Staphyloc
c 621	6	20.0	1380	11	ABD06721	Abd06721 Pseudomon
c 622	6	20.0	1380	14	AEB64924	Aeb64924 Rice geno
623	6	20.0	1387	13	ADX62879	Adx62879 Plant ful
624	6	20.0	1393	13	ADX62830	Adx62830 Plant ful
c 625	6	20.0	1394	10	ABX74527	Abx74527 Human cDN
c 626	6	20.0	1417	6	ABL99780	Abl99780 Human sec
c 627	6	20.0	1430	2	AAT66904	Aat66904 Abl inter
628	6	20.0	1437	5	AAH65230	Aah65230 C glutami
629	6	20.0	1439	4	AAK81211	Aak81211 Human imm
630	6	20.0	1439	4	AAK81212	Aak81212 Human imm
631	6	20.0	1440	3	AAA49203	Aaa49203 Corn puta
632	6	20.0	1440	4	AAK81210	Aak81210 Human imm
c 633	6	20.0	1440	13	ADS62968	Ads62968 Bacterial
c 634	6	20.0	1440	13	ADS59801	Ads59801 Bacterial
c 635	6	20.0	1440	13	ADS62425	Ads62425 Bacterial
c 636	6	20.0	1442	6	ABK63417	Abk63417 Rat seque
c 637	6	20.0	1442	10	ADB57812	Adb57812 Toxicity-
c 638	6	20.0	1442	10	ADB52336	Adb52336 Primary r
c 639	6	20.0	1442	11	ADW22355	Adw22355 Rat hepat
640	6	20.0	1443	10	ADC92879	Adc92879 E. faeciu
641	6	20.0	1448	4	ABL09695	Abl09695 Drosophil
642	6	20.0	1452	6	ABQ69871	Abq69871 Listeria
643	6	20.0	1462	4	ABL05821	Abl05821 Drosophil
644	6	20.0	1464	10	ACF79984	Acf79984 Acinetoba
c 645	6	20.0	1466	2	AAX98009	Aax98009 Human sec
c 646	6	20.0	1466	8	ADA40082	Ada40082 Human sec
c 647	6	20.0	1466	9	ADA11554	Ada11554 Human cDN
c 648	6	20.0	1466	10	ADA56257	Ada56257 Gene enco
c 649	6	20.0	1467	10	ACC61538	Acc61538 Gene sequ
c 650	6	20.0	1467	10	ADK62547	Adk62547 Disease t
651	6	20.0	1479	12	ADQ97176	Adq97176 Human can
c 652	6	20.0	1481	14	ADZ62542	Adz62542 Murine H2
653	6	20.0	1483	11	ADL65454	Adl65454 C. glutam
c 654	6	20.0	1484	3	AAC47540	Aac47540 Arabidops
c 655	6	20.0	1485	13	ADS62804	Ads62804 Bacterial
c 656	6	20.0	1486	3	AAC40456	Aac40456 Arabidops
c 657	6	20.0	1487	6	ABQ76296	Abq76296 S. cerevi
c 658	6	20.0	1491	3	AAA95814	Aaa95814 Soybean M
c 659	6	20.0	1491	14	ADU63872	Adu63872 Human glu
c 660	6	20.0	1494	5	AAS70042	Aas70042 DNA encod
661	6	20.0	1494	9	ADB23089	Adb23089 Soybean m

	662	6	20.0	1500	4	AAF67893 Aaf67893 Corynebac
c	663	6	20.0	1503	11	ACL30037 Acl30037 Rice abio
	664	6	20.0	1509	3	AAF12970 Aaf12970 Aspergill
	665	6	20.0	1509	13	ADU57011 Adu57011 Aspergill
	666	6	20.0	1509	14	ADZ95014 Adz95014 Aspergill
	667	6	20.0	1510	8	ACA44694 Aca44694 Prokaryot
c	668	6	20.0	1521	10	ACC60988 Acc60988 Gene sequ
c	669	6	20.0	1521	10	ADK62609 Adk62609 Disease t
c	670	6	20.0	1521	13	ADS46816 Ads46816 Bacterial
	671	6	20.0	1524	12	ADH78727 Adh78727 Potato AG
	672	6	20.0	1527	13	ADT15870 Adt15870 Plant cDN
	673	6	20.0	1527	14	ACL67609 Acl67609 M. xanthu
c	674	6	20.0	1529	13	ADR21637 Adr21637 Human enz
c	675	6	20.0	1531	12	ADO62068 Transcrip
c	676	6	20.0	1536	4	AAH00675 Aah00675 Saccharom
	677	6	20.0	1536	8	ACA47448 Aca47448 Prokaryot
c	678	6	20.0	1536	10	ACC60919 Acc60919 Gene sequ
c	679	6	20.0	1536	10	ADK62005 Adk62005 Disease t
c	680	6	20.0	1536	13	ADT47454 Adt47454 Bacterial
	681	6	20.0	1540	12	ADH78725 Potato AG
c	682	6	20.0	1551	4	AAD06388 Aad06388 Human glu
c	683	6	20.0	1551	4	AAS10863 Aas10863 Human cDN
c	684	6	20.0	1551	6	ABK40235 DNA encod
c	685	6	20.0	1551	10	ACF80575 Acf80575 Human glu
	686	6	20.0	1552	3	AAC50194 Aac50194 Arabidops
c	687	6	20.0	1552	13	ADX33721 Adx33721 Plant ful
	688	6	20.0	1563	14	ACL72415 Acl72415 M. xanthu
c	689	6	20.0	1568	4	ABL17401 Abl17401 Drosophil
c	690	6	20.0	1570	5	AAS64752 DNA encod
	691	6	20.0	1572	9	ADB09800 Adb09800 Alloiococ
	692	6	20.0	1581	13	ADX51138 Adx51138 Plant ful
c	693	6	20.0	1581	13	ADO84514 Plant ful
c	694	6	20.0	1590	3	AAC49836 Aac49836 Arabidops
c	695	6	20.0	1592	6	AAH99924 Aah99924 Nucleotid
c	696	6	20.0	1593	6	AAH99925 Aah99925 Nucleotid
	697	6	20.0	1596	3	AAC38094 Aac38094 Arabidops
c	698	6	20.0	1596	14	AEA49116 Aea49116 L. rhamno
c	699	6	20.0	1602	8	ADA71352 Ada71352 Rice gene
	700	6	20.0	1607	4	AAF71526 Aaf71526 Corynebac
c	701	6	20.0	1611	4	AAD06389 Aad06389 Human glu
c	702	6	20.0	1614	6	ABZ14755 Abz14755 Arabidops
	703	6	20.0	1617	10	ABZ39640 Abz39640 N. gonorr
c	704	6	20.0	1618	3	AAA54527 Aaa54527 Phytyl/pr
c	705	6	20.0	1618	13	ADS17339 Ads17339 Tocophero
c	706	6	20.0	1619	13	ADR42505 Adr42505 Human 158
c	707	6	20.0	1619	13	ADR42461 Adr42461 Human 158
c	708	6	20.0	1619	13	ADR42504 Adr42504 Human 158
c	709	6	20.0	1619	13	ADR42506 Adr42506 Human 158
c	710	6	20.0	1620	13	ADR42494 Adr42494 Human 158
c	711	6	20.0	1620	13	ADR42492 Adr42492 Human 158
c	712	6	20.0	1620	13	ADR42457 Adr42457 Human 158
	713	6	20.0	1622	3	AAC50544 Aac50544 Arabidops
	714	6	20.0	1624	13	ADX46756 Adx46756 Plant ful
	715	6	20.0	1625	3	AAC33995 Aac33995 Arabidops
	716	6	20.0	1630	2	AAQ66684 Aaq66684 Acy B2 ge
c	717	6	20.0	1632	12	ADQ28918 Adq28918 Porcine l
c	718	6	20.0	1632	12	ADQ28922 Adq28922 Porcine l
c	719	6	20.0	1632	12	ADQ28924 Adq28924 Porcine l
c	720	6	20.0	1632	12	ADQ28925 Adq28925 Porcine l
c	721	6	20.0	1632	12	ADQ28920 Adq28920 Porcine l
c	722	6	20.0	1632	12	ADQ28923 Adq28923 Porcine l
c	723	6	20.0	1632	12	ADQ28921 Adq28921 Porcine l
c	724	6	20.0	1632	12	ADQ28917 Adq28917 Porcine l
c	725	6	20.0	1632	12	ADQ28919 Adq28919 Porcine l
c	726	6	20.0	1632	12	ADQ28926 Adq28926 Porcine l
c	727	6	20.0	1637	4	AAH14022 Aah14022 Human cDN
c	728	6	20.0	1640	5	AAH46546 Aah46546 2-hydroxy
c	729	6	20.0	1641	9	ADB09011 Adb09011 Alloiococ
c	730	6	20.0	1641	9	ADB09007 Adb09007 Alloiococ
c	731	6	20.0	1641	9	ADB09009 Adb09009 Alloiococ
c	732	6	20.0	1641	9	ADB09013 Adb09013 Alloiococ
c	733	6	20.0	1641	12	ADP87482 Adp87482 Rabbit li
c	734	6	20.0	1642	2	AAT71753 Aat71753 Human glu
c	735	6	20.0	1643	12	ADH71693 Adh71693 Human gen
	736	6	20.0	1644	5	AAH65320 Aah65320 C glutami
	737	6	20.0	1644	13	ADX45823 Adx45823 Plant ful
c	738	6	20.0	1648	12	ADH71691 Adh71691 Human gen
c	739	6	20.0	1648	12	ADH71677 Adh71677 Human gen
c	740	6	20.0	1659	4	AAH16963 Aah16963 Human cDN
c	741	6	20.0	1660	13	ADO83587 Ado83587 Plant ful
c	742	6	20.0	1661	1	AAN80113 Aan80113 Encodes r
c	743	6	20.0	1661	2	AAX26682 Aax26682 Complete
c	744	6	20.0	1661	3	AAA48444 Aaa48444 Human lys
c	745	6	20.0	1662	3	AAZ51820 Aaz51820 Orpinomyc
c	746	6	20.0	1665	13	ADO81879 Ado81879 Plant ful
c	747	6	20.0	1667	2	AAZ42152 Aaz42152 Human nor
	748	6	20.0	1668	10	ADF00125 Adf00125 Bacterial
c	749	6	20.0	1668	12	ADH71685 Adh71685 Human gen
c	750	6	20.0	1668	12	ADH71687 Adh71687 Human gen
c	751	6	20.0	1673	13	ADX15211 Adx15211 Plant ful
	752	6	20.0	1676	13	ADX12785 Adx12785 Plant ful
c	753	6	20.0	1678	2	AAT09973 Aat09973 E4 promot
c	754	6	20.0	1678	2	AAT09967 Aat09967 E4 promot
c	755	6	20.0	1678	2	AAX00466 Aax00466 Tomato E4
	756	6	20.0	1686	4	AAH24904 Aah24904 Nucleotid
c	757	6	20.0	1689	5	AAS91605 DNA encod
c	758	6	20.0	1695	12	ADP87484 Adp87484 Rabbit li
	759	6	20.0	1700	14	ADZ62299 Adz62299 Murine 26
c	760	6	20.0	1701	3	AAA63884 Aaa63884 cDNA enco
	761	6	20.0	1701	4	ABL07907 Abl07907 Drosophil
c	762	6	20.0	1705	13	ACN42732 Acn42732 Human dia
c	763	6	20.0	1707	14	ADY69086 SLC22A8 c
c	764	6	20.0	1707	14	AEB94228 Aeb94228 Human org
c	765	6	20.0	1712	6	ABK50884 Abk50884 DNA encod
c	766	6	20.0	1716	12	ADM66967 Adm66967 Human adi
c	767	6	20.0	1717	2	AAZ09683 Aaz09683 Rabbit li
c	768	6	20.0	1717	12	ADG98215 Adg98215 DNA encod
	769	6	20.0	1722	6	ABQ76709 Abq76709 Human mac
c	770	6	20.0	1722	10	ADD29622 Add29622 Human tum
c	771	6	20.0	1722	12	ADH71669 Adh71669 Human gen
	772	6	20.0	1740	2	AAV42803 Aav42803 Human CMV
c	773	6	20.0	1741	4	AAF28294 Aaf28294 Modified
c	774	6	20.0	1741	4	AAF28293 Aaf28293 Unmodifie
	775	6	20.0	1743	13	ADR19895 Adr19895 HCMV AD16
c	776	6	20.0	1758	10	ADK68151 Adk68151 Novel NOV
c	777	6	20.0	1758	12	ADH71699 Adh71699 Human gen
c	778	6	20.0	1758	13	ADR49140 Adr49140 Human NOV
c	779	6	20.0	1762	10	ADK68153 Adk68153 Novel NOV
c	780	6	20.0	1762	12	ADH71701 Adh71701 Human gen
c	781	6	20.0	1762	13	ADR49142 Adr49142 Human NOV
	782	6	20.0	1767	4	AAF71525 Aaf71525 Corynebac
c	783	6	20.0	1776	6	ABQ86172 Abq86172 Novel hum
c	784	6	20.0	1780	10	ADB57974 Adb57974 Toxicity-
c	785	6	20.0	1780	10	ADB52455 Adb52455 Primary r
c	786	6	20.0	1780	11	ADW22432 Adw22432 Rat chole
c	787	6	20.0	1780	11	ADW22367 Adw22367 Rat hepat
c	788	6	20.0	1785	6	ABQ86173 Abq86173 Novel hum
c	789	6	20.0	1792	6	ABS69894 Abs69894 Human lys
	790	6	20.0	1806	8	ACA39740 Aca39740 Prokaryot
	791	6	20.0	1812	3	AAA16649 Aaa16649 Human sec
c	792	6	20.0	1823	12	ADN04489 Adn04489 Antipsori
c	793	6	20.0	1823	13	ADP24401 Adp24401 PRO polyp
	794	6	20.0	1825	10	ADI22667 Adi22667 Human liv
	795	6	20.0	1825	12	ADN05308 Adn05308 Antipsori
	796	6	20.0	1827	13	ADT17992 Adt17992 Plant cDN
c	797	6	20.0	1830	8	ADA69851 Ada69851 Rice gene
c	798	6	20.0	1833	6	ABK91247 Abk91247 Human cDN
c	799	6	20.0	1833	10	ADF66647 Adf66647 Human tra
	800	6	20.0	1833	13	ADT47176 Adt47176 Bacterial
	801	6	20.0	1835	4	AAH14894 Aah14894 Human cDN
c	802	6	20.0	1840	14	ADZ62639 Adz62639 Murine Es
	803	6	20.0	1850	13	ADX50124 Adx50124 Plant ful
c	804	6	20.0	1851	2	AAQ01760 Aaq01760 DNA seque
	805	6	20.0	1860	4	AAS53351 Aas53351 Haemophil
	806	6	20.0	1860	8	ACA34217 Aca34217 Prokaryot
	807	6	20.0	1870	3	AAC49812 Aac49812 Arabidops

c 808	6	20.0	1879	4	ABL16989	Abl16989 Drosophil
c 809	6	20.0	1885	6	ABK63543	Abk63543 Rat seque
c 810	6	20.0	1885	10	ADB59072	Adb59072 Toxicity-
c 811	6	20.0	1885	10	ADB53820	Adb53820 Primary r
812	6	20.0	1890	3	AAC47103	Aac47103 Arabidops
813	6	20.0	1897	10	ADF82451	Adf82451 Leukaemia
814	6	20.0	1902	10	ACF79985	Acf79985 Acinetoba
c 815	6	20.0	1908	3	AAC59401	Aac59401 Human sec
816	6	20.0	1920	14	ACL68348	Acl68348 M. xanthu
817	6	20.0	1934	10	ADC29972	Adc29972 Human nov
c 818	6	20.0	1941	6	ABK63610	Abk63610 Rat seque
c 819	6	20.0	1941	12	ADP72999	Adp72999 Renal tox
820	6	20.0	1944	13	ADT15425	Adt15425 Plant cDN
821	6	20.0	1945	6	ABA04998	Aba04998 Human zin
c 822	6	20.0	1948	4	AAL07173	Aal07173 Human rep
823	6	20.0	1969	5	AAS77736	Aas77736 DNA encod
c 824	6	20.0	1971	10	ABZ58585	Abz58585 Corynebac
c 825	6	20.0	1977	3	AAC43618	Aac43618 Arabidops
c 826	6	20.0	1986	6	ABQ76564	Abq76564 C. albica
c 827	6	20.0	1986	13	ADR89411	Adr89411 AXMI-009
828	6	20.0	1989	5	AAH65321	Aah65321 C glutami
c 829	6	20.0	1992	6	ABN70681	Abn70681 Streptoco
c 830	6	20.0	2000	6	ABZ17401	Abz17401 Arabidops
c 831	6	20.0	2000	8	ADA71929	Ada71929 Rice gene
c 832	6	20.0	2000	8	ADA72812	Ada72812 Rice gene
833	6	20.0	2000	10	ADC08433	Adc08433 Rice DNA
834	6	20.0	2000	11	ACL36248	Acl36248 Rice stre
c 835	6	20.0	2000	11	ACL37188	Acl37188 Rice stre
c 836	6	20.0	2000	11	ACL34869	Acl34869 Rice stre
c 837	6	20.0	2000	11	ACL38760	Acl38760 Rice stre
c 838	6	20.0	2000	11	ACL36700	Acl36700 Rice stre
c 839	6	20.0	2000	11	ACL35500	Acl35500 Rice stre
c 840	6	20.0	2000	11	ACL36969	Acl36969 Rice stre
841	6	20.0	2000	11	ACL37544	Acl37544 Rice stre
842	6	20.0	2000	12	ADJ41141	Adj41141 Plant cDN
c 843	6	20.0	2004	3	AAC69803	Aac69803 Human bre
c 844	6	20.0	2004	10	ACC78880	Acc78880 Human glu
c 845	6	20.0	2004	12	ADN49695	Adn49695 Human glu
c 846	6	20.0	2004	13	ADU74371	Adu74371 Human glu
c 847	6	20.0	2011	13	ADX37022	Adx37022 Plant ful
c 848	6	20.0	2016	13	ADR89409	Adr89409 AXMI-009
c 849	6	20.0	2022	8	ABZ74890	Abz74890 Mouse acy
c 850	6	20.0	2025	8	ABT19381	Abt19381 Aspergill
c 851	6	20.0	2025	8	ABT21201	Abt21201 Aspergill
c 852	6	20.0	2037	11	ADM07136	Adm07136 Aspergill
c 853	6	20.0	2039	13	ADR24487	Adr24487 Breast ca
c 854	6	20.0	2049	13	ADR89407	Adr89407 AXMI-009
855	6	20.0	2056	6	ABT11019	Abt11019 Human bre
856	6	20.0	2056	6	ABN96880	Abn96880 Gene #337
c 857	6	20.0	2058	12	ADH71671	Adh71671 Human gen
c 858	6	20.0	2082	13	ADX32529	Adx32529 Plant ful
c 859	6	20.0	2086	4	AAH46826	Aah46826 Human nov
c 860	6	20.0	2086	4	AAS12522	Aas12522 Gene #15
c 861	6	20.0	2086	10	ABQ77259	Abq77259 Human gon
c 862	6	20.0	2100	8	ACA47741	Aca47741 Prokaryot
c 863	6	20.0	2103	3	AAA98001	Aaa98001 Human T g
c 864	6	20.0	2105	8	ABT20603	Abt20603 Aspergill
c 865	6	20.0	2105	8	ABT18787	Abt18787 Aspergill
c 866	6	20.0	2106	4	ABL16927	Abl16927 Drosophil
c 867	6	20.0	2108	5	AAF56464	Aaf56464 Neisseria
c 868	6	20.0	2109	5	AAF56463	Aaf56463 Neisseria
c 869	6	20.0	2111	5	AAF56458	Aaf56458 Neisseria
c 870	6	20.0	2112	3	AAZ54330	Aaz54330 Neisseria
c 871	6	20.0	2112	3	AAZ54329	Aaz54329 Neisseria
c 872	6	20.0	2112	3	AAA75745	Aaa75745 DNA encod
c 873	6	20.0	2112	5	AAF56462	Aaf56462 Neisseria
c 874	6	20.0	2112	5	AAF56459	Aaf56459 Neisseria
c 875	6	20.0	2112	5	AAF56456	Aaf56456 Neisseria
c 876	6	20.0	2112	5	AAF56460	Aaf56460 Neisseria
c 877	6	20.0	2112	5	AAF56461	Aaf56461 Neisseria
c 878	6	20.0	2112	5	AAF56466	Aaf56466 Neisseria
c 879	6	20.0	2112	5	AAF56467	Aaf56467 Neisseria
c 880	6	20.0	2113	5	AAF56457	Aaf56457 Neisseria
c 881	6	20.0	2113	5	AAF56465	Aaf56465 Neisseria
c 882	6	20.0	2121	5	AAC85822	Aac85822 hOAT3 DNA
c 883	6	20.0	2128	10	ADA53748	Ada53748 Human cod
c 884	6	20.0	2135	2	AAV12393	Aav12393 Human ost
885	6	20.0	2139	13	ADR13684	Adr13684 Amidase c
c 886	6	20.0	2161	12	ADG32241	Adg32241 DNA encod
c 887	6	20.0	2162	11	ACN92124	Acn92124 Breast ca
888	6	20.0	2175	6	ABN86188	Abn86188 Human ins
889	6	20.0	2175	6	ABQ77707	Abq77707 Insulin-l
c 890	6	20.0	2177	10	ADD29601	Add29601 Human tum
891	6	20.0	2178	3	AAC77914	Aac77914 Human can
c 892	6	20.0	2179	3	AAA11146	Aaa11146 Human cer
c 893	6	20.0	2179	14	ADY74828	Ady74828 Rat organ
c 894	6	20.0	2183	4	AAK94590	Aak94590 Human ful
c 895	6	20.0	2183	12	ADL31490	Adl31490 Full leng
c 896	6	20.0	2184	13	ACN42237	Acn42237 Human dia
c 897	6	20.0	2185	13	ADS13024	Ads13024 DNA seque
c 898	6	20.0	2186	14	ADU63878	Adu63878 Recombina
c 899	6	20.0	2190	8	ACA25334	Aca25334 Prokaryot
c 900	6	20.0	2194	4	ABL13311	Abl13311 Drosophil
901	6	20.0	2196	2	AAQ67901	Aaq67901 Syndecan
902	6	20.0	2196	2	AAV41533	Aav41533 Nucleotid
903	6	20.0	2196	2	AAV15947	Aav15947 Mouse syn
904	6	20.0	2196	8	ACA60751	Aca60751 Mouse syn
c 905	6	20.0	2202	13	ADS48132	Ads48132 Bacterial
c 906	6	20.0	2203	13	ACN42236	Acn42236 Human dia
907	6	20.0	2204	6	ABK50208	Abk50208 cDNA enco
908	6	20.0	2206	2	AAQ07043	Aaq07043 Virginia
c 909	6	20.0	2223	13	ADX14951	Adx14951 Plant ful
c 910	6	20.0	2228	13	ADR42455	Adr42455 Human 158
c 911	6	20.0	2228	13	ADR42486	Adr42486 Human 158
c 912	6	20.0	2228	13	ADR42488	Adr42488 Human 158
c 913	6	20.0	2230	3	AAC54329	Aac54329 Arabidops
c 914	6	20.0	2236	12	ADP99203	Adp99203 Human tra
c 915	6	20.0	2242	10	ADB63743	Adb63743 Human cDN
c 916	6	20.0	2245	13	ADS49039	Ads49039 Bacterial
c 917	6	20.0	2258	13	ACN42235	Acn42235 Human dia
918	6	20.0	2267	4	ABL26950	Abl26950 Drosophil
c 919	6	20.0	2275	12	ADN04372	Adn04372 Antipsori
c 920	6	20.0	2275	13	ADP24196	Adp24196 PRO polyp
c 921	6	20.0	2275	13	ADS19469	Ads19469 Beta-gluc
c 922	6	20.0	2275	14	AEB34810	Aeb34810 DNA encod
c 923	6	20.0	2279	9	ADA37283	Ada37283 Acid beta
924	6	20.0	2283	5	AAS88224	Aas88224 DNA encod
c 925	6	20.0	2289	13	ADS45529	Ads45529 Bacterial
926	6	20.0	2290	14	AEB67701	Aeb67701 Rice geno
c 927	6	20.0	2292	10	ACF72290	Acf72290 Photorhab
c 928	6	20.0	2294	13	ACN42233	Acn42233 Human dia
929	6	20.0	2297	10	ADA52853	Ada52853 Human cod
c 930	6	20.0	2313	13	ACN42232	Acn42232 Human dia
c 931	6	20.0	2316	11	ADR42062	Adr42062 Human can
c 932	6	20.0	2316	11	ADR42105	Adr42105 Human can
933	6	20.0	2324	2	AAQ88240	Aaq88240 Neisseria
c 934	6	20.0	2327	2	AAX34303	Aax34303 Hybrid lo
935	6	20.0	2334	10	ABZ38548	Abz38548 N. gonorr
936	6	20.0	2337	10	ADB63376	Adb63376 Human cDN
c 937	6	20.0	2346	4	ABL03597	Abl03597 Drosophil
c 938	6	20.0	2350	6	AAD42877	Aad42877 Human DNA
c 939	6	20.0	2350	10	ADH62608	Adh62608 Human car
940	6	20.0	2352	10	ADF81920	Adf81920 Leukaemia
941	6	20.0	2355	11	ADP21270	Adp21270 Gene enco
942	6	20.0	2355	11	ADP21262	Adp21262 Gene enco
943	6	20.0	2364	5	AAF94358	Aaf94358 Haemophil
944	6	20.0	2364	6	ABK64922	Abk64922 DNA encod
c 945	6	20.0	2371	10	ADF37971	Adf37971 Synchroni
c 946	6	20.0	2373	10	ADD82134	Add82134 Murine hn
947	6	20.0	2383	2	AAQ07042	Aaq07042 Washingto
c 948	6	20.0	2391	4	AAK77091	Aak77091 Human imm
949	6	20.0	2394	12	ADQ76240	Adq76240 Bacillus
950	6	20.0	2397	3	AAC50585	Aac50585 Arabidops
c 951	6	20.0	2397	6	ABK49425	Abk49425 DNA encod
c 952	6	20.0	2397	10	ADG42574	Adg42574 Novel hum
c 953	6	20.0	2397	12	ADH71673	Adh71673 Human gen

c 954	6	20.0	2400	6	ABQ70661	Abq70661 Listeria
c 955	6	20.0	2407	4	AAH18551	Aah18551 Human cDN
956	6	20.0	2413	13	ADX28964	Adx28964 Plant ful
957	6	20.0	2429	10	ADB63638	Adb63638 Human cDN
c 958	6	20.0	2433	12	ADH71683	Adh71683 Human gen
c 959	6	20.0	2446	13	ADR08383	Adr08383 Full leng
960	6	20.0	2461	10	ADF82241	Adf82241 Leukaemia
c 961	6	20.0	2481	10	ADK68155	Adk68155 Novel NOV
c 962	6	20.0	2481	12	ADH71703	Adh71703 Human gen
c 963	6	20.0	2481	13	ADR49144	Adr49144 Human NOV
964	6	20.0	2488	2	AAQ07041	Aaq07041 Idaho all
c 965	6	20.0	2503	5	AAS71417	Aas71417 DNA encod
c 966	6	20.0	2509	10	ADH78814	Adh78814 Human api
c 967	6	20.0	2521	12	ADQ83233	Adq83233 Human tum
c 968	6	20.0	2521	12	ADQ85144	Adq85144 Human tum
c 969	6	20.0	2521	13	ADQ83913	Adq83913 Human tum
c 970	6	20.0	2526	5	AAS66674	Aas66674 DNA encod
c 971	6	20.0	2526	6	ABA90335	Aba90335 Human pol
c 972	6	20.0	2526	6	ABS63432	Abs63432 Human cDN
c 973	6	20.0	2530	12	ADJ27229	Adj27229 Human TRI
c 974	6	20.0	2531	6	ABS63433	Abs63433 Human cDN
c 975	6	20.0	2531	10	ADK68149	Adk68149 Novel NOV
c 976	6	20.0	2531	12	ADH71697	Adh71697 Human gen
c 977	6	20.0	2531	13	ADR49138	Adr49138 Human NOV
c 978	6	20.0	2539	12	ADH71689	Adh71689 Human gen
979	6	20.0	2547	6	ABK75344	Abk75344 Bacillus
c 980	6	20.0	2548	12	ADH71705	Adh71705 Human gen
c 981	6	20.0	2549	8	ABX05171	Abx05171 Human nov
982	6	20.0	2555	4	ABL06246	Abl06246 Drosophil
c 983	6	20.0	2555	6	AAL40488	Aal40488 158P1D7 S
c 984	6	20.0	2555	13	ADR42487	Adr42487 Human 158
c 985	6	20.0	2555	13	ADR42453	Adr42453 Human 158
c 986	6	20.0	2555	13	ADR42451	Adr42451 Human 158
c 987	6	20.0	2555	13	ADR42499	Adr42499 Human 158
c 988	6	20.0	2555	13	ADR42493	Adr42493 Human 158
c 989	6	20.0	2563	2	AAQ50008	Aaq50008 Aspergill
990	6	20.0	2568	12	ADN74168	Adn74168 Thale cre
991	6	20.0	2569	10	ADD44980	Add44980 Rat gene
992	6	20.0	2569	10	ADD44984	Add44984 Rat gene
993	6	20.0	2571	2	AAV26970	Aav26970 Feline im
c 994	6	20.0	2574	8	AAD56188	Aad56188 Human LRR
c 995	6	20.0	2576	11	ACN90350	Acn90350 Breast ca
996	6	20.0	2576	13	ADX12775	Adx12775 Plant ful
c 997	6	20.0	2586	10	ADE76203	Ade76203 Human glu
c 998	6	20.0	2588	6	AAL49802	Aal49802 Human chl
c 999	6	20.0	2593	8	AAD56186	Aad56186 Human LRR
1000	6	20.0	2604	13	ADX14545	Adx14545 Plant ful

ALIGNMENTS

RESULT 1
AAV81465
ID AAV81465 standard; DNA; 65 BP.
XX
AC AAV81465;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE Ribosome-inactivating protein coding sequence fragment.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; ss.
XX
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX
PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 22; 39pp; English.
XX
CC This sequence encodes a fragment of the ribosome-inactivating protein
CC (RIP) of the invention. The RIP is designated bouganin, and comprises a
CC linear polypeptide (26 kDa) with a pI of 9.0, where the amino-terminal
CC end exhibits 50 % homology with the sequence shown in AAW67752. The
CC proteins and conjugates form compositions in treating various human
CC diseases or conditions, including cancer, graft-versus-host disease,
CC organ transplant rejection, type I diabetes, multiple sclerosis,
CC rheumatoid arthritis, systemic lupus erythematosus, and myasthenia
CC gravis. The proteins are also useful as therapeutic anti-viral agents in
CC plants and mammals. Compositions containing the polynucleotide encoding
CC bouganin are useful in gene therapy. Bouganin possesses low non-specific
CC toxicity, which makes it very suitable for use as the toxic agent in
CC various immunotoxins. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 65 BP; 19 A; 18 C; 15 G; 13 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.61e-15	Length:	65
Score:	21.00	Matches:	21
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	70.0%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-1 (1-30) x AAV81465 (1-65)

```
Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63
```

RESULT 2
AAV81468
ID AAV81468 standard; DNA; 363 BP.
XX
AC AAV81468;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE Ribosome-inactivating protein, coding sequence fragment.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; ss.
XX
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX

```
PR   06-JUN-1997;   97EP-00201725.
XX
PA   (PANG-) PANGENETICS BV.
XX
PI   Stirpe F,  Bolognesi A;
XX
DR   WPI; 1999-045796/04.
XX
PT   New type-1 ribosome-inactivating protein bouganin - useful in forming
PT   immunotoxins for use in medicine and plant protection.
XX
PS   Example 8; Page 24; 39pp; English.
XX
CC   This sequence represents a fragment of the DNA encoding the ribosome-
CC   inactivating protein (RIP) of the invention. The RIP is designated
CC   bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,
CC   where the amino-terminal end exhibits 50 % homology with the sequence
CC   shown in AAW67752. The proteins and conjugates form compositions in
CC   treating various human diseases or conditions, including cancer, graft-
CC   versus-host disease, organ transplant rejection, type I diabetes,
CC   multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC   and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC   viral agents in plants and mammals. Compositions containing the
CC   polynucleotide encoding bouganin are useful in gene therapy. Bouganin
CC   possesses low non-specific toxicity, which makes it very suitable for use
CC   as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC   correct OS field.)
XX
SQ   Sequence 363 BP; 110 A; 68 C; 85 G; 100 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.43e-07        Length:         363
Score:                  14.00           Matches:        14
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            46.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-1 (1-30) x AAV81468 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 3
AAF31245
ID   AAF31245 standard; DNA; 1238 BP.
XX
AC   AAF31245;
XX
DT   09-APR-2001  (first entry)
XX
DE   Human immune response molecule (IMUN) coding sequence SEQ ID NO: 12.
XX
KW   Human; IMUN; immune response molecule; autoimmune disorder;
KW   inflammatory disorder; cell proliferation disorder; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200102569-A2.
XX
PD   11-JAN-2001.
XX
PF   06-JUL-2000; 2000WO-US018505.
XX
PR   06-JUL-1999;   99US-0142572P.
PR   09-SEP-1999;   99US-0153170P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Tang YT,  Yue H,  Yang J,  Azimzai Y,  Baughn MR,  Lu DAM;
XX
DR   WPI; 2001-123113/13.
DR   P-PSDB; AAB67048.
XX
PT   Novel human immune response molecules (IMUN), useful for diagnosing,
PT   treating and preventing disorders associated with abnormal expression of
PT   IMUN, e.g. Addison's disease, allergies, anemia, asthma and
PT   atherosclerosis.
XX
PS   Claim 5; Page 90; 95pp; English.
XX
CC   The present invention provides the protein and coding sequences for ten
CC   human immune response molecules (designated IMUN-1 to IMUN-10). The
CC   sequences can be used in the diagnosis, treatment and prevention of
CC   autoimmune and inflammatory disorders such as AIDS, atherosclerosis,
CC   asthma, allergies, Crohn's disease, multiple sclerosis, irritable bowel
CC   syndrome, psoriasis, rheumatoid arthritis and infections, and cell
CC   proliferation disorders including arteriosclerosis, cirrhosis and cancer
XX
SQ   Sequence 1238 BP; 363 A; 249 C; 302 G; 324 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              15.8            Length:         1238
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     4               Gaps:           0

US-10-758-902-1 (1-30) x AAF31245 (1-1238)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db        994 ACAGTGTCATTTAATTTGGGAGAG 1017

RESULT 4
ADP07317
ID   ADP07317 standard; DNA; 2143 BP.
XX
AC   ADP07317;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human WT1 DNA.
XX
KW   ds; proliferative disease; breast; methylation; CpG; bisulfite; human.
XX
OS   Homo sapiens.
XX
PN   DE10255104-A1.
XX
PD   11-MAR-2004.
XX
PF   26-NOV-2002; 2002DE-01055104.
XX
PR   27-AUG-2002; 2002DE-01039313.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Maier S;
XX
DR   WPI; 2004-284340/27.
DR   GENBANK; NM_004906.
XX
PT   Analyzing proliferative diseases of breast cells, useful e.g. for
PT   diagnosis, prognosis and treatment of breast cancer, by determining
PT   methylation status of specific genes.
XX
PS   Claim 1; Page; 22pp; German.
XX
CC   This invention describes a novel method of analysing proliferative
CC   diseases of breast cells by determining the methylation status of certain
CC   genes. The invention also describes nucleic acids or their complements,
CC   oligomers, especially oligonucleotides or peptide nucleic acid oligomers,
CC   that hybridise to, or are identical with, any of the nucleic acids, the
```

CC preparation of an oligomer array for analysing proliferative diseases of
CC breast cells that are associated with the methylation status of CpG
CC dinucleotides of the genes by bonding at least one oligomer to a solid
CC phase and a kit comprising a bisulfite reagent and the oligomer. The
CC nucleic acids are genomic sequences (5'- and/or regulatory and/or CpG-
CC rich regions). The base sequence of the oligomer includes at least one
CC CpG island, especially with C in the middle third of the sequence. The
CC process involves a genomic DNA sample treated chemically, specifically
CC with a bisulfite reagent, to convert non-methylated C to uracil or some
CC other base having base-pairing properties different from those of C.
CC Fragments of the treated DNA are then amplified, using primers and a
CC polymerase and the methylation status of the genomic CpG dinucleotides is
CC determined by analysis of the amplicons, particularly by hybridisation to
CC the oligomer, optionally with extension of the hybridised oligomer by at
CC least one base, or detection is by sequencing. The amplification may use
CC methylation-specific primers. Alternatively, genomic DNA is extracted
CC from a sample and digested with methylation-specific restriction enzymes,
CC then the digestion fragments detected, optionally after amplification. In
CC either method, more than 10 fragments of 100-200 bp are amplified in a
CC single reaction vessel, using a heat-resistant DNA polymerase in PCR. The
CC amplicons carry detectable markers, e.g. fluorophores, radioisotopes
CC and/or releasable fragments of known mass that can be detected by mass
CC spectrometry. The method is used for characterisation, classification,
CC differentiation, staging, phase-estimation, diagnosis and/or therapy of
CC proliferative diseases of breast cells. The method provides very specific
CC classification of proliferative diseases, allowing better treatment. It
CC can both characterise methylation status and detect single-nucleotide
CC polymorphisms. This sequence represents human gene used to illustrate the
CC method of the invention. NOTE: This sequence does not appear in the
CC printed specification but has been retrieved from Genbank.
XX
SQ Sequence 2143 BP; 619 A; 431 C; 498 G; 595 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	26.1	Length:	2143
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-1 (1-30) x ADP07317 (1-2143)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db       1436 ACAGTGTCATTTAATTTGGGAGAG 1459
```

RESULT 5
ADQ67284
ID ADQ67284 standard; cDNA; 2291 BP.
XX
AC ADQ67284;
XX
DT 07-OCT-2004 (first entry)
XX
DE Novel human cDNA sequence #2257.
XX
KW ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX
OS Homo sapiens.
XX
PN EP1440981-A2.
XX
PD 28-JUL-2004.
XX
PF 21-JAN-2004; 2004EP-00001196.
XX
PR 21-JAN-2003; 2003JP-00102206.
PR 09-MAY-2003; 2003JP-00131392.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX
DR WPI; 2004-535376/52.
DR P-PSDB; ADQ67591.
XX
PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 4445; 2449pp; English.
XX
CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.
XX
SQ Sequence 2291 BP; 642 A; 393 C; 498 G; 758 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	27.8	Length:	2291
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-1 (1-30) x ADQ67284 (1-2291)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db       1604 ACAGTGTCATTTAATTTGGGAGAG 1627
```

RESULT 6
ADE54051
ID ADE54051 standard; cDNA; 2772 BP.
XX
AC ADE54051;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human prostate cancer cDNA #398.
XX
KW Human; prostate cancer; ss; cDNA combination; differential expression;
KW gene.
XX
OS Homo sapiens.
XX
PN US2003190640-A1.
XX
PD 09-OCT-2003.
XX
PF 29-MAY-2002; 2002US-00252157.
XX
PR 31-MAY-2001; 2001US-0295048P.
XX
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
XX
PI Faris M, Pearson CI;
XX
DR WPI; 2003-831619/77.
XX
PT New combination comprising cDNAs that are differentially expressed in
PT prostate cancer, useful for diagnosing, treating or monitoring the
PT progression of treatment of prostate cancer.
XX

PS Claim 1; SEQ ID NO 398; 42pp; English.
XX
CC The invention relates to a combination comprising a number of cDNAs
CC expressed in prostate cancer. The invention also relates to a method for
CC detecting differential expression of one or more cDNAs in a sample
CC containing nucleic acids by hybridising a substrate with the nucleic
CC acids, thus forming one or more hybridisation complexes, detecting
CC hybridisation complex formation and comparing the complexes formed with
CC standard complexes, where differences between the standard and the sample
CC complex formation indicate differential expression of cDNAs in the
CC sample. The differential expression is diagnostic of prostate cancer. The
CC invention also relates to proteins and antibodies related to the cDNAs.
CC The combination is useful for diagnosing, treating or monitoring the
CC progression of treatment of prostate cancer. The antibodies are useful
CC for detecting prostate cancer. This sequence represents a human prostate
CC cancer cDNA of the invention.
XX
SQ Sequence 2772 BP; 740 A; 680 C; 664 G; 688 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	33.1	Length:	2772
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-1 (1-30) x ADE54051 (1-2772)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db       2634 ACAGTGTCATTTAATTTGGGAGAG 2657
```

RESULT 7
AAV81463
ID AAV81463 standard; DNA; 23 BP.
XX
AC AAV81463;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE PCR primer 102 for Ribosome-inactivating protein, bouganin.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; PCR primer; ss.
XX
OS Synthetic.
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX
PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 22; 39pp; English.
XX
CC This sequence represents a PCR primer for DNA encoding the ribosome-
CC inactivating protein (RIP) of the invention. The RIP is designated
CC bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,
CC where the amino-terminal end exhibits 50 % homology with the sequence
CC shown in AAW67752. The proteins and conjugates form compositions in
CC treating various human diseases or conditions, including cancer, graft-
CC versus-host disease, organ transplant rejection, type I diabetes,
CC multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC viral agents in plants and mammals. Compositions containing the
CC polynucleotide encoding bouganin are useful in gene therapy. Bouganin
CC possesses low non-specific toxicity, which makes it very suitable for use
CC as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 23 BP; 5 A; 4 C; 5 G; 2 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.:	5.76	Length:	23
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-1 (1-30) x AAV81463 (1-23)

```
Qy          9 GlyGluAlaTyrGluTyrPro 15
              |||||||||||||||||||||
Db          1 GGNGARGCNTAYGARTAYCCN 21
```

RESULT 8
AAV81464/c
ID AAV81464 standard; DNA; 23 BP.
XX
AC AAV81464;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE PCR primer 116 for Ribosome-inactivating protein, bouganin.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; PCR primer; ss.
XX
OS Synthetic.
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX
PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 22; 39pp; English.
XX
CC This sequence represents a PCR primer for DNA encoding the ribosome-
CC inactivating protein (RIP) of the invention. The RIP is designated
CC bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,
CC where the amino-terminal end exhibits 50 % homology with the sequence
CC shown in AAW67752. The proteins and conjugates form compositions in
CC treating various human diseases or conditions, including cancer, graft-

```
CC   versus-host disease, organ transplant rejection, type I diabetes,
CC   multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC   and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC   viral agents in plants and mammals. Compositions containing the
CC   polynucleotide encoding bouganin are useful in gene therapy. Bouganin
CC   possesses low non-specific toxicity, which makes it very suitable for use
CC   as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC   correct OS field.)
XX
SQ   Sequence 23 BP; 1 A; 4 C; 5 G; 6 T; 0 U; 7 Other;

Alignment Scores:
Pred. No.:              5.76          Length:        23
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x AAV81464 (1-23)

Qy         23 AsnGluLeuAlaLysGlyThr 29
              |||||||||||||||||||
Db         23 AAYGARCTNGCNAARGGNACN 3

RESULT 9
AAV81466
ID   AAV81466 standard; DNA; 25 BP.
XX
AC   AAV81466;
XX
DT   27-AUG-2003  (revised)
DT   16-APR-1999  (first entry)
XX
DE   PCR primer 125 for Ribosome-inactivating protein, bouganin.
XX
KW   Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW   graft-versus-host disease; organ transplant rejection; type I diabetes;
KW   rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW   anti-viral agent; gene therapy; toxic agent; immunotoxin; PCR primer; ss.
XX
OS   Synthetic.
OS   Bougainvillea spectabilis.
XX
PN   WO9855623-A1.
XX
PD   10-DEC-1998.
XX
PF   08-JUN-1998;   98WO-NL000336.
XX
PR   06-JUN-1997;   97EP-00201725.
XX
PA   (PANG-) PANGENETICS BV.
XX
PI   Stirpe F,  Bolognesi A;
XX
DR   WPI; 1999-045796/04.
XX
PT   New type-1 ribosome-inactivating protein bouganin - useful in forming
PT   immunotoxins for use in medicine and plant protection.
XX
PS   Example 8; Page 22; 39pp; English.
XX
CC   This sequence represents a PCR primer for DNA encoding the ribosome-
CC   inactivating protein (RIP) of the invention. The RIP is designated
CC   bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,
CC   where the amino-terminal end exhibits 50 % homology with the sequence
CC   shown in AAW67752. The proteins and conjugates form compositions in
CC   treating various human diseases or conditions, including cancer, graft-
CC   versus-host disease, organ transplant rejection, type I diabetes,
CC   multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC   and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC   viral agents in plants and mammals. Compositions containing the
CC   polynucleotide encoding bouganin are useful in gene therapy. Bouganin
CC   possesses low non-specific toxicity, which makes it very suitable for use
CC   as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC   correct OS field.)
XX
SQ   Sequence 25 BP; 8 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.21          Length:        25
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x AAV81466 (1-25)

Qy         17 PheIleGlnAspLeuArgAsn 23
              |||||||||||||||||||||
Db          3 TTTATACAAGATTTGCGCAAC 23

RESULT 10
ABV18359/c
ID   ABV18359 standard; cDNA; 431 BP.
XX
AC   ABV18359;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 18350.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005171.
XX
PR   17-FEB-2000; 2000US-0183319P.
PR   16-MAR-2000; 2000US-0189862P.
PR   25-MAY-2000; 2000US-0207454P.
PR   09-JUN-2000; 2000US-0211314P.
PR   18-JUL-2000; 2000US-0219007P.
PR   13-DEC-2000; 2000US-0255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS   Claim 1; Page 3027; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for: (a) assessing whether
CC   a patient is afflicted with prostate cancer; (b) monitoring the
CC   progression of prostate cancer in a patient; (c) assessing the efficacy
CC   of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC   the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC   determining whether prostate cancer has metastasized in a patient; (h)
CC   assessing the aggressiveness or indolence of prostate cancer in a patient
CC   ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
```

XX
SQ Sequence 431 BP; 118 A; 104 C; 79 G; 128 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	83.5	Length:	431
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-1 (1-30) x ABV18359 (1-431)

```
Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        253 AATACAGTTTCCTTCAATTTA 233
```

RESULT 11
ABQ62599
ID ABQ62599 standard; DNA; 439 BP.
XX
AC ABQ62599;
XX
DT 16-AUG-2002 (first entry)
XX
DE Mycobacterium tuberculosis BAC vector clone Rv149SP6.
XX
KW Mycobacterium tuberculosis; Mycobacterium bovis; mycobacterium;
KW detection; BAC vector; bacterial artificial chromosome; tuberculosis;
KW gene; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9954487-A2.
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-IB000740.
XX
PR 16-APR-1998; 98US-00060756.
XX
PA (INSP) INST PASTEUR.
XX
PI Cole S, Buchrieser-Brosch R, Gordon S, Billault A;
XX
DR WPI; 2000-013262/01.
XX
PT Isolation of polynucleotides from mycobacterial genomes, useful for
PT detection of Mycobacteria and for combating tuberculosis.
XX
PS Claim 23; Page 50; 161pp; English.
XX
CC The present invention describes a method for isolating a polynucleotide
CC of interest that is present or is expressed in a genome of a first
CC mycobacterium strain and that is absent or altered in a genome of a
CC second mycobacterium strain, which is different from the first strain
CC using a bacterial artificial chromosome (BAC) vector. Recombinant BAC
CC vectors, which are preferably immobilised, can be used to detect
CC mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological
CC samples. The polynucleotides identified are useful as probes or primers
CC for detecting a given mycobacterium of interest. By aligning the
CC polynucleotides contained in the recombinant BAC vectors it is possible
CC to physically map a polynucleotide of mycobacterial origin in a
CC biological sample. The methods and vectors from the present invention are
CC useful in providing information for combating tuberculosis. It is
CC possible to compare genomes between different strains or species and
CC their non-pathogenic strains or species counterparts. ABQ62492 to
CC ABQ63228 and ABB81227 to ABB81230 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 439 BP; 83 A; 143 C; 117 G; 96 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	84.9	Length:	439
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x ABQ62599 (1-439)

```
Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db        364 CAGGATCTCAGAAACGAGCTG 384
```

RESULT 12
ADP95365/c
ID ADP95365 standard; cDNA; 471 BP.
XX
AC ADP95365;
XX
DT 09-SEP-2004 (first entry)
XX
DE Cotton expressed sequence tag, EST, #4376.
XX
KW Cotton; ss; EST; expressed sequence tag; plant; plant protection;
KW plant improvement; marker-assisted breeding.
XX
OS Gossypium hirsutum; variety Nucotton33B.
XX
PN US2004123338-A1.
XX
PD 24-JUN-2004.
XX
PF 08-DEC-2000; 2000US-00732627.
XX
PR 10-DEC-1999; 99US-0170255P.
XX
PA (FINC/) FINCHER K L.
XX
PI Fincher KL;
XX
DR WPI; 2004-479807/45.
XX
PT New substantially purified nucleic acid molecule that encodes a cotton
PT protein or its fragment, useful as molecular tool for the targeting and
PT isolation of novel genes for plant protection and improvement.
XX
PS Claim 1; SEQ ID NO 4376; 30pp; English.
XX
CC The invention relates to a substantially purified nucleic acid molecule
CC that encodes a cotton protein or its fragment comprising an EST
CC (expressed sequence tag) appearing as ADP90990-ADP95919. Also included
CC are a substantially purified cotton protein or its fragment encoded by a
CC nucleic acid molecule above and a transformed plant (having a nucleic
CC acid molecule which comprises: an exogenous promoter region which
CC functions in a plant cell to cause the production of a mRNA molecule; a
CC structural nucleic acid molecule comprising one of the ESTs or their
CC complements; a 3' non-translated sequence that functions in the plant
CC cell to cause termination of transcription and addition of polyadenylated
CC ribonucleotides to a 3' end of the mRNA molecule). The ESTs are useful as
CC molecular tool for the targeting and isolation of novel genes for plant
CC protection and improvement. The ESTs are useful for developing new
CC strategies for understanding critical plant developmental and metabolic
CC pathways, for isolating genes and promoters, for identifying and mapping
CC the genes involved in developmental and metabolic pathways, and for
CC determining gene function. The cotton nucleic acid molecules are useful
CC as molecular tags to isolate genetic regions, isolate genes, map genes,
CC and determine gene function. The nucleic acid molecules are useful for
CC determining if genes are members of a particular gene family and for use
CC in marker-assisted breeding programs. The present sequence is one of the
CC 4930 cotton ESTs of the invention. NOTE: The sequences are not displayed
CC in the specification but are available in electronic format from the
CC USPTO at seqdata.uspto.gov/sequence.html?DocID=20040123338.
XX

```
SQ   Sequence 471 BP; 134 A; 103 C; 103 G; 130 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              90.6          Length:         471
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.3%         Indels:         0
DB:                     12            Gaps:           0

US-10-758-902-1 (1-30) x ADP95365 (1-471)

Qy          4 ValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||
Db        379 GTGAGCTTTAATTTGGGGGAA 359

RESULT 13
AAS35302/c
ID   AAS35302 standard; cDNA; 472 BP.
XX
AC   AAS35302;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Human cardiovascular system antigen cDNA polynucleotide SEQ ID No 187.
XX
KW   Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
KW   chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog;
KW   antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW   cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW   ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm;
KW   hyperproliferative disorder; breast; liver; cardiovascular disorder; ss;
KW   cerebrovascular disorder; nervous system disorder; bacterial infection;
KW   fungal infection; viral infection; ocular disorder; endocrine disorder;
KW   gastrointestinal disorder; renal disorder; respiratory disorder;
KW   wound healing; skin aging; organ transplantation; tissue regeneration;
KW   anti-infertility.
XX
OS   Homo sapiens.
XX
PN   WO200155321-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001340.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0231243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
PR   08-SEP-2000; 2000US-0231414P.
PR   08-SEP-2000; 2000US-0232080P.
PR   08-SEP-2000; 2000US-0232081P.
PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0233064P.
PR   14-SEP-2000; 2000US-0233065P.
PR   21-SEP-2000; 2000US-0234223P.
PR   21-SEP-2000; 2000US-0234274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
PR   27-SEP-2000; 2000US-0235836P.
PR   29-SEP-2000; 2000US-0236327P.
PR   29-SEP-2000; 2000US-0236367P.
PR   29-SEP-2000; 2000US-0236368P.
PR   29-SEP-2000; 2000US-0236369P.
PR   29-SEP-2000; 2000US-0236370P.
PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   02-OCT-2000; 2000US-0237040P.
PR   13-OCT-2000; 2000US-0239935P.
PR   13-OCT-2000; 2000US-0239937P.
PR   20-OCT-2000; 2000US-0240960P.
PR   20-OCT-2000; 2000US-0241221P.
PR   20-OCT-2000; 2000US-0241785P.
PR   20-OCT-2000; 2000US-0241786P.
PR   20-OCT-2000; 2000US-0241787P.
PR   20-OCT-2000; 2000US-0241808P.
PR   20-OCT-2000; 2000US-0241809P.
PR   20-OCT-2000; 2000US-0241826P.
PR   01-NOV-2000; 2000US-0244617P.
PR   08-NOV-2000; 2000US-0246474P.
PR   08-NOV-2000; 2000US-0246475P.
PR   08-NOV-2000; 2000US-0246476P.
PR   08-NOV-2000; 2000US-0246477P.
PR   08-NOV-2000; 2000US-0246478P.
PR   08-NOV-2000; 2000US-0246523P.
PR   08-NOV-2000; 2000US-0246524P.
PR   08-NOV-2000; 2000US-0246525P.
PR   08-NOV-2000; 2000US-0246526P.
PR   08-NOV-2000; 2000US-0246527P.
PR   08-NOV-2000; 2000US-0246528P.
PR   08-NOV-2000; 2000US-0246532P.
```

PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-451930/48.
DR P-PSDB; AAU22028.
XX
PT New cardiovascular system related polynucleotides and polypeptides,
PT useful for diagnosing, treating and/or preventing disorders of the
PT cardiovascular system.
XX
PS Claim 1; SEQ ID NO 187; 674pp; English.
XX
CC Sequences AAS35126-AAS35740 represent cDNA molecules, which encode the
CC cardiovascular system antigen polypeptides of the invention.
CC Cardiovascular system antigens and their associated polynucleotides are
CC useful in the diagnosis, treatment and prevention of various types of
CC disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
CC chickens or sheep. A pathological condition can be determined by
CC detecting the presence or absence of a mutation in a cardiovascular
CC system antigen polynucleotide. The treatable disorders include autoimmune
CC diseases such as rheumatoid arthritis, hyperproliferative disorders such
CC as neoplasms of the breast or liver, cardiovascular disorders such as
CC cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,
CC nervous system disorders such as Alzheimer's disease, infections caused
CC by bacteria, viruses and fungi, ocular disorders such as corneal
CC infection, endocrine disorders such as premature labour and infertility,
CC gastrointestinal disorders such as Crohn's disease, renal disorders such
CC as glomerulonephritis and respiratory disorders such as asthma and
CC pleurisy. The polypeptides can also be used to aid wound healing, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, to regenerate tissues and in chemotaxis. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

Alignment Scores:

Pred. No.:	90.7	Length:	472
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-1 (1-30) x AAS35302 (1-472)

```
Qy          4 ValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||
Db        245 GTTTCCTTCAAYCTAGGAGAA 225
```

RESULT 14
ADE45381/c
ID ADE45381 standard; cDNA; 472 BP.
XX
AC ADE45381;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cardiovascular system related polynucleotide #177.
XX
KW Human; cardiovascular system related polypeptide; cancer;
KW proliferative disorder; foetal abnormality; developmental abnormality;
KW haematopoietic disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003059908-A1.
XX
PD 27-MAR-2003.
XX
PF 07-MAR-2002; 2002US-00091504.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764869.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI; 2003-743766/70.
DR P-PSDB; ADE45996.
XX
PT New cardiovascular system related polynucleotides and polypeptides,
PT useful for preventing, treating, or ameliorating a medical condition,
PT such as cancer of cardiovascular tissues and cancer metastases.
XX
PS Claim 1; SEQ ID NO 187; 262pp; English.
XX
CC The invention relates to human cardiovascular system related polypeptides
CC and the polynucleotides encoding them. The polypeptides, polynucleotides
CC and antibodies to the polypeptides are useful for diagnosing a
CC pathological condition or a susceptibility to a pathological condition,
CC for preventing, treating, or ameliorating a medical condition, such as
CC cancer of cardiovascular system tissues, proliferative disorders, foetal
CC and developmental abnormalities, haematopoietic disorders, diseases of
CC the immune system, AIDS, autoimmune diseases (e.g., rheumatoid
CC arthritis), inflammation, allergies, neurological disorders (e.g.,
CC Alzheimer's disease, Parkinson's disease), cognitive disorders,
CC schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis,
CC diabetes, atherosclerosis, cardiovascular disorders, angiogenic
CC disorders, kidney disorders, gastrointestinal disorders, pregnancy-
CC related disorders, endocrine disorders and infections. The nucleic acids
CC are also useful for chromosome identification, radiation hybrid mapping
CC or long-range restriction mapping. The polypeptides and polynucleotides
CC may also be used as food additives or preservatives to increase or
CC decrease storage capabilities, fat content or other nutritional
CC components. This sequence represents a human cardiovascular system
CC related polynucleotide of the invention.
XX
SQ Sequence 472 BP; 110 A; 105 C; 118 G; 126 T; 0 U; 13 Other;

Alignment Scores:
Pred. No.: 90.7 Length: 472
Score: 7.00 Matches: 7

```
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            23.3%           Indels:        0
DB:                     10              Gaps:          0

US-10-758-902-1 (1-30) x ADE45381 (1-472)

Qy          4 ValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||
Db        245 GTTTCCTTCAAYCTAGGAGAA 225

RESULT 15
ADJ06799/c
ID   ADJ06799 standard; DNA; 472 BP.
XX
AC   ADJ06799;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human cardiovascular system associated gene SeqID187.
XX
KW   autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;
KW   breast neoplasms; liver neoplasm; cardiovascular disorder;
KW   cardiac arrest; cerebrovascular disorder; cerebral ischaemia;
KW   angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW   ocular disorder; corneal infection; wound healing;
KW   epithelial cell proliferation; skin aging; sunburn;
KW   organ transplantation; cell culture; tissue regeneration; chemotaxis;
KW   food additive; preservative; cardiovascular system associated antigen;
KW   nuclear factor kappaB; NFkappaB; promoter element; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   US2004005575-A1.
XX
PD   08-JAN-2004.
XX
PF   26-AUG-2002; 2002US-00227577.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0231243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
PR   08-SEP-2000; 2000US-0231414P.
PR   08-SEP-2000; 2000US-0232080P.
PR   08-SEP-2000; 2000US-0232081P.
PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0233064P.
PR   14-SEP-2000; 2000US-0233065P.
PR   21-SEP-2000; 2000US-0234223P.
PR   21-SEP-2000; 2000US-0234274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
PR   27-SEP-2000; 2000US-0235836P.
PR   29-SEP-2000; 2000US-0236327P.
PR   29-SEP-2000; 2000US-0236367P.
PR   29-SEP-2000; 2000US-0236368P.
PR   29-SEP-2000; 2000US-0236369P.
PR   29-SEP-2000; 2000US-0236370P.
PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   02-OCT-2000; 2000US-0237040P.
PR   13-OCT-2000; 2000US-0239935P.
PR   13-OCT-2000; 2000US-0239937P.
PR   20-OCT-2000; 2000US-0240960P.
PR   20-OCT-2000; 2000US-0241221P.
PR   20-OCT-2000; 2000US-0241785P.
PR   20-OCT-2000; 2000US-0241786P.
PR   20-OCT-2000; 2000US-0241787P.
PR   20-OCT-2000; 2000US-0241808P.
PR   20-OCT-2000; 2000US-0241809P.
PR   20-OCT-2000; 2000US-0241826P.
PR   01-NOV-2000; 2000US-0244617P.
PR   08-NOV-2000; 2000US-0246474P.
PR   08-NOV-2000; 2000US-0246475P.
PR   08-NOV-2000; 2000US-0246476P.
PR   08-NOV-2000; 2000US-0246477P.
PR   08-NOV-2000; 2000US-0246478P.
PR   08-NOV-2000; 2000US-0246523P.
PR   08-NOV-2000; 2000US-0246524P.
PR   08-NOV-2000; 2000US-0246525P.
PR   08-NOV-2000; 2000US-0246526P.
PR   08-NOV-2000; 2000US-0246527P.
PR   08-NOV-2000; 2000US-0246528P.
PR   08-NOV-2000; 2000US-0246532P.
PR   08-NOV-2000; 2000US-0246609P.
PR   08-NOV-2000; 2000US-0246610P.
PR   08-NOV-2000; 2000US-0246611P.
PR   08-NOV-2000; 2000US-0246613P.
PR   17-NOV-2000; 2000US-0249207P.
PR   17-NOV-2000; 2000US-0249208P.
PR   17-NOV-2000; 2000US-0249209P.
```

PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764869.
PR 07-MAR-2002; 2002US-00091504.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI; 2004-081713/08.
DR P-PSDB; ADJ07414.
XX
PT New cardiovascular system-related nucleic acid molecule, useful for
PT diagnosing, preventing or treating diseases of the cardiovascular system,
PT and in chromosome mapping, drug screening or in pharmacogenomics.
XX
PS Claim 1; SEQ ID NO 187; 262pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule encoding a
CC human cardiovascular system associated polypeptide (or antigens), or its
CC fragment. Also included recombinant vectors, recombinant host cells, an
CC isolated human cardiovascular system associated polypeptide (including
CC its fragment, allelic variant, species homologue or epitope), an isolated
CC antibody that binds specifically to a human cardiovascular system
CC associated polypeptide, diagnosing a pathological condition or
CC susceptibility to a pathological condition (comprising determining the
CC presence or absence of a mutation in human cardiovascular system
CC associated nucleic acid and diagnosing a condition based on the presence
CC or absence of the mutation), identifying a binding partner to human
CC cardiovascular system associated polypeptides, the gene corresponding to
CC the human cardiovascular system associated cDNA sequence and identifying
CC an activity in a biological assay comprising expressing the human
CC cardiovascular system associated cDNA in a cell, isolating the
CC supernatant, detecting an activity in a biological assay and identifying
CC the protein in the supernatant having the activity. The human
CC cardiovascular system associated nucleic acids and polypeptides are used
CC to prevent, treat or ameliorate a medical condition (for example in
CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep), for
CC example autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders, for example neoplasms of the breast or

Alignment Scores:

Pred. No.:	90.7	Length:	472
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-1 (1-30) x ADJ06799 (1-472)

```
Qy          4 ValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||
Db        245 GTTTCCTTCAAYCTAGGAGAA 225
```

RESULT 16
ADT06364/c
ID ADT06364 standard; DNA; 484 BP.
XX
AC ADT06364;
XX
DT 30-DEC-2004 (first entry)
XX
DE Nicotiana tabacum oxidative stress-associated DNA sequence #106.
XX
KW ds; hydrogen peroxide; signaling pathway; catalase deficient plant;
KW plant; stress tolerance; oxidative stress; tobacco.
XX
OS Nicotiana tabacum.
XX
PN WO2004087952-A2.
XX
PD 14-OCT-2004.
XX
PF 31-MAR-2004; 2004WO-EP050398.
XX
PR 31-MAR-2003; 2003EP-00100850.
PR 27-MAY-2003; 2003EP-00101544.
XX
PA (VIBV-) VIB VZW.
PA (UYGE-) UNIV GENT.
XX
PI Van Breusegem F, Inze DG, Vandenabeele S;
XX
DR WPI; 2004-737731/72.
XX
PT Isolating a gene involved in the hydrogen peroxide induced signaling
PT pathway, useful for obtaining oxidative stress, comprises growing
PT catalase deficient plant.
XX
PS Claim 10; SEQ ID NO 106; 322pp; English.
XX
CC The invention relates to a method for isolating a gene involved in the
CC hydrogen peroxide induced signaling pathway comprising growing at least
CC one catalase deficient plant and one control plant. The isolated gene or
CC the encoded protein is useful for obtaining stress tolerance, i.e.
CC oxidative stress. The method is useful for isolating a gene involved in
CC the hydrogen peroxide induced signaling pathway. This sequence
CC corresponds to a gene of the invention.
XX
SQ Sequence 484 BP; 125 A; 82 C; 120 G; 157 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	92.8	Length:	484
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-1 (1-30) x ADT06364 (1-484)

```
Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||||
Db        251 AACACCGTCAGCTTCAACCTC 231
```

RESULT 17
ABV48145/c
ID ABV48145 standard; cDNA; 498 BP.

XX
AC ABV48145;
XX
DT 17-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 48136.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 9448; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
XX
SQ Sequence 498 BP; 138 A; 125 C; 98 G; 137 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	95.3	Length:	498
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-1 (1-30) x ABV48145 (1-498)

```
Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        305 AATACAGTTTCCTTCAATTTA 285
```

RESULT 18
ABQ92793/c
ID ABQ92793 standard; DNA; 543 BP.
XX
AC ABQ92793;
XX
DT 29-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
DE Triticum tauschii/wheat D genome microsatellite marker cfd61.
XX
KW Microsatellite marker; wheat; D genome; mapping; genotyping;
KW polymorphism; phenotypic trait; QTL; quantitative trait locus;
KW disease-associated gene; development factor; quality factor;
KW resistance factor; wheat product; identification; detection;
KW genetically modified wheat; ds.
XX
OS Aegilops tauschii.
OS Triticum aestivum.
XX
PN EP1217079-A1.
XX
PD 26-JUN-2002.
XX
PF 22-DEC-2000; 2000EP-00403659.
XX
PR 22-DEC-2000; 2000EP-00403659.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Bernard M, Sourdille P, Guyomarch H;
XX
DR WPI; 2002-550410/59.
XX
PT Map of wheat D genome comprising the genome location of a microsatellite
PT marker, useful for e.g. identifying genes responsible for a desired
PT phenotypic trait, especially quantitative trait loci in wheat, and
PT diseases.
XX
PS Claim 1; Page 31; 105pp; English.
XX
CC The invention relates to a map of the bread wheat D genome comprising the
CC genome location of a microsatellite marker selected from a group of 185
CC such markers (ABQ92733-ABQ92917). The invention also encompasses the use
CC of left (ABQ92918-ABQ93102) and right (ABQ93103-ABQ93287) primers to
CC amplify and detect the microsatellite markers, and to identify genes
CC responsible for a phenotypic trait of interest in wheat. Wheat is an
CC allohexaploid species consisting of 3 diploid genomes designated A, B and
CC D, resulting from two successive intercrossings involving at least three
CC different species. The D genome is thought to have been introduced in the
CC most recent intercrossing, between the amphiploid AABB and Triticum
CC tauschii (DD), probably involving only a limited number of genotypes of
CC both species. Due to its polyploid genome, the large size of its genome,
CC and its low level of polymorphism, the genetic mapping of wheat has to
CC date been difficult. Microsatellites are tandemly repeated sequences
CC between one and six nucleotides long, and are very polymorphic in length,
CC mainly due to polymerase slippage during replication. This high degree of
CC polymorphism makes them especially suitable for the genetic mapping of
CC species which show little intraspecies polymorphism, such as wheat. In
CC addition, microsatellites are codominant, and exhibit Mendelian
CC inheritance. The 185 microsatellite markers of the invention are
CC developed from the ancestral diploid donor species Triticum tauschii and
CC map to the wheat D genome, which is less polymorphic than the A or B
CC genomes. These microsatellite markers thus help to overcome some of the
CC problems associated with the genetic mapping of wheat. The wheat D genome
CC map and the microsatellite markers and associated primers of the
CC invention are useful for identifying genes responsible for a phenotypic
CC trait of interest, most notably QTLs (quantitative trait loci). In
CC particular they may be used for analysing genes and alleles implicated in
CC disease and for identifying development factors, quality factors and
CC factors conferring resistance to pathogens and xenobiotics. The
CC microsatellite markers, and associated primers may be also be used in
CC mapping and genotyping diploid and polyploid species of Triticum,
CC particularly Aegilops, Triticum monococcum, Triticum durum, Triticum
CC aestivum, or related species; for identifying cultivars and hybrids of
CC Triticum and related species; to assess whether or not a product
CC comprises wheat or a related species; and to assess whether or not a
CC product comprises genetically modified wheat. The present sequence
CC represents a specifically claimed Triticum tauschii/wheat genome D
CC microsatellite marker of the invention. (Updated on 29-AUG-2003 to

```
CC   standardise OS field)
XX
SQ   Sequence 543 BP; 188 A; 161 C; 111 G; 83 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              103          Length:        543
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     6            Gaps:          0

US-10-758-902-1 (1-30) x ABQ92793 (1-543)

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||||||||||||
Db        488 TTGAGGAACGAACTTGCCAAA 468

RESULT 19
ACH38914/c
ID   ACH38914 standard; cDNA; 555 BP.
XX
AC   ACH38914;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human foetal brain cDNA #281.
XX
KW   Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW   genome mapping; biodiversity; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Claim 1; SEQ ID NO 26126; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 555 BP; 120 A; 161 C; 167 G; 100 T; 0 U; 7 Other;

Alignment Scores:
Pred. No.:              105          Length:        555
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     9            Gaps:          0

US-10-758-902-1 (1-30) x ACH38914 (1-555)

Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||
Db        184 AGTTTCAATCTGGGTGAGGCC 164

RESULT 20
ACL61717/c
ID   ACL61717 standard; cDNA; 562 BP.
XX
AC   ACL61717;
XX
DT   24-MAR-2005  (first entry)
XX
DE   Human colon cancer differentially expressed polynucleotide, SEQ ID:7852.
XX
KW   Differential expression; diagnosis; therapy; drug screening; cancer;
KW   neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO2005000087-A2.
XX
PD   06-JAN-2005.
XX
PF   13-MAY-2004; 2004WO-US015421.
XX
PR   03-JUN-2003; 2003US-0475872P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Randazzo F,  Moler E,  Escobedo J,  Garcia PD;
XX
DR   WPI; 2005-075421/08.
XX
PT   New isolated polynucleotides, which are differentially expressed in colon
PT   cancer cell, useful for treating cancer, e.g. colon cancer, breast
PT   cancer, or pancreatic cancer.
XX
PS   Claim 1; SEQ ID NO 7852; 97pp; English.
XX
CC   The invention relates to 9672 polynucleotides (ACL53866-ACL63537) which
CC   are differentially expressed in colon cancer cells. The invention also
CC   relates to vectors and host cells comprising a differentially expressed
CC   polynucleotide of the invention; a method for detecting a cancerous cell
CC   by detection of a gene product of the polynucleotides; a method for
CC   inhibiting a cancerous phenotype of a cell by inhibiting a gene product
CC   of the polynucleotides; a method of treating an individual with cancer by
CC   administration of a modulator of a gene product of the polynucleotides;
CC   and an isolated antibody that specifically binds to a polypeptide encoded
CC   by one of the 9672 polynucleotides. The polynucleotides, polypeptides,
CC   antibodies, and methods are useful for the detection of cancerous cells;
CC   for the diagnosis, prognosis and management of cancer; for the
CC   identification of agents that modulate the phenotype of cancerous cells;
CC   for the identification of therapeutic targets for cancer chemotherapy;
CC   and for the treatment of cancer, especially colon cancer and metastasized
CC   colon cancer, but also breast or pancreatic cancer. The polynucleotides
CC   are also useful as a source of probes or primers for use in diagnostic
CC   methods. The differentially expressed polynucleotides or their encoded
```

CC proteins can additionally be used as vaccines to modulate primary immune
CC responses for the prevention or treatment of cancer. The present sequence
CC represents a specifically claimed polynucleotide which is differentially
CC expressed in colon cancer. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 562 BP; 119 A; 168 C; 171 G; 104 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	106	Length:	562
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	14	Gaps:	0

US-10-758-902-1 (1-30) x ACL61717 (1-562)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||
Db        125 AGTTTCAATCTGGGTGAGGCC 105
```

RESULT 21
ABV55005
ID ABV55005 standard; cDNA; 588 BP.
XX
AC ABV55005;
XX
DT 17-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 54996.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 10627; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
XX
SQ Sequence 588 BP; 167 A; 143 C; 138 G; 140 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	111	Length:	588
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-1 (1-30) x ABV55005 (1-588)

```
Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        120 AATACAGTTTCCTTCAATTTA 140
```

RESULT 22
ABK77612
ID ABK77612 standard; DNA; 588 BP.
XX
AC ABK77612;
XX
DT 13-AUG-2002 (first entry)
XX
DE Bacillus clausii genomic sequence tag (GST) #455.
XX
KW Differential gene expression; genomic sequenced tag; GST;
KW altered culture condition; environmental stress;
KW physiological provocation; ds.
XX
OS Bacillus clausii.
XX
PN WO200229113-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031437.
XX
PR 06-OCT-2000; 2000US-00680598.
PR 27-MAR-2001; 2001US-0279526P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
XX
PI Berka R, Clausen IG;
XX
DR WPI; 2002-416684/44.
XX
PT Monitoring differential expression of several genes in first Bacillus
PT cell relative to expression of same genes in one or more second Bacillus
PT cells, by using substrate containing Bacillus genomic sequenced tag
PT array.
XX
PS Claim 11; SEQ ID NO 4903; 200pp; English.
XX
CC The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC isolated from Bacillus cells to a substrate containing array of Bacillus
CC genomic sequenced tags (GST), examining the array, and determining
CC relative gene expression by an observed hybridisation reporter signal of
CC a spot in the array. The method is useful for measuring the expression of
CC genes in a first Bacillus cell relative to expression of the same genes
CC in one or more second Bacillus cells. The method is useful for monitoring
CC global expression of several genes from a Bacillus cell, discovering new
CC genes, identifying possible functions of unknown open reading frames and
CC monitoring gene copy number variation and stability. Monitoring changes
CC in expression of genes may be used to provide a representation of the way
CC in which Bacillus cells adapt to changes in culture conditions,

CC environmental stress or other physiological provocation. Extensive follow
CC -up characterisation is unnecessary, when one spot on an array equals one
CC gene or one open reading frame, since sequence information is available.
CC This sequence represents a genomic sequence tag (GST) used in the method
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 588 BP; 173 A; 132 C; 159 G; 122 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	111	Length:	588
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x ABK77612 (1-588)

```
Qy          9 GlyGluAlaTyrGluTyrPro 15
              |||||||||||||||||||||
Db        470 GGAGAAGCATATGAGTATCCA 490
```

RESULT 23
ADH82120
ID ADH82120 standard; DNA; 651 BP.
XX
AC ADH82120;
XX
DT 22-APR-2004 (first entry)
XX
DE Enterococcus faecalis polynucleotide #5.
XX
KW Enterococcus faecalis infection; transcription regulatory element;
KW antibacterial; gene; ds.
XX
OS Enterococcus faecalis.
XX
PN US6617156-B1.
XX
PD 09-SEP-2003.
XX
PF 13-AUG-1998; 98US-00134000.
XX
PR 15-AUG-1997; 97US-0055778P.
XX
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2003-895394/82.
DR P-PSDB; ADH85525.
XX
PT New nucleic acid comprising a sequence encoding an Enterococcus fecalis
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating E. fecalis infection.
XX
PS Disclosure; SEQ ID NO 5; 193pp; English.
XX
CC The invention relates to Enterococcus faecalis polynucleotides and
CC polypeptides. The invention also relates to a recombinant expression
CC vector comprising a polynucleotide operably linked to a transcription
CC regulatory element, a cell comprising a recombinant vector, a method for
CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
CC a sequence not given in the specification, a recombinant vector
CC comprising the nucleic acid and a cell comprising the recombinant vector.
CC The polynucleotides can be used to detect the presence of E. faecalis in
CC a sample. The sequences are useful for preparing a composition for
CC diagnosing or treating Enterococcus faecalis infection. This sequence
CC represents an E. faecalis polynucleotide of the invention.
XX
SQ Sequence 651 BP; 212 A; 117 C; 157 G; 165 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	122	Length:	651
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-1 (1-30) x ADH82120 (1-651)

```
Qy         24 GluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||
Db        496 GAATTAGCAAAAGGTACGCCG 516
```

RESULT 24
ABK77619
ID ABK77619 standard; DNA; 693 BP.
XX
AC ABK77619;
XX
DT 13-AUG-2002 (first entry)
XX
DE Bacillus clausii genomic sequence tag (GST) #462.
XX
KW Differential gene expression; genomic sequenced tag; GST;
KW altered culture condition; environmental stress;
KW physiological provocation; ds.
XX
OS Bacillus clausii.
XX
PN WO200229113-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031437.
XX
PR 06-OCT-2000; 2000US-00680598.
PR 27-MAR-2001; 2001US-0279526P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
XX
PI Berka R, Clausen IG;
XX
DR WPI; 2002-416684/44.
XX
PT Monitoring differential expression of several genes in first Bacillus
PT cell relative to expression of same genes in one or more second Bacillus
PT cells, by using substrate containing Bacillus genomic sequenced tag
PT array.
XX
PS Claim 11; SEQ ID NO 4910; 200pp; English.
XX
CC The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC isolated from Bacillus cells to a substrate containing array of Bacillus
CC genomic sequenced tags (GST), examining the array, and determining
CC relative gene expression by an observed hybridisation reporter signal of
CC a spot in the array. The method is useful for measuring the expression of
CC genes in a first Bacillus cell relative to expression of the same genes
CC in one or more second Bacillus cells. The method is useful for monitoring
CC global expression of several genes from a Bacillus cell, discovering new
CC genes, identifying possible functions of unknown open reading frames and
CC monitoring gene copy number variation and stability. Monitoring changes
CC in expression of genes may be used to provide a representation of the way
CC in which Bacillus cells adapt to changes in culture conditions,
CC environmental stress or other physiological provocation. Extensive follow
CC -up characterisation is unnecessary, when one spot on an array equals one
CC gene or one open reading frame, since sequence information is available.
CC This sequence represents a genomic sequence tag (GST) used in the method

```
CC   of the invention. Note: The sequence data for this patent did not form
CC   part of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 693 BP; 205 A; 152 C; 185 G; 149 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:              129           Length:        693
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-1 (1-30) x ABK77619 (1-693)

Qy          9 GlyGluAlaTyrGluTyrPro 15
              |||||||||||||||||||||
Db        573 GGAGAAGCATATGAGTATCCA 593

RESULT 25
AAA27409
ID   AAA27409 standard; cDNA; 731 BP.
XX
AC   AAA27409;
XX
DT   10-AUG-2000  (first entry)
XX
DE   Soybean glutamyl-tRNA synthetase partial coding sequence # 1.
XX
KW   Soybean glutamyl-tRNA synthetase; aminoacyl-tRNA synthetase; AARS;
KW   herbicide; plant toxin; protein synthesis inhibition; enzyme; ss.
XX
OS   Glycine max.
XX
FH   Key             Location/Qualifiers
FT   CDS             159. .733
FT                   /*tag=  a
FT                   /partial
FT                   /product= "soybean glutamyl-tRNA synthetase # 1"
FT                   /note= "Partial soybean glutamyl-tRNA synthetase
FT                   sequence: encodes first 191 amino-acids of AAY94278"
XX
PN   WO200028057-A2.
XX
PD   18-MAY-2000.
XX
PF   09-NOV-1999;   99WO-US026478.
XX
PR   10-NOV-1998;   98US-0107789P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Famodu OO,  Simmons C;
XX
DR   WPI; 2000-387421/33.
DR   P-PSDB; AAY94278.
XX
PT   New polynucleotide encoding plant aminoacyl-tRNA synthase and the encoded
PT   polypeptide, useful e.g. for regulating gene expression.
XX
PS   Claim 12; Page 53; 74pp; English.
XX
CC   The present sequence is a partial coding sequence for soybean glutamyl-
CC   tRNA synthetase. Glutamyl-tRNA synthetase is an aminoacyl-tRNA synthetase
CC   (AARS). AARSs charge (acylate) specific tRNAs with amino acids for use in
CC   protein synthesis. Glutamyl-tRNA synthetase therefore charges a glutamyl-
CC   tRNA with glutamate. Since this enzyme has a crucial role in protein
CC   synthesis and therefore life, any agent that inhibits or disrupts protein
CC   synthesis is likely to be toxic. The present sequence could therefore be
CC   used as a basis for testing whether the encoded aminoacyl-tRNA synthetase
CC   is sensitive to known inhibitors or other chemicals and hence could be
CC   used in the discovery of potential herbicides
XX
SQ   Sequence 731 BP; 197 A; 168 C; 181 G; 185 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              135           Length:        731
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x AAA27409 (1-731)

Qy         24 GluLeuAlaLysGlyThrPro 30
              |||||||||||||||||||||
Db        582 GAGCTAGCAAAAGGAACTCCT 602

RESULT 26
ABZ83251/c
ID   ABZ83251 standard; cDNA; 1024 BP.
XX
AC   ABZ83251;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Toxicologically relevant human nucleotide sequence #410.
XX
KW   Toxicologically relevant gene; toxicological response; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003016500-A2.
XX
PD   27-FEB-2003.
XX
PF   16-AUG-2002; 2002WO-US026514.
XX
PR   16-AUG-2001; 2001US-0313080P.
XX
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI   Neft RE,  Dunn RT,  Adkins K,  Pickett GG,  Kier LD,  Schmeiser K;
PI   Alen P;
XX
DR   WPI; 2003-268322/26.
XX
PT   Determining a toxicological response to an agent, useful for screening of
PT   drugs, comprises comparing the expression profile of one or more human
PT   toxic response genes to a reference gene expression profile indicative of
PT   toxicity.
XX
PS   Claim 1; Page 147; 455pp; English.
XX
CC   The present invention describes a method (M1) for determining a
CC   toxicological response to an agent, which comprises comparing the
CC   expression profile of one or more human toxic response genes to a
CC   reference gene expression profile indicative of toxicity, and so
CC   determining the presence of a toxic response to the agent. Also
CC   described: (1) an array comprising one or more polynucleotides selected
CC   from the genes corresponding to the partial sequences given in ABZ82842
CC   to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC   ; and (2) determining if a gene putatively identified to be a toxic
CC   response gene plays a role on toxic response pathways by determining the
CC   expression profile of the gene after exposure of cells or a human subject
CC   to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC   exposing cells to an agent or isolating cells from a human subject who
CC   was exposed to an agent; (b) obtaining the test gene expression profile
CC   for a putatively identified toxic response gene after exposure to a known
CC   toxic pharmaceutical or industrial agent; and (c) comparing the test
CC   profile to the expression profile of a gene with a similar function or
CC   comparing the test profile to the expression profile of that gene after
CC   exposure to other known toxic compounds. The methods are useful for
```

CC predicting and determining toxicological responses on a cellular, organ
CC or system level. The arrays comprising the human genes are useful for
CC toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ Sequence 1024 BP; 206 A; 362 C; 308 G; 148 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	184	Length:	1024
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-1 (1-30) x ABZ83251 (1-1024)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db        829 AGTTTCAATCTGGGTGAGGCC 809
```

RESULT 27
AAQ86989/c
ID AAQ86989 standard; cDNA; 1146 BP.
XX
AC AAQ86989;
XX
DT 25-MAR-2003 (revised)
DT 08-NOV-1995 (first entry)
XX
DE Creatine-kinase subunit B cDNA.
XX
KW Creatine-kinase; subunit B; dimeric enzyme; vector; prokaryote host;
KW Escherichia coli; myocardial infarction; reperfusion; diagnostic; ss.
XX
OS Homo sapiens.
XX
PN WO9512662-A1.
XX
PD 11-MAY-1995.
XX
PF 02-NOV-1994; 94WO-US012624.
XX
PR 02-NOV-1993; 93US-00146655.
XX
PA (GENZ) GENZYME CORP.
XX
PI Ziegler RJ, Long S;
XX
DR WPI; 1995-185770/24.
DR P-PSDB; AAR72986.
XX
PT Prodn. of eukaryotic hetero:dimeric enzyme - in an active form using a
PT prokaryotic host.
XX
PS Disclosure; Page 9-10; 22pp; English.
XX
CC Creatine-kinase (CK) is produced by constructing 2 vectors separately
CC contg. DNA encoding the CK subunit B (AAR72986) and subunit M (AAR72987),
CC transforming a prokaryotic host, pref. E. coli, with both vectors, and
CC culturing transformants under conditions appropriate for expression of
CC the dimeric enzyme. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1146 BP; 235 A; 377 C; 357 G; 177 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	204	Length:	1146
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-1 (1-30) x AAQ86989 (1-1146)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db        786 AGTTTCAATCTGGGTGAGGCC 766
```

RESULT 28
ACA49107/c
ID ACA49107 standard; DNA; 1167 BP.
XX
AC ACA49107;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #30764.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Salmonella paratyphi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU45237.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 36977; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target

```
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1167 BP; 234 A; 318 C; 309 G; 305 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              207          Length:        1167
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     8            Gaps:          0

US-10-758-902-1 (1-30) x ACA49107 (1-1167)

Qy         22 ArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||
Db       1035 CGGAACGAACTCGCCAAAGGG 1015

RESULT 29
ACN39756/c
ID   ACN39756 standard; cDNA; 1355 BP.
XX
AC   ACN39756;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Tumour-associated antigenic target (TAT) cDNA DNA325945, SEQ ID NO:4100.
XX
KW   Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW   tumour; diagnosis; cell proliferative disorder; breast cancer;
KW   colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW   central nervous system cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; melanoma; leukaemia; hybridisation probe;
KW   chromosome identification; chromosome mapping; gene mapping;
KW   gene therapy; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004030615-A2.
XX
PD   15-APR-2004.
XX
PF   29-SEP-2003; 2003WO-US028547.
XX
PR   02-OCT-2002; 2002US-0414971P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wu TD,  Zhang Z,  Zhou Y;
XX
DR   WPI; 2004-347921/32.
XX
PT   New tumor-associated antigenic target polypeptides and nucleic acids,
PT   useful in preparing a medicament for treating or detecting a
PT   proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT   prostate cancer or tumor.
XX
PS   Claim 1; SEQ ID NO 4100; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods and compositions for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT nucleic acid of the invention
XX
SQ   Sequence 1355 BP; 269 A; 446 C; 409 G; 231 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              238          Length:        1355
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     13           Gaps:          0

US-10-758-902-1 (1-30) x ACN39756 (1-1355)

Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||
Db        799 AGTTTCAATCTGGGTGAGGCC 779

RESULT 30
ABL62370/c
ID   ABL62370 standard; DNA; 1360 BP.
XX
AC   ABL62370;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Colon adenocarcinoma related gene sequence SEQ ID NO:707.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   25-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235637P.
PR   26-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
```

PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 707; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 1360 BP; 277 A; 442 C; 410 G; 231 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	238	Length:	1360
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x ABL62370 (1-1360)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db        794 AGTTTCAATCTGGGTGAGGCC 774
```

RESULT 31
ABN95771/c
ID ABN95771 standard; DNA; 1360 BP.
XX
AC ABN95771;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #2269 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030589.
XX
PR 02-OCT-2000; 2000US-0237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR WPI; 2002-426119/45.
XX
PT Diagnosing and detecting the progression of liver cancer, hepatocellular
PT carcinoma or metastatic liver tumor in a patient, involves detecting the
PT level of expression of two or more genes in a liver tissue sample.
XX
PS Claim 1; SEQ ID NO 2269; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1360 BP; 277 A; 442 C; 410 G; 231 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	238	Length:	1360
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x ABN95771 (1-1360)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db        794 AGTTTCAATCTGGGTGAGGCC 774
```

RESULT 32
AAQ51619/c
ID AAQ51619 standard; DNA; 1376 BP.
XX
AC AAQ51619;
XX
DT 25-MAR-2003 (revised)
DT 26-MAY-1994 (first entry)
XX
DE Human creatine kinase subunit B.
XX
KW Creatine kinase; isoform; mutant; subunit B; subunit M; lys-M; lys-B;

KW myocardial infarction; MI; electrophoresis; lysine; ss.
XX
OS Homo sapiens.
XX
PN EP571085-A1.
XX
PD 24-NOV-1993.
XX
PF 21-APR-1993; 93EP-00303115.
XX
PR 21-APR-1992; 92US-00871469.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Perryman M, Kesterson R, Friedman DL, Roberts R;
XX
DR WPI; 1993-370481/47.
XX
PT Mutant isoforms of creatinine kinase, e.g. lys-M or lys-B - used as
PT standards in non-denaturing electrophoresis to assess damage from
PT myocardial infarction.
XX
PS Claim 4; Fig 4; 22pp; English.
XX
CC Nucleotide sequences of human creatine kinase M or B subunits are given
CC in AAQ51619-20. The mutant CK M or B subunits of the invention are stable
CC to proteolytic cleavage of C-terminal lysine. The mutant lys-M CK subunit
CC differs from wild-type human M CK subunit by a single base substitution
CC at position 1219. The lysine codon, AAG, has been converted to TAG
CC (position 1219-1221) which acts as a stop codon. Expressed mutant M CK
CC protein differs from wild-type M CK subunit due to the lack of a carboxy
CC terminal lysine gp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1376 BP; 282 A; 452 C; 410 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	241	Length:	1376
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-1 (1-30) x AAQ51619 (1-1376)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||||
Db        809 AGTTTCAATCTGGGTGAGGCC 789
```

RESULT 33
ABQ54381
ID ABQ54381 standard; cDNA; 1390 BP.
XX
AC ABQ54381;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HOPJG01 cDNA, SEQ ID NO:261.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; chromosome 14q32; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US018569.
XX
PR 07-JUN-2000; 2000US-0209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR P-PSDB; ABP41304.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.
XX
PS Claim 1; SEQ ID NO 261; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents cDNA encoding a human ovarian antigen of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1390 BP; 228 A; 414 C; 440 G; 302 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.:	243	Length:	1390
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x ABQ54381 (1-1390)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||||
Db        614 AGTTTCAATCTGGGTGAGGCC 634
```

RESULT 34
ADZ48855/c
ID ADZ48855 standard; DNA; 1431 BP.
XX
AC ADZ48855;

XX
DT 30-JUN-2005 (first entry)
XX
DE Insulin signaling pathway related gene, SEQ ID 184.
XX
KW Antidiabetic; Gene Therapy; Non-insulin dependent diabetes;
KW insulin resistance; gene; ds.
XX
OS Homo sapiens.
XX
PN US2005085436-A1.
XX
PD 21-APR-2005.
XX
PF 08-JUL-2004; 2004US-00887553.
XX
PR 08-JUL-2003; 2003US-0485883P.
XX
PA (LIHH/) LI H.
PA (MAJJ/) MA J.
XX
PI Li H, Ma J;
XX
DR WPI; 2005-305194/31.
XX
PT Treating, preventing or ameliorating pathological conditions associated
PT with dysregulation of the insulin signaling pathway (ISP) comprises
PT administering to a subject an amount of a modulator of any of the
PT proteins regulated by ISP.
XX
PS Disclosure; SEQ ID NO 184; 70pp; English.
XX
CC The present invention relates to a method for treating, preventing or
CC ameliorating pathological conditions associated with dysregulation of the
CC insulin signaling pathway (ISP). The method comprises administering to a
CC subject a modulator for ISP-regulated proteins or a pharmaceutical
CC composition comprising the described modulator. The method is useful for
CC treating, preventing or ameliorating pathological conditions associated
CC with dysregulation of the ISP such as Type II diabetes or Type A syndrome
CC of insulin resistance. The present sequence is a human homolog of a
CC Drosophila gene regulated by ISP. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20050085436.
XX
SQ Sequence 1431 BP; 273 A; 482 C; 435 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	250	Length:	1431
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	14	Gaps:	0

US-10-758-902-1 (1-30) x ADZ48855 (1-1431)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db        866 AGTTTCAATCTGGGTGAGGCC 846
```

RESULT 35
AEA81138/c
ID AEA81138 standard; DNA; 1431 BP.
XX
AC AEA81138;
XX
DT 25-AUG-2005 (first entry)
XX
DE Human creatine kinase, brain (CKB) DNA.
XX
KW screening; obesity; nutritional disorder; anorectic; ds; gene;
KW creatine kinase; CKB.
XX
OS Homo sapiens.
XX
PN US2005136465-A1.
XX
PD 23-JUN-2005.
XX
PF 22-DEC-2004; 2004US-00019829.
XX
PR 22-DEC-2003; 2003EP-00104902.
XX
PA (CLER/) CLERC R G.
PA (DUCH/) DUCHATEAU-NGUYEN G.
PA (GARD/) GARDES C.
PA (MIZR/) MIZRAHI J.
PA (OSTE/) OSTENSON C.
XX
PI Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;
XX
DR WPI; 2005-457507/46.
DR P-PSDB; AEA81150.
XX
PT Screening test compounds that reduce and/or prevent obesity involves
PT contacting cell expressing gene from alpha-two-glycoprotein.
XX
PS Claim 1; SEQ ID NO 5; 21pp; English.
XX
CC The invention relates to a novel method for screening for test compounds
CC that reduce and/or prevent obesity. The method comprises contacting a
CC cell expressing a gene selected from SEQ ID NO. 1-12 or 25-85, with a
CC compound. The method of the invention demonstrates anorectic applications
CC and may be useful for screening for compounds that reduce and/or prevent
CC obesity. The current sequence is that of the human creatine kinase, brain
CC (CKB) DNA of the invention. The sequence listing for the specification
CC can be located via the USPTO web-site.
XX
SQ Sequence 1431 BP; 273 A; 482 C; 435 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	250	Length:	1431
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	14	Gaps:	0

US-10-758-902-1 (1-30) x AEA81138 (1-1431)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db        866 AGTTTCAATCTGGGTGAGGCC 846
```

RESULT 36
ADP10454/c
ID ADP10454 standard; DNA; 1432 BP.
XX
AC ADP10454;
XX
DT 12-AUG-2004 (first entry)
XX
DE Reference mRNA sequences for marker probe #131.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX

PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 80; SEQ ID NO 463; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
CC and monitoring of allograft rejection and other disorders.
XX
SQ Sequence 1432 BP; 273 A; 482 C; 436 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	250	Length:	1432
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-1 (1-30) x ADP10454 (1-1432)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||
Db        867 AGTTTCAATCTGGGTGAGGCC 847
```

RESULT 37
ADR14270/c
ID ADR14270 standard; DNA; 1432 BP.
XX
AC ADR14270;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human NF-kappaB pathway-associated gene SeqID271.
XX
KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnerary; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; gene; ds; human.
XX
OS Homo sapiens.
XX
PN WO2004065577-A2.
XX
PD 05-AUG-2004.
XX
PF 13-JAN-2004; 2004WO-US000798.
XX
PR 14-JAN-2003; 2003US-0440068P.
PR 12-MAY-2003; 2003US-0469757P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Nadler SG, Neubauer MG, Feder JN, Carman J;
XX
DR WPI; 2004-562168/54.
DR P-PSDB; ADR14271.
XX
PT New isolated polynucleotides and polypeptides associated with NF-kappaB
PT pathway, useful for diagnosing, treating, or preventing disorders or
PT diseases associated with NF-kappaB pathway.
XX
PS Claim 1; SEQ ID NO 271; 237pp; English.
XX
CC This invention relates to the novel association of protein sequences (and
CC the genes which encode them) to the NF-kappaB pathway. The invention may
CC be useful for the production of compounds with an antiinflammatory,
CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
CC vulnerary activity or for gene therapy. The proteins and nucleotides are
CC useful for diagnosing, preventing, treating, or ameliorating conditions
CC or diseases associated with the NF-kappaB pathway. The condition is an
CC immune disorder, an inflammatory disorder, an inflammatory disorder
CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
CC immune activity, disorders related to aberrant acute phase responses,
CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
CC organ transplant rejection, conditions related to organ transplant
CC rejection, disorders related to aberrant signal transduction,
CC proliferating disorders, cancers and HIV propagation in cells infected
CC with other viruses. The present sequence is that of a human gene which is
CC subject to the novel association with the NF-kappaB pathway of the
CC invention. Note: This sequence does not appear in the specification but
CC was obtained by the indexer from Genbank.
XX
SQ Sequence 1432 BP; 273 A; 482 C; 436 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	250	Length:	1432
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-1 (1-30) x ADR14270 (1-1432)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||
Db        867 AGTTTCAATCTGGGTGAGGCC 847
```

RESULT 38
ADX07813/c

ID ADX07813 standard; DNA; 1432 BP.
XX
AC ADX07813;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 2378.
XX
KW cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2005012875-A2.
XX
PD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR WPI; 2005-163068/17.
DR P-PSDB; ADX07814.
XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 2378; 141pp; English.
XX
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[[5-(1,1-Dimethylethyl)-2-
CC oxazolyl]methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
CC sequence encodes a biomarker used in the method of the invention.
XX
SQ Sequence 1432 BP; 273 A; 482 C; 436 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	250	Length:	1432
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	14	Gaps:	0

US-10-758-902-1 (1-30) x ADX07813 (1-1432)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||
Db        867 AGTTTCAATCTGGGTGAGGCC 847
```

RESULT 39
ADZ22658/c
ID ADZ22658 standard; DNA; 1432 BP.
XX
AC ADZ22658;
XX
DT 16-JUN-2005 (first entry)
XX
DE Creatine kinase brain (CKB) DNA.
XX
KW prognosis; nervous system tumor; cytostatic; neoplasm;
KW neurological disease; gene; ds; Creatine kinase brain; CKB.
XX
OS Homo sapiens.
XX
PN WO2005030992-A2.
XX
PD 07-APR-2005.
XX
PF 01-OCT-2004; 2004WO-FR050475.
XX
PR 01-OCT-2003; 2003FR-00011483.
XX
PA (INMR) BIOMERIEUX SA.
PA (BERA-) CENT BERARD LEON.
XX
PI Combaret V, Krause A, Puisieux A, Lacroix B;
XX
DR WPI; 2005-273392/28.
XX
PT Prognosis of neuroblastoma, based on measuring expression of one or more
PT specific target genes, for example insulin-like growth factor binding
PT protein-7, that are differentially expressed between patients with good
PT and poor prognosis.
XX
PS Claim 1; SEQ ID NO 33; 104pp; French.
XX
CC The invention describes a method for prognosis of neuroblastoma
CC comprising: extracting a biological material from a patient sample;
CC contacting the material with at least one reagent (R) specific for any of
CC 37 target genes (TG) of, e.g. 2667, 762 and 580 base pairs in length (SEQ
CC ID NOs: 1-37) fully defined in the specification, provided that when the
CC gene is any of SEQ ID NOs: 11, 17 or 37, then at least two (R), specific
CC for different TG are used; and determining expression of at least one TG
CC (or at least two for SEQ ID NOs: 11, 17 and 37). The method provides a
CC very reliable differentiation between patients with good or poor
CC prognoses. This sequence represents a neoblastoma prognosis method target
CC gene.
XX
SQ Sequence 1432 BP; 273 A; 482 C; 436 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	250	Length:	1432
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	14	Gaps:	0

US-10-758-902-1 (1-30) x ADZ22658 (1-1432)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||
Db        867 AGTTTCAATCTGGGTGAGGCC 847
```

RESULT 40
AEA04437/c
ID AEA04437 standard; cDNA; 1432 BP.
XX
AC AEA04437;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human cDNA from gene under-expressed in cancer, CKB.
XX
KW Tumor marker; ss; gene; colon tumor; cancer; cytostatic; neoplasm;
KW diagnostic; microarray; drug screening.

XX
OS Homo sapiens.
XX
PN WO2005044990-A2.
XX
PD 19-MAY-2005.
XX
PF 01-NOV-2004; 2004WO-US036404.
XX
PR 04-NOV-2003; 2003US-00700439.
XX
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Burgess C, Myerow S, Thiagalingam A, Maimonis P, Molino G;
PI Burgart L, Boardman LA, Thibodeau S, Lewis M;
XX
DR WPI; 2005-372198/38.
DR P-PSDB; AEA04530.
DR REFSEQ; NM_001823.
XX
PT Detecting expression of one or more nucleic acid sequences in biological
PT sample, useful for detecting cancer, comprises detecting a change in the
PT expression level of one or more nucleic acid sequences relative to a
PT control expression level.
XX
PS Claim 1; SEQ ID NO 82; 256pp; English.
XX
CC The invention relates to detecting differential expression of one or more
CC nucleic acid sequences (appearing as AEA04356-AEA04448 in a biological
CC sample comprising obtaining the sample from a subject, and detecting a
CC change in the expression level of one or more nucleic acid sequences
CC relative to a control expression level of the nucleic acid sequences, is
CC new. Also included are detecting cancer (or a pre-malignant condition
CC thereof) in a subject (comprising comparing the expression level of one
CC or more nucleic acid sequences in a biological sample from the subject
CC with a control expression level of the nucleic acid sequences, where a
CC change of at least two-fold in the expression level of the nucleic acid
CC sequences is indicative of cancer or pre-malignant condition), monitoring
CC the onset (or progression, or regression) of cancer (or a pre-malignant
CC condition) in a subject (by detecting in a biological sample of the
CC subject at a first point in time the expression of one or more nucleic
CC acid sequences, repeating the first step at a subsequent point in time
CC and comparing the expression level detected, where a change in the
CC expression level is indicative of progression of cancer or its pre-
CC malignant condition in the subject), determining prognosis for cancer or
CC its pre-malignant condition in a subject (comprising detecting in a
CC biological sample of the subject, the expression level of one or more
CC nucleic acid sequences, comparing the expression level with a reference
CC expression level of the nucleic acid sequences and evaluating the
CC prognosis of the subject based on the comparison), determining the
CC efficacy of a test compound for inhibiting cancer in a subject,
CC determining the efficacy of a therapy for inhibiting cancer in a subject,
CC selecting a composition for inhibiting cancer in a subject, inhibiting
CC cancer in a subject, a polypeptide encoded by the nucleic acids above
CC (appearing as AEA04449-AEA04541), an antibody that specifically binds to
CC the polypeptide sequence, and detecting in a biological sample the
CC presence of a polypeptide. The method is useful for detecting
CC differential expression of one or more nucleic acid sequences in a
CC biological sample, which is useful for detecting cancer (especially colon
CC cancer), monitoring the onset, progression, or regression of cancer or a
CC pre-malignant condition, or determining prognosis for cancer or its pre-
CC malignant condition in a subject, or for determining the efficacy of a
CC test compound for inhibiting cancer in a subject. The compound is useful
CC for inhibiting cancer in a subject. The antibodies may also be used to
CC treat cancer. The present sequence is a cDNA from a human gene under-
CC expressed in cancer samples.
XX
SQ Sequence 1432 BP; 273 A; 482 C; 436 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	250	Length:	1432
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	14	Gaps:	0

US-10-758-902-1 (1-30) x AEA04437 (1-1432)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||
Db        867 AGTTTCAATCTGGGTGAGGCC 847
```

Search completed: February 20, 2006, 01:09:35
Job time : 167.693 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 01:03:22 ; Search time 45.5866 Seconds
(without alignments)
1169.792 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 30
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2599867

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160837_4110/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10758902_@CGN_1_1_237_@runat_17022006_160837_4110 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	70.0	65	3	US-09-445-160B-5	Sequence 5, Appli
	2	14	46.7	363	3	US-09-445-160B-8	Sequence 8, Appli
	3	7	23.3	23	3	US-09-445-160B-3	Sequence 3, Appli
c	4	7	23.3	23	3	US-09-445-160B-4	Sequence 4, Appli
	5	7	23.3	25	3	US-09-445-160B-6	Sequence 6, Appli
	6	7	23.3	439	3	US-09-060-756-98	Sequence 98, Appl
	7	7	23.3	439	3	US-09-670-314-98	Sequence 98, Appl
c	8	7	23.3	601	3	US-09-949-016-124164	Sequence 124164,
c	9	7	23.3	601	3	US-09-949-016-124165	Sequence 124165,
	10	7	23.3	601	3	US-09-949-016-146880	Sequence 146880,
	11	7	23.3	601	3	US-09-949-016-148868	Sequence 148868,
	12	7	23.3	651	3	US-09-134-000C-5	Sequence 5, Appli
	13	7	23.3	731	3	US-09-831-683B-13	Sequence 13, Appl
c	14	7	23.3	1414	3	US-09-949-016-2364	Sequence 2364, Ap
c	15	7	23.3	2343	2	US-09-018-760-3	Sequence 3, Appli
	16	7	23.3	2556	3	US-08-811-682-18	Sequence 18, Appl
c	17	7	23.3	3016	3	US-09-023-655-259	Sequence 259, App
	18	7	23.3	3225	2	US-08-482-090-14	Sequence 14, Appl
	19	7	23.3	3225	2	US-08-481-700B-7	Sequence 7, Appli
	20	7	23.3	3225	2	US-09-007-383-14	Sequence 14, Appl
	21	7	23.3	9471	3	US-08-811-682-1	Sequence 1, Appli
c	22	7	23.3	10713	3	US-09-949-016-15928	Sequence 15928, A
c	23	7	23.3	10968	2	US-08-680-327-2	Sequence 2, Appli
c	24	7	23.3	10968	3	US-09-228-246-1	Sequence 1, Appli
	25	7	23.3	37059	3	US-09-949-016-15865	Sequence 15865, A
	26	7	23.3	68529	3	US-09-949-016-12140	Sequence 12140, A
	27	7	23.3	68529	3	US-09-949-016-15671	Sequence 15671, A
c	28	7	23.3	93894	3	US-09-949-016-13629	Sequence 13629, A
c	29	7	23.3	110243	3	US-09-949-016-13698	Sequence 13698, A
	30	7	23.3	113538	3	US-09-949-016-16329	Sequence 16329, A
	31	7	23.3	143644	3	US-09-949-016-15238	Sequence 15238, A
c	32	7	23.3	145241	3	US-09-949-016-17394	Sequence 17394, A
c	33	7	23.3	145241	3	US-09-949-016-17395	Sequence 17395, A
	34	7	23.3	187848	3	US-09-949-016-12111	Sequence 12111, A
	35	6	20.0	50	3	US-10-131-827-7466	Sequence 7466, Ap
	36	6	20.0	70	3	US-09-121-286-4	Sequence 4, Appli
	37	6	20.0	70	3	US-09-121-286-19	Sequence 19, Appl
	38	6	20.0	93	3	US-09-513-999C-18774	Sequence 18774, A
c	39	6	20.0	105	2	US-08-611-757-84	Sequence 84, Appl
c	40	6	20.0	105	6	PCT-US95-05980-84	Sequence 84, Appl
c	41	6	20.0	114	3	US-09-641-931F-43	Sequence 43, Appl
	42	6	20.0	139	3	US-09-513-999C-27754	Sequence 27754, A
	43	6	20.0	147	3	US-09-513-999C-13216	Sequence 13216, A
	44	6	20.0	196	3	US-09-270-767-27150	Sequence 27150, A
c	45	6	20.0	219	3	US-09-248-796A-12324	Sequence 12324, A
c	46	6	20.0	226	3	US-09-270-767-25231	Sequence 25231, A
c	47	6	20.0	258	3	US-09-513-999C-26204	Sequence 26204, A
	48	6	20.0	285	3	US-09-248-796A-3910	Sequence 3910, Ap
	49	6	20.0	308	3	US-09-513-999C-21934	Sequence 21934, A
c	50	6	20.0	309	3	US-09-270-767-7193	Sequence 7193, Ap
c	51	6	20.0	309	3	US-09-270-767-22475	Sequence 22475, A
	52	6	20.0	332	3	US-09-188-930-83	Sequence 83, Appl
	53	6	20.0	332	3	US-09-312-283C-83	Sequence 83, Appl
c	54	6	20.0	457	3	US-09-270-767-9928	Sequence 9928, Ap
c	55	6	20.0	460	3	US-09-621-976-13826	Sequence 13826, A
	56	6	20.0	481	3	US-09-949-016-52690	Sequence 52690, A
c	57	6	20.0	483	3	US-09-821-687-1	Sequence 1, Appli
	58	6	20.0	492	3	US-09-134-000C-1371	Sequence 1371, Ap
c	59	6	20.0	500	3	US-09-621-976-3868	Sequence 3868, Ap
	60	6	20.0	514	2	US-08-705-625-1	Sequence 1, Appli
	61	6	20.0	514	3	US-09-220-574-1	Sequence 1, Appli
c	62	6	20.0	546	3	US-09-437-054A-13	Sequence 13, Appl
c	63	6	20.0	552	3	US-09-307-973A-5	Sequence 5, Appli
c	64	6	20.0	555	3	US-09-134-000C-3370	Sequence 3370, Ap
c	65	6	20.0	564	3	US-09-252-991A-5360	Sequence 5360, Ap
	66	6	20.0	567	3	US-09-949-016-52691	Sequence 52691, A
	67	6	20.0	578	3	US-09-533-559-1570	Sequence 1570, Ap
	68	6	20.0	601	3	US-09-949-016-24378	Sequence 24378, A
c	69	6	20.0	601	3	US-09-949-016-24400	Sequence 24400, A
c	70	6	20.0	601	3	US-09-949-016-24401	Sequence 24401, A
c	71	6	20.0	601	3	US-09-949-016-24402	Sequence 24402, A
c	72	6	20.0	601	3	US-09-949-016-24403	Sequence 24403, A
c	73	6	20.0	601	3	US-09-949-016-28322	Sequence 28322, A
c	74	6	20.0	601	3	US-09-949-016-28371	Sequence 28371, A
	75	6	20.0	601	3	US-09-949-016-30794	Sequence 30794, A
c	76	6	20.0	601	3	US-09-949-016-31770	Sequence 31770, A
	77	6	20.0	601	3	US-09-949-016-44718	Sequence 44718, A
	78	6	20.0	601	3	US-09-949-016-58571	Sequence 58571, A
	79	6	20.0	601	3	US-09-949-016-69509	Sequence 69509, A
c	80	6	20.0	601	3	US-09-949-016-70587	Sequence 70587, A
	81	6	20.0	601	3	US-09-949-016-70665	Sequence 70665, A
	82	6	20.0	601	3	US-09-949-016-70666	Sequence 70666, A

83	6	20.0	601	3	US-09-949-016-70667	Sequence 70667, A
84	6	20.0	601	3	US-09-949-016-70668	Sequence 70668, A
85	6	20.0	601	3	US-09-949-016-72655	Sequence 72655, A
86	6	20.0	601	3	US-09-949-016-74697	Sequence 74697, A
87	6	20.0	601	3	US-09-949-016-74896	Sequence 74896, A
88	6	20.0	601	3	US-09-949-016-75095	Sequence 75095, A
89	6	20.0	601	3	US-09-949-016-75294	Sequence 75294, A
90	6	20.0	601	3	US-09-949-016-75493	Sequence 75493, A
91	6	20.0	601	3	US-09-949-016-82616	Sequence 82616, A
92	6	20.0	601	3	US-09-949-016-83868	Sequence 83868, A
c 93	6	20.0	601	3	US-09-949-016-84109	Sequence 84109, A
94	6	20.0	601	3	US-09-949-016-84393	Sequence 84393, A
95	6	20.0	601	3	US-09-949-016-89715	Sequence 89715, A
96	6	20.0	601	3	US-09-949-016-106051	Sequence 106051,
97	6	20.0	601	3	US-09-949-016-106250	Sequence 106250,
98	6	20.0	601	3	US-09-949-016-106449	Sequence 106449,
99	6	20.0	601	3	US-09-949-016-106648	Sequence 106648,
100	6	20.0	601	3	US-09-949-016-106847	Sequence 106847,
101	6	20.0	601	3	US-09-949-016-135512	Sequence 135512,
102	6	20.0	601	3	US-09-949-016-135532	Sequence 135532,
103	6	20.0	601	3	US-09-949-016-136375	Sequence 136375,
104	6	20.0	601	3	US-09-949-016-142952	Sequence 142952,
c 105	6	20.0	601	3	US-09-949-016-149287	Sequence 149287,
c 106	6	20.0	601	3	US-09-949-016-151148	Sequence 151148,
c 107	6	20.0	601	3	US-09-949-016-153495	Sequence 153495,
108	6	20.0	601	3	US-09-949-016-157402	Sequence 157402,
109	6	20.0	601	3	US-09-949-016-157509	Sequence 157509,
110	6	20.0	601	3	US-09-949-016-165523	Sequence 165523,
c 111	6	20.0	601	3	US-09-949-016-170477	Sequence 170477,
112	6	20.0	601	3	US-09-949-016-180151	Sequence 180151,
113	6	20.0	601	3	US-09-949-016-180152	Sequence 180152,
c 114	6	20.0	601	3	US-09-949-016-183080	Sequence 183080,
115	6	20.0	601	3	US-09-949-016-187004	Sequence 187004,
c 116	6	20.0	601	3	US-09-949-016-187901	Sequence 187901,
117	6	20.0	601	3	US-09-949-016-190898	Sequence 190898,
118	6	20.0	601	3	US-09-949-016-190899	Sequence 190899,
119	6	20.0	601	3	US-09-949-016-190900	Sequence 190900,
120	6	20.0	601	3	US-09-949-016-190901	Sequence 190901,
121	6	20.0	601	3	US-09-949-016-190991	Sequence 190991,
122	6	20.0	601	3	US-09-949-016-190992	Sequence 190992,
123	6	20.0	601	3	US-09-949-016-190993	Sequence 190993,
124	6	20.0	601	3	US-09-949-016-190994	Sequence 190994,
c 125	6	20.0	601	3	US-09-949-016-193894	Sequence 193894,
c 126	6	20.0	601	3	US-09-949-016-194400	Sequence 194400,
127	6	20.0	601	3	US-09-949-016-199549	Sequence 199549,
c 128	6	20.0	601	3	US-09-949-016-199571	Sequence 199571,
c 129	6	20.0	601	3	US-09-949-016-199572	Sequence 199572,
c 130	6	20.0	601	3	US-09-949-016-199573	Sequence 199573,
c 131	6	20.0	601	3	US-09-949-016-199574	Sequence 199574,
c 132	6	20.0	601	3	US-09-949-016-202381	Sequence 202381,
133	6	20.0	601	3	US-09-949-002-4575	Sequence 4575, Ap
134	6	20.0	601	3	US-09-949-002-4576	Sequence 4576, Ap
135	6	20.0	601	3	US-09-949-002-4577	Sequence 4577, Ap
136	6	20.0	601	3	US-09-949-002-4578	Sequence 4578, Ap
137	6	20.0	601	3	US-09-949-002-4579	Sequence 4579, Ap
c 138	6	20.0	642	3	US-09-270-767-1394	Sequence 1394, Ap
c 139	6	20.0	642	3	US-09-270-767-16676	Sequence 16676, A
c 140	6	20.0	648	3	US-09-533-559-4497	Sequence 4497, Ap
141	6	20.0	666	3	US-09-435-019-11	Sequence 11, Appl
c 142	6	20.0	666	3	US-09-435-019-12	Sequence 12, Appl
143	6	20.0	666	3	US-10-065-200A-11	Sequence 11, Appl
c 144	6	20.0	666	3	US-10-065-200A-12	Sequence 12, Appl
145	6	20.0	684	3	US-09-533-559-7530	Sequence 7530, Ap
c 146	6	20.0	690	3	US-09-134-001C-1404	Sequence 1404, Ap
c 147	6	20.0	732	3	US-09-437-054A-15	Sequence 15, Appl
148	6	20.0	760	3	US-09-533-559-7777	Sequence 7777, Ap
c 149	6	20.0	789	3	US-09-280-116-114	Sequence 114, App
c 150	6	20.0	789	3	US-09-902-540-2956	Sequence 2956, Ap
151	6	20.0	885	3	US-09-270-767-11551	Sequence 11551, A
152	6	20.0	886	3	US-09-949-016-5376	Sequence 5376, Ap
153	6	20.0	909	3	US-09-252-991A-2103	Sequence 2103, Ap
154	6	20.0	923	3	US-09-573-080A-172	Sequence 172, App
155	6	20.0	933	3	US-09-543-681A-604	Sequence 604, App
156	6	20.0	934	3	US-09-270-767-6409	Sequence 6409, Ap
157	6	20.0	934	3	US-09-270-767-21691	Sequence 21691, A
c 158	6	20.0	936	2	US-08-033-797-1	Sequence 1, Appli
c 159	6	20.0	936	2	US-08-472-265-1	Sequence 1, Appli
c 160	6	20.0	936	2	US-08-472-263-1	Sequence 1, Appli
161	6	20.0	936	3	US-09-134-001C-1398	Sequence 1398, Ap
c 162	6	20.0	948	3	US-09-248-796A-2650	Sequence 2650, Ap
163	6	20.0	981	3	US-09-902-540-6237	Sequence 6237, Ap
c 164	6	20.0	982	2	US-08-822-028-1	Sequence 1, Appli
c 165	6	20.0	982	3	US-08-479-285-1	Sequence 1, Appli
c 166	6	20.0	982	3	US-08-961-309-40	Sequence 40, Appl
c 167	6	20.0	982	3	US-09-503-653A-1	Sequence 1, Appli
168	6	20.0	1002	3	US-09-252-991A-2014	Sequence 2014, Ap
169	6	20.0	1017	3	US-09-573-080A-177	Sequence 177, App
c 170	6	20.0	1028	3	US-09-157-077-6	Sequence 6, Appli
171	6	20.0	1065	3	US-09-328-352-3699	Sequence 3699, Ap
172	6	20.0	1125	3	US-09-270-767-11171	Sequence 11171, A
173	6	20.0	1182	3	US-09-248-796A-5505	Sequence 5505, Ap
174	6	20.0	1188	3	US-09-540-236-600	Sequence 600, App
c 175	6	20.0	1233	3	US-09-583-110-1302	Sequence 1302, Ap
c 176	6	20.0	1275	3	US-09-107-433-2599	Sequence 2599, Ap
177	6	20.0	1341	3	US-09-252-991A-5248	Sequence 5248, Ap
c 178	6	20.0	1365	2	US-08-114-072-1	Sequence 1, Appli
c 179	6	20.0	1365	6	PCT-US94-09361-1	Sequence 1, Appli
c 180	6	20.0	1380	3	US-09-252-991A-5325	Sequence 5325, Ap
c 181	6	20.0	1430	2	US-08-549-004A-15	Sequence 15, Appl
c 182	6	20.0	1430	3	US-09-051-982A-15	Sequence 15, Appl
183	6	20.0	1440	3	US-09-857-612A-7	Sequence 7, Appli
184	6	20.0	1443	3	US-09-107-532A-2506	Sequence 2506, Ap
c 185	6	20.0	1463	3	US-09-270-767-13986	Sequence 13986, A
186	6	20.0	1500	3	US-09-602-787A-301	Sequence 301, App
187	6	20.0	1509	3	US-09-533-559-5493	Sequence 5493, Ap
c 188	6	20.0	1521	3	US-09-487-558B-89	Sequence 89, Appl
189	6	20.0	1527	3	US-09-902-540-4072	Sequence 4072, Ap
c 190	6	20.0	1551	3	US-09-715-858-5	Sequence 5, Appli
191	6	20.0	1563	3	US-09-902-540-8878	Sequence 8878, Ap
c 192	6	20.0	1611	3	US-09-715-858-7	Sequence 7, Appli
c 193	6	20.0	1618	3	US-09-560-761B-15	Sequence 15, Appl
194	6	20.0	1635	3	US-09-248-796A-12936	Sequence 12936, A
195	6	20.0	1638	3	US-09-248-796A-10381	Sequence 10381, A
c 196	6	20.0	1642	2	US-08-713-928B-3	Sequence 3, Appli
197	6	20.0	1653	3	US-09-248-796A-2471	Sequence 2471, Ap
c 198	6	20.0	1662	3	US-09-390-234-17	Sequence 17, Appl
c 199	6	20.0	1662	3	US-09-603-311-17	Sequence 17, Appl
200	6	20.0	1668	3	US-09-543-681A-410	Sequence 410, App
c 201	6	20.0	1678	2	US-08-261-677-10	Sequence 10, Appl
c 202	6	20.0	1678	2	US-08-384-556A-6	Sequence 6, Appli
c 203	6	20.0	1678	2	US-08-331-355A-10	Sequence 10, Appl
c 204	6	20.0	1678	6	PCT-US94-12364-10	Sequence 10, Appl
c 205	6	20.0	1678	6	PCT-US95-07753-6	Sequence 6, Appli
c 206	6	20.0	1701	3	US-09-264-737-3	Sequence 3, Appli
207	6	20.0	1703	3	US-09-057-996-3	Sequence 3, Appli
c 208	6	20.0	1717	3	US-09-595-682B-20	Sequence 20, Appl
209	6	20.0	1740	3	US-08-796-101-50	Sequence 50, Appl
c 210	6	20.0	1741	3	US-09-586-216C-11	Sequence 11, Appl
c 211	6	20.0	1741	3	US-09-586-216C-13	Sequence 13, Appl
c 212	6	20.0	1792	3	US-09-782-378A-16	Sequence 16, Appl
c 213	6	20.0	1891	3	US-08-973-462-3	Sequence 3, Appli
214	6	20.0	1914	3	US-09-614-221A-272	Sequence 272, App
215	6	20.0	1920	3	US-09-902-540-4811	Sequence 4811, Ap
216	6	20.0	1922	3	US-09-949-016-5462	Sequence 5462, Ap
217	6	20.0	1980	3	US-09-248-796A-10706	Sequence 10706, A
c 218	6	20.0	2121	3	US-09-614-891-4	Sequence 4, Appli
219	6	20.0	2196	2	US-08-472-217-3	Sequence 3, Appli
220	6	20.0	2196	3	US-08-760-534A-3	Sequence 3, Appli
221	6	20.0	2196	3	US-09-336-757-3	Sequence 3, Appli
c 222	6	20.0	2242	3	US-10-104-047-1897	Sequence 1897, Ap
c 223	6	20.0	2294	3	US-09-949-016-5458	Sequence 5458, Ap
c 224	6	20.0	2327	3	US-09-157-077-1	Sequence 1, Appli
225	6	20.0	2337	3	US-10-104-047-1530	Sequence 1530, Ap
226	6	20.0	2429	3	US-10-104-047-1792	Sequence 1792, Ap
c 227	6	20.0	2526	3	US-09-964-956-3	Sequence 3, Appli
c 228	6	20.0	2531	3	US-09-964-956-4	Sequence 4, Appli

c 229	6	20.0	2555	3	US-09-935-430-656	Sequence 656, App
c 230	6	20.0	2563	2	US-08-423-441-1	Sequence 1, Appli
231	6	20.0	2606	3	US-10-104-047-17	Sequence 17, Appl
c 232	6	20.0	2610	3	US-09-614-221A-212	Sequence 212, App
c 233	6	20.0	2711	3	US-10-104-047-15	Sequence 15, Appl
234	6	20.0	2749	9	5240849-1	Patent No. 5240849
235	6	20.0	2754	3	US-09-902-540-5587	Sequence 5587, Ap
c 236	6	20.0	2796	2	US-08-261-677-8	Sequence 8, Appli
c 237	6	20.0	2796	2	US-08-384-556A-4	Sequence 4, Appli
c 238	6	20.0	2796	2	US-08-331-355A-8	Sequence 8, Appli
c 239	6	20.0	2796	3	US-08-777-147-5	Sequence 5, Appli
c 240	6	20.0	2796	3	US-09-157-077-8	Sequence 8, Appli
c 241	6	20.0	2796	6	PCT-US94-12364-8	Sequence 8, Appli
c 242	6	20.0	2796	6	PCT-US95-07753-4	Sequence 4, Appli
c 243	6	20.0	2832	3	US-09-583-110-2133	Sequence 2133, Ap
c 244	6	20.0	2838	3	US-09-107-433-737	Sequence 737, App
c 245	6	20.0	2838	3	US-09-964-956-1	Sequence 1, Appli
246	6	20.0	2989	3	US-09-068-195-10	Sequence 10, Appl
247	6	20.0	3114	3	US-08-637-732A-2	Sequence 2, Appli
c 248	6	20.0	3223	3	US-09-949-016-3258	Sequence 3258, Ap
249	6	20.0	3270	3	US-08-637-732A-1	Sequence 1, Appli
c 250	6	20.0	3307	3	US-09-023-655-306	Sequence 306, App
c 251	6	20.0	3319	3	US-09-949-016-3257	Sequence 3257, Ap
252	6	20.0	3340	3	US-09-228-986-5	Sequence 5, Appli
253	6	20.0	3340	3	US-10-101-464A-5	Sequence 5, Appli
c 254	6	20.0	3436	3	US-09-710-279-3556	Sequence 3556, Ap
c 255	6	20.0	3452	3	US-09-821-687-3	Sequence 3, Appli
256	6	20.0	3566	2	US-08-415-788-1	Sequence 1, Appli
257	6	20.0	3566	2	US-08-415-788-4	Sequence 4, Appli
258	6	20.0	3566	2	US-08-415-788-6	Sequence 6, Appli
259	6	20.0	3567	2	US-08-415-788-2	Sequence 2, Appli
260	6	20.0	3567	3	US-08-637-732A-3	Sequence 3, Appli
c 261	6	20.0	3667	3	US-09-221-017B-727	Sequence 727, App
262	6	20.0	4105	3	US-09-634-238-182	Sequence 182, App
263	6	20.0	4148	3	US-09-435-019-13	Sequence 13, Appl
c 264	6	20.0	4148	3	US-09-435-019-15	Sequence 15, Appl
265	6	20.0	4148	3	US-10-065-200A-13	Sequence 13, Appl
c 266	6	20.0	4148	3	US-10-065-200A-15	Sequence 15, Appl
c 267	6	20.0	4562	3	US-09-949-016-5195	Sequence 5195, Ap
c 268	6	20.0	4784	3	US-09-634-238-24	Sequence 24, Appl
269	6	20.0	4787	3	US-09-949-016-14085	Sequence 14085, A
270	6	20.0	4787	3	US-09-949-016-14086	Sequence 14086, A
271	6	20.0	4886	3	US-09-949-016-17118	Sequence 17118, A
272	6	20.0	4902	3	US-09-902-540-2065	Sequence 2065, Ap
273	6	20.0	4953	3	US-09-602-787A-13	Sequence 13, Appl
274	6	20.0	4953	3	US-09-602-787A-55	Sequence 55, Appl
c 275	6	20.0	5113	3	US-09-560-385A-11	Sequence 11, Appl
c 276	6	20.0	5170	3	US-09-560-385A-3	Sequence 3, Appli
c 277	6	20.0	5264	3	US-09-560-385A-9	Sequence 9, Appli
c 278	6	20.0	5280	3	US-09-560-385A-1	Sequence 1, Appli
c 279	6	20.0	5361	3	US-08-973-462-2	Sequence 2, Appli
c 280	6	20.0	5373	3	US-09-560-385A-7	Sequence 7, Appli
281	6	20.0	5428	3	US-09-625-972-21	Sequence 21, Appl
c 282	6	20.0	5433	3	US-09-560-385A-5	Sequence 5, Appli
c 283	6	20.0	5496	3	US-08-600-982-23	Sequence 23, Appl
c 284	6	20.0	5496	6	PCT-US94-10261A-23	Sequence 23, Appl
285	6	20.0	5565	3	US-09-068-195-21	Sequence 21, Appl
286	6	20.0	5688	3	US-09-487-558B-135	Sequence 135, App
287	6	20.0	5840	3	US-09-949-016-5692	Sequence 5692, Ap
c 288	6	20.0	6152	3	US-08-973-462-1	Sequence 1, Appli
289	6	20.0	6240	3	US-09-634-238-21	Sequence 21, Appl
290	6	20.0	6447	3	US-08-675-566-16	Sequence 16, Appl
291	6	20.0	6827	3	US-08-961-527-60	Sequence 60, Appl
292	6	20.0	7070	2	US-08-619-554-3	Sequence 3, Appli
293	6	20.0	7141	3	US-09-631-594-73	Sequence 73, Appl
294	6	20.0	7151	3	US-09-839-477-7	Sequence 7, Appli
295	6	20.0	7360	2	US-08-611-107-9	Sequence 9, Appli
296	6	20.0	7360	2	US-08-422-560A-9	Sequence 9, Appli
297	6	20.0	7360	3	US-08-468-793-9	Sequence 9, Appli
c 298	6	20.0	7620	2	US-07-767-135-1	Sequence 1, Appli
c 299	6	20.0	7620	2	US-07-841-652-1	Sequence 1, Appli
300	6	20.0	8424	3	US-09-543-681A-808	Sequence 808, App
301	6	20.0	9003	3	US-09-949-016-16062	Sequence 16062, A
302	6	20.0	9369	3	US-09-949-016-17071	Sequence 17071, A
303	6	20.0	9472	2	US-08-325-547-9	Sequence 9, Appli
304	6	20.0	9480	3	US-09-657-013-35	Sequence 35, Appl
305	6	20.0	9641	3	US-09-625-972-22	Sequence 22, Appl
306	6	20.0	9790	3	US-09-949-016-17204	Sequence 17204, A
307	6	20.0	10087	3	US-09-657-013-29	Sequence 29, Appl
c 308	6	20.0	10470	3	US-08-956-171E-20	Sequence 20, Appl
c 309	6	20.0	10470	3	US-08-781-986A-20	Sequence 20, Appl
c 310	6	20.0	10528	3	US-09-902-540-945	Sequence 945, App
311	6	20.0	10669	3	US-08-961-527-57	Sequence 57, Appl
312	6	20.0	11376	3	US-09-949-016-16035	Sequence 16035, A
c 313	6	20.0	11887	3	US-08-961-527-146	Sequence 146, App
c 314	6	20.0	13290	3	US-09-949-016-13937	Sequence 13937, A
c 315	6	20.0	13290	3	US-09-949-016-13938	Sequence 13938, A
316	6	20.0	13332	3	US-09-902-540-1047	Sequence 1047, Ap
317	6	20.0	18248	3	US-09-949-016-12452	Sequence 12452, A
318	6	20.0	18249	3	US-09-949-016-17256	Sequence 17256, A
319	6	20.0	22121	3	US-09-949-016-14359	Sequence 14359, A
320	6	20.0	22121	3	US-09-949-016-14909	Sequence 14909, A
321	6	20.0	24602	3	US-09-902-540-1202	Sequence 1202, Ap
c 322	6	20.0	24639	3	US-09-949-016-14068	Sequence 14068, A
c 323	6	20.0	24715	3	US-09-949-016-12979	Sequence 12979, A
324	6	20.0	24984	3	US-09-949-016-14950	Sequence 14950, A
c 325	6	20.0	25124	3	US-09-949-016-15982	Sequence 15982, A
c 326	6	20.0	25686	3	US-09-902-540-1246	Sequence 1246, Ap
327	6	20.0	25814	3	US-09-949-016-16927	Sequence 16927, A
c 328	6	20.0	26454	3	US-09-902-540-1251	Sequence 1251, Ap
c 329	6	20.0	26769	3	US-09-949-016-14934	Sequence 14934, A
c 330	6	20.0	27757	3	US-09-949-016-12407	Sequence 12407, A
c 331	6	20.0	27757	3	US-09-949-016-14545	Sequence 14545, A
332	6	20.0	27908	3	US-09-949-016-12397	Sequence 12397, A
333	6	20.0	27909	3	US-09-949-016-17082	Sequence 17082, A
c 334	6	20.0	29103	3	US-09-902-540-1236	Sequence 1236, Ap
c 335	6	20.0	30246	3	US-08-956-171E-56	Sequence 56, Appl
c 336	6	20.0	30246	3	US-08-781-986A-56	Sequence 56, Appl
c 337	6	20.0	31035	3	US-09-949-016-12272	Sequence 12272, A
c 338	6	20.0	31035	3	US-09-949-016-17266	Sequence 17266, A
c 339	6	20.0	31078	3	US-09-949-016-14435	Sequence 14435, A
c 340	6	20.0	31391	3	US-09-949-016-17200	Sequence 17200, A
341	6	20.0	32584	3	US-09-949-016-16766	Sequence 16766, A
c 342	6	20.0	33140	3	US-09-596-002-23	Sequence 23, Appl
c 343	6	20.0	33675	3	US-09-921-992-2	Sequence 2, Appli
c 344	6	20.0	34185	3	US-09-545-481-3	Sequence 3, Appli
345	6	20.0	34677	3	US-09-949-002-593	Sequence 593, App
346	6	20.0	35630	3	US-09-949-016-13832	Sequence 13832, A
c 347	6	20.0	37711	3	US-09-949-016-12832	Sequence 12832, A
c 348	6	20.0	37712	3	US-09-949-016-16704	Sequence 16704, A
349	6	20.0	37976	3	US-09-949-016-13441	Sequence 13441, A
c 350	6	20.0	40897	3	US-09-949-016-13910	Sequence 13910, A
c 351	6	20.0	40897	3	US-09-949-016-13911	Sequence 13911, A
c 352	6	20.0	40897	3	US-09-949-016-13912	Sequence 13912, A
c 353	6	20.0	40897	3	US-09-949-016-13913	Sequence 13913, A
c 354	6	20.0	40897	3	US-09-949-016-14409	Sequence 14409, A
c 355	6	20.0	40897	3	US-09-949-016-14410	Sequence 14410, A
c 356	6	20.0	40897	3	US-09-949-016-14411	Sequence 14411, A
c 357	6	20.0	40897	3	US-09-949-016-14412	Sequence 14412, A
c 358	6	20.0	41132	3	US-09-949-016-12021	Sequence 12021, A
c 359	6	20.0	41136	3	US-09-949-016-13021	Sequence 13021, A
360	6	20.0	41696	3	US-09-949-016-12444	Sequence 12444, A
361	6	20.0	41927	3	US-09-902-540-1268	Sequence 1268, Ap
c 362	6	20.0	44479	3	US-09-949-016-17176	Sequence 17176, A
c 363	6	20.0	44998	3	US-09-949-016-12824	Sequence 12824, A
c 364	6	20.0	44999	3	US-09-949-016-14832	Sequence 14832, A
c 365	6	20.0	44999	3	US-09-949-016-14833	Sequence 14833, A
c 366	6	20.0	44999	3	US-09-949-016-17108	Sequence 17108, A
c 367	6	20.0	44999	3	US-09-949-016-17109	Sequence 17109, A
368	6	20.0	45900	3	US-09-949-016-17599	Sequence 17599, A
c 369	6	20.0	46288	3	US-09-949-016-14999	Sequence 14999, A
c 370	6	20.0	46311	3	US-09-949-016-15000	Sequence 15000, A
c 371	6	20.0	46447	3	US-09-949-016-15071	Sequence 15071, A
c 372	6	20.0	46447	3	US-09-949-016-15072	Sequence 15072, A
c 373	6	20.0	46447	3	US-09-949-016-15073	Sequence 15073, A
c 374	6	20.0	46447	3	US-09-949-016-15074	Sequence 15074, A

c 375	6	20.0	46447	3	US-09-949-016-15075	Sequence 15075, A
c 376	6	20.0	46447	3	US-09-949-016-15076	Sequence 15076, A
c 377	6	20.0	46447	3	US-09-949-016-15077	Sequence 15077, A
c 378	6	20.0	49313	3	US-09-949-016-15063	Sequence 15063, A
c 379	6	20.0	49313	3	US-09-949-016-15064	Sequence 15064, A
c 380	6	20.0	49313	3	US-09-949-016-15065	Sequence 15065, A
c 381	6	20.0	49313	3	US-09-949-016-15066	Sequence 15066, A
c 382	6	20.0	49313	3	US-09-949-016-15067	Sequence 15067, A
c 383	6	20.0	49313	3	US-09-949-016-15068	Sequence 15068, A
c 384	6	20.0	49313	3	US-09-949-016-15069	Sequence 15069, A
c 385	6	20.0	49313	3	US-09-949-016-15070	Sequence 15070, A
386	6	20.0	50269	3	US-09-949-016-17598	Sequence 17598, A
387	6	20.0	51547	3	US-09-949-016-16405	Sequence 16405, A
388	6	20.0	51807	3	US-09-949-016-15333	Sequence 15333, A
389	6	20.0	53799	3	US-10-042-665A-3	Sequence 3, Appli
390	6	20.0	54707	3	US-09-949-016-11861	Sequence 11861, A
c 391	6	20.0	57320	3	US-09-949-016-13983	Sequence 13983, A
c 392	6	20.0	59853	3	US-09-949-016-13618	Sequence 13618, A
c 393	6	20.0	59853	3	US-09-949-016-13619	Sequence 13619, A
c 394	6	20.0	59853	3	US-09-949-016-13620	Sequence 13620, A
c 395	6	20.0	59853	3	US-09-949-016-13621	Sequence 13621, A
c 396	6	20.0	59853	3	US-09-949-016-13622	Sequence 13622, A
c 397	6	20.0	59853	3	US-09-949-016-13623	Sequence 13623, A
c 398	6	20.0	59853	3	US-09-949-016-13624	Sequence 13624, A
c 399	6	20.0	59853	3	US-09-949-016-13625	Sequence 13625, A
400	6	20.0	65300	3	US-09-949-016-16813	Sequence 16813, A
c 401	6	20.0	65848	3	US-09-949-016-13285	Sequence 13285, A
402	6	20.0	67156	3	US-09-949-016-12284	Sequence 12284, A
403	6	20.0	67157	3	US-09-949-016-16558	Sequence 16558, A
404	6	20.0	68719	3	US-09-949-016-12799	Sequence 12799, A
405	6	20.0	68720	3	US-09-949-016-14296	Sequence 14296, A
406	6	20.0	69199	3	US-09-949-016-13881	Sequence 13881, A
c 407	6	20.0	70014	3	US-09-949-016-17110	Sequence 17110, A
408	6	20.0	74940	3	US-09-949-016-17512	Sequence 17512, A
409	6	20.0	75394	3	US-09-949-016-11754	Sequence 11754, A
410	6	20.0	75929	3	US-09-949-016-15543	Sequence 15543, A
411	6	20.0	75929	3	US-09-949-016-15544	Sequence 15544, A
c 412	6	20.0	79787	3	US-09-949-016-13637	Sequence 13637, A
413	6	20.0	80355	3	US-09-949-016-12735	Sequence 12735, A
414	6	20.0	80357	3	US-09-949-016-13572	Sequence 13572, A
c 415	6	20.0	81819	3	US-09-949-016-16661	Sequence 16661, A
c 416	6	20.0	81819	3	US-09-949-016-16662	Sequence 16662, A
c 417	6	20.0	82494	3	US-09-949-016-16937	Sequence 16937, A
c 418	6	20.0	83938	3	US-09-949-016-16068	Sequence 16068, A
419	6	20.0	84571	3	US-09-949-016-17420	Sequence 17420, A
420	6	20.0	84839	3	US-09-949-016-15816	Sequence 15816, A
421	6	20.0	86127	3	US-09-949-016-12209	Sequence 12209, A
422	6	20.0	86128	3	US-09-949-016-15608	Sequence 15608, A
c 423	6	20.0	87190	3	US-09-949-016-16335	Sequence 16335, A
424	6	20.0	87216	3	US-09-949-016-15891	Sequence 15891, A
425	6	20.0	87323	3	US-09-949-016-13828	Sequence 13828, A
c 426	6	20.0	87594	3	US-09-949-016-12135	Sequence 12135, A
c 427	6	20.0	87611	3	US-09-949-016-16139	Sequence 16139, A
c 428	6	20.0	89210	3	US-09-949-016-16988	Sequence 16988, A
c 429	6	20.0	89220	3	US-09-949-016-12655	Sequence 12655, A
c 430	6	20.0	89224	3	US-09-949-016-15572	Sequence 15572, A
c 431	6	20.0	93493	3	US-09-949-016-12063	Sequence 12063, A
c 432	6	20.0	95020	3	US-09-949-016-13272	Sequence 13272, A
c 433	6	20.0	96845	3	US-09-949-016-13658	Sequence 13658, A
434	6	20.0	101835	3	US-09-949-016-14695	Sequence 14695, A
c 435	6	20.0	102520	3	US-09-949-016-17367	Sequence 17367, A
c 436	6	20.0	102526	3	US-09-949-016-12448	Sequence 12448, A
437	6	20.0	105210	3	US-09-949-016-14158	Sequence 14158, A
438	6	20.0	107140	3	US-09-949-016-14834	Sequence 14834, A
439	6	20.0	112114	3	US-09-949-016-17292	Sequence 17292, A
c 440	6	20.0	121068	3	US-09-949-016-14138	Sequence 14138, A
441	6	20.0	126176	3	US-09-949-016-16137	Sequence 16137, A
c 442	6	20.0	126176	3	US-09-949-016-16137	Sequence 16137, A
443	6	20.0	126176	3	US-09-949-016-16138	Sequence 16138, A
c 444	6	20.0	126176	3	US-09-949-016-16138	Sequence 16138, A
445	6	20.0	126237	3	US-09-949-016-16674	Sequence 16674, A
446	6	20.0	126237	3	US-09-949-016-16675	Sequence 16675, A
447	6	20.0	128175	3	US-09-949-016-16268	Sequence 16268, A
448	6	20.0	130563	3	US-09-949-016-12273	Sequence 12273, A
449	6	20.0	130724	3	US-09-949-016-13753	Sequence 13753, A
450	6	20.0	131379	3	US-09-949-016-16050	Sequence 16050, A
c 451	6	20.0	137046	3	US-09-949-016-12427	Sequence 12427, A
c 452	6	20.0	137048	3	US-09-949-016-13438	Sequence 13438, A
c 453	6	20.0	137394	3	US-09-949-016-13872	Sequence 13872, A
c 454	6	20.0	137743	3	US-09-949-016-12178	Sequence 12178, A
c 455	6	20.0	147840	3	US-09-949-016-15236	Sequence 15236, A
c 456	6	20.0	148609	3	US-09-949-016-12860	Sequence 12860, A
c 457	6	20.0	148609	3	US-09-949-016-16787	Sequence 16787, A
458	6	20.0	154605	3	US-09-949-016-11894	Sequence 11894, A
459	6	20.0	157644	3	US-09-949-016-16179	Sequence 16179, A
460	6	20.0	157644	3	US-09-949-016-16180	Sequence 16180, A
c 461	6	20.0	163662	3	US-09-949-016-12545	Sequence 12545, A
c 462	6	20.0	163664	3	US-09-949-016-13546	Sequence 13546, A
c 463	6	20.0	168174	3	US-10-071-411A-63	Sequence 63, Appl
c 464	6	20.0	168273	3	US-10-071-411A-2	Sequence 2, Appli
c 465	6	20.0	169998	3	US-09-676-610B-24	Sequence 24, Appl
c 466	6	20.0	174170	3	US-09-949-016-14810	Sequence 14810, A
c 467	6	20.0	174170	3	US-09-949-016-14811	Sequence 14811, A
c 468	6	20.0	174318	3	US-09-949-016-11880	Sequence 11880, A
c 469	6	20.0	174318	3	US-09-949-016-14812	Sequence 14812, A
c 470	6	20.0	174318	3	US-09-949-016-14813	Sequence 14813, A
c 471	6	20.0	179904	3	US-09-949-002-577	Sequence 577, App
c 472	6	20.0	179905	3	US-09-949-002-705	Sequence 705, App
473	6	20.0	185765	3	US-09-949-002-674	Sequence 674, App
474	6	20.0	185766	3	US-09-949-002-707	Sequence 707, App
475	6	20.0	187169	3	US-09-949-016-12776	Sequence 12776, A
c 476	6	20.0	187580	3	US-09-949-016-13266	Sequence 13266, A
477	6	20.0	191569	3	US-09-949-016-15940	Sequence 15940, A
478	6	20.0	193303	3	US-09-497-855A-37	Sequence 37, Appl
479	6	20.0	193303	3	US-09-497-855A-44	Sequence 44, Appl
c 480	6	20.0	197496	3	US-09-877-177A-10	Sequence 10, Appl
481	6	20.0	212139	3	US-09-949-016-16065	Sequence 16065, A
c 482	6	20.0	227979	3	US-09-949-016-11842	Sequence 11842, A
c 483	6	20.0	228851	3	US-09-949-016-13781	Sequence 13781, A
c 484	6	20.0	229354	3	US-09-705-400-64	Sequence 64, Appl
485	6	20.0	231129	3	US-09-949-016-16110	Sequence 16110, A
486	6	20.0	250352	3	US-09-949-016-14724	Sequence 14724, A
487	6	20.0	251769	3	US-09-949-016-13185	Sequence 13185, A
488	6	20.0	251769	3	US-09-949-016-13186	Sequence 13186, A
c 489	6	20.0	264206	3	US-09-949-016-12731	Sequence 12731, A
c 490	6	20.0	264304	3	US-09-949-016-13249	Sequence 13249, A
c 491	6	20.0	264665	3	US-09-949-016-13747	Sequence 13747, A
c 492	6	20.0	265038	3	US-09-949-016-15779	Sequence 15779, A
493	6	20.0	266748	3	US-09-949-016-13187	Sequence 13187, A
494	6	20.0	266748	3	US-09-949-016-13188	Sequence 13188, A
495	6	20.0	276237	3	US-09-949-016-17504	Sequence 17504, A
496	6	20.0	278866	3	US-09-949-016-13922	Sequence 13922, A
497	6	20.0	278866	3	US-09-949-016-13923	Sequence 13923, A
498	6	20.0	278866	3	US-09-949-016-13924	Sequence 13924, A
499	6	20.0	278866	3	US-09-949-016-13925	Sequence 13925, A
500	6	20.0	278866	3	US-09-949-016-13926	Sequence 13926, A
501	6	20.0	278866	3	US-09-949-016-14699	Sequence 14699, A
502	6	20.0	278866	3	US-09-949-016-14700	Sequence 14700, A
503	6	20.0	278866	3	US-09-949-016-14701	Sequence 14701, A
504	6	20.0	278866	3	US-09-949-016-14702	Sequence 14702, A
505	6	20.0	278866	3	US-09-949-016-14703	Sequence 14703, A
c 506	6	20.0	304533	3	US-09-949-016-15371	Sequence 15371, A
c 507	6	20.0	304533	3	US-09-949-016-15372	Sequence 15372, A
508	6	20.0	312474	3	US-09-949-016-17434	Sequence 17434, A
c 509	6	20.0	312957	3	US-09-949-001-31	Sequence 31, Appl
c 510	6	20.0	312972	3	US-09-949-001-34	Sequence 34, Appl
511	6	20.0	319608	3	US-09-539-333D-1	Sequence 1, Appli
512	6	20.0	319608	3	US-09-679-409-1	Sequence 1, Appli
c 513	6	20.0	325034	3	US-09-949-016-14957	Sequence 14957, A
c 514	6	20.0	363032	3	US-09-949-016-12415	Sequence 12415, A
c 515	6	20.0	363033	3	US-09-949-016-15754	Sequence 15754, A
516	6	20.0	373182	3	US-09-949-016-17371	Sequence 17371, A
c 517	6	20.0	373182	3	US-09-949-016-17371	Sequence 17371, A
518	6	20.0	373694	3	US-09-949-016-12062	Sequence 12062, A
c 519	6	20.0	373694	3	US-09-949-016-12062	Sequence 12062, A
c 520	6	20.0	374159	3	US-09-949-016-15868	Sequence 15868, A

521	6	20.0	387902	3	US-09-949-016-14543	Sequence 14543, A
c 522	6	20.0	389504	3	US-09-949-016-11774	Sequence 11774, A
c 523	6	20.0	421491	3	US-09-949-016-12805	Sequence 12805, A
c 524	6	20.0	421494	3	US-09-949-016-14060	Sequence 14060, A
525	6	20.0	421883	3	US-09-949-016-12557	Sequence 12557, A
c 526	6	20.0	422592	3	US-09-949-016-14182	Sequence 14182, A
527	6	20.0	455726	3	US-09-949-016-14157	Sequence 14157, A
c 528	6	20.0	455726	3	US-09-949-016-14157	Sequence 14157, A
529	6	20.0	462589	3	US-09-949-016-12900	Sequence 12900, A
530	6	20.0	476044	3	US-09-949-016-12412	Sequence 12412, A
531	6	20.0	481115	3	US-09-949-016-11940	Sequence 11940, A
c 532	6	20.0	481115	3	US-09-949-016-11940	Sequence 11940, A
533	6	20.0	670689	3	US-09-949-016-12505	Sequence 12505, A
c 534	6	20.0	670689	3	US-09-949-016-12505	Sequence 12505, A
535	6	20.0	670690	3	US-09-949-016-14207	Sequence 14207, A
c 536	6	20.0	670690	3	US-09-949-016-14207	Sequence 14207, A
537	6	20.0	678533	3	US-09-949-016-14577	Sequence 14577, A
c 538	6	20.0	678533	3	US-09-949-016-14577	Sequence 14577, A
539	6	20.0	678533	3	US-09-949-016-14578	Sequence 14578, A
c 540	6	20.0	678533	3	US-09-949-016-14578	Sequence 14578, A
541	6	20.0	1230025	3	US-09-198-452A-1	Sequence 1, Appli
c 542	6	20.0	1230025	3	US-09-198-452A-1	Sequence 1, Appli
543	6	20.0	1230230	3	US-09-438-185A-1	Sequence 1, Appli
c 544	6	20.0	1230230	3	US-09-438-185A-1	Sequence 1, Appli
c 545	6	20.0	1664976	3	US-08-916-421B-1	Sequence 1, Appli
c 546	6	20.0	1664976	3	US-09-692-570-1	Sequence 1, Appli
547	6	20.0	1830121	3	US-09-557-884-1	Sequence 1, Appli
c 548	6	20.0	1830121	3	US-09-557-884-1	Sequence 1, Appli
549	6	20.0	1830121	3	US-09-643-990A-1	Sequence 1, Appli
c 550	6	20.0	1830121	3	US-09-643-990A-1	Sequence 1, Appli
551	6	20.0	1830121	3	US-10-158-865-1	Sequence 1, Appli
c 552	6	20.0	1830121	3	US-10-158-865-1	Sequence 1, Appli
553	6	20.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 554	6	20.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
555	6	20.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 556	6	20.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 557	5	16.7	17	3	US-08-584-040-4131	Sequence 4131, Ap
c 558	5	16.7	17	3	US-08-584-040-4132	Sequence 4132, Ap
c 559	5	16.7	17	3	US-09-371-772B-1898	Sequence 1898, Ap
c 560	5	16.7	17	3	US-09-371-772B-1899	Sequence 1899, Ap
c 561	5	16.7	17	3	US-09-371-772B-6616	Sequence 6616, Ap
562	5	16.7	17	3	US-09-866-108A-7137	Sequence 7137, Ap
563	5	16.7	17	3	US-09-866-108A-7138	Sequence 7138, Ap
564	5	16.7	17	3	US-09-866-108A-7139	Sequence 7139, Ap
c 565	5	16.7	17	3	US-09-685-664B-1898	Sequence 1898, Ap
c 566	5	16.7	17	3	US-09-685-664B-1899	Sequence 1899, Ap
567	5	16.7	18	3	US-08-637-732A-17	Sequence 17, Appl
c 568	5	16.7	19	3	US-09-696-791-62	Sequence 62, Appl
c 569	5	16.7	19	3	US-09-696-791-63	Sequence 63, Appl
c 570	5	16.7	20	2	US-08-507-431-8	Sequence 8, Appli
c 571	5	16.7	20	2	US-08-902-655A-8	Sequence 8, Appli
c 572	5	16.7	20	3	US-09-116-622-8	Sequence 8, Appli
c 573	5	16.7	20	3	US-09-219-277-8	Sequence 8, Appli
c 574	5	16.7	20	3	US-09-599-661-8	Sequence 8, Appli
c 575	5	16.7	20	3	US-09-021-701-1165	Sequence 1165, Ap
c 576	5	16.7	20	3	US-09-198-452A-4485	Sequence 4485, Ap
c 577	5	16.7	20	3	US-09-198-452A-6092	Sequence 6092, Ap
578	5	16.7	20	3	US-09-967-655-47	Sequence 47, Appl
c 579	5	16.7	20	3	US-10-131-827-8840	Sequence 8840, Ap
c 580	5	16.7	21	2	US-08-265-484B-32	Sequence 32, Appl
c 581	5	16.7	21	3	US-09-050-159-69	Sequence 69, Appl
582	5	16.7	21	3	US-09-422-978-10949	Sequence 10949, A
583	5	16.7	23	3	US-09-312-405-7	Sequence 7, Appli
584	5	16.7	23	3	US-09-446-301A-23	Sequence 23, Appl
585	5	16.7	23	3	US-09-099-932-21	Sequence 21, Appl
586	5	16.7	23	3	US-10-392-970-21	Sequence 21, Appl
c 587	5	16.7	24	3	US-09-352-654A-38	Sequence 38, Appl
c 588	5	16.7	24	3	US-09-348-097-38	Sequence 38, Appl
c 589	5	16.7	24	3	US-09-350-275-38	Sequence 38, Appl
590	5	16.7	24	3	US-09-585-174-42	Sequence 42, Appl
c 591	5	16.7	24	3	US-09-909-558-38	Sequence 38, Appl
c 592	5	16.7	25	3	US-09-343-634-1	Sequence 1, Appli
593	5	16.7	25	3	US-09-866-108A-12029	Sequence 12029, A
594	5	16.7	25	3	US-09-866-108A-12030	Sequence 12030, A
595	5	16.7	25	3	US-09-866-108A-12031	Sequence 12031, A
596	5	16.7	25	3	US-09-866-108A-12032	Sequence 12032, A
597	5	16.7	25	3	US-09-866-108A-12033	Sequence 12033, A
598	5	16.7	25	3	US-09-866-108A-12034	Sequence 12034, A
599	5	16.7	25	3	US-09-866-108A-12035	Sequence 12035, A
600	5	16.7	25	3	US-09-866-108A-12036	Sequence 12036, A
601	5	16.7	25	3	US-09-866-108A-12037	Sequence 12037, A
602	5	16.7	25	3	US-09-866-108A-12038	Sequence 12038, A
603	5	16.7	25	3	US-09-866-108A-12039	Sequence 12039, A
c 604	5	16.7	25	3	US-10-161-025-1	Sequence 1, Appli
605	5	16.7	25	3	US-09-396-196G-5366	Sequence 5366, Ap
606	5	16.7	25	3	US-09-396-196G-9205	Sequence 9205, Ap
607	5	16.7	25	3	US-09-396-196G-9206	Sequence 9206, Ap
608	5	16.7	25	3	US-09-396-196G-9207	Sequence 9207, Ap
c 609	5	16.7	25	3	US-09-396-196G-10955	Sequence 10955, A
610	5	16.7	25	3	US-09-396-196G-19551	Sequence 19551, A
c 611	5	16.7	25	3	US-09-396-196G-30477	Sequence 30477, A
c 612	5	16.7	25	3	US-09-396-196G-30478	Sequence 30478, A
c 613	5	16.7	25	3	US-09-396-196G-50836	Sequence 50836, A
c 614	5	16.7	25	3	US-09-396-196G-68462	Sequence 68462, A
c 615	5	16.7	25	3	US-09-396-196G-80590	Sequence 80590, A
616	5	16.7	25	3	US-09-396-196G-90368	Sequence 90368, A
c 617	5	16.7	25	3	US-09-396-196G-95475	Sequence 95475, A
618	5	16.7	27	6	PCT-US96-05800-5	Sequence 5, Appli
c 619	5	16.7	28	2	US-08-117-364A-4	Sequence 4, Appli
c 620	5	16.7	28	2	US-08-457-733-4	Sequence 4, Appli
c 621	5	16.7	28	3	US-08-457-996A-4	Sequence 4, Appli
c 622	5	16.7	29	3	US-08-753-750B-32	Sequence 32, Appl
c 623	5	16.7	29	3	US-08-753-750B-49	Sequence 49, Appl
624	5	16.7	29	3	US-09-957-974-10	Sequence 10, Appl
625	5	16.7	30	3	US-08-882-649A-14	Sequence 14, Appl
c 626	5	16.7	30	3	US-09-889-611A-7	Sequence 7, Appli
627	5	16.7	30	3	US-09-880-727-14	Sequence 14, Appl
628	5	16.7	31	3	US-09-027-089-10	Sequence 10, Appl
629	5	16.7	33	3	US-09-610-215-9	Sequence 9, Appli
c 630	5	16.7	35	3	US-09-646-561-65	Sequence 65, Appl
631	5	16.7	36	3	US-09-070-408-4	Sequence 4, Appli
632	5	16.7	36	3	US-09-070-408-9	Sequence 9, Appli
c 633	5	16.7	37	2	US-07-826-928A-35	Sequence 35, Appl
c 634	5	16.7	37	2	US-08-257-073-141	Sequence 141, App
635	5	16.7	37	3	US-09-614-679A-2	Sequence 2, Appli
636	5	16.7	39	3	US-08-952-445-34	Sequence 34, Appl
637	5	16.7	39	3	US-09-981-430-34	Sequence 34, Appl
638	5	16.7	39	3	US-09-935-338-103	Sequence 103, App
c 639	5	16.7	41	3	US-09-716-964B-165	Sequence 165, App
640	5	16.7	45	2	US-08-082-849B-24	Sequence 24, Appl
c 641	5	16.7	45	2	US-08-464-136-59	Sequence 59, Appl
c 642	5	16.7	45	2	US-08-349-131-59	Sequence 59, Appl
c 643	5	16.7	45	3	US-08-470-297A-59	Sequence 59, Appl
c 644	5	16.7	45	3	US-08-471-622A-59	Sequence 59, Appl
c 645	5	16.7	45	6	PCT-US91-07149-59	Sequence 59, Appl
646	5	16.7	45	6	PCT-US94-01624-24	Sequence 24, Appl
c 647	5	16.7	46	2	US-08-397-602A-5	Sequence 5, Appli
c 648	5	16.7	46	2	US-08-082-849B-26	Sequence 26, Appl
c 649	5	16.7	46	6	PCT-US94-01624-26	Sequence 26, Appl
650	5	16.7	47	3	US-09-422-978-2914	Sequence 2914, Ap
651	5	16.7	47	3	US-09-422-978-3159	Sequence 3159, Ap
c 652	5	16.7	50	3	US-10-131-827-5519	Sequence 5519, Ap
c 653	5	16.7	50	3	US-10-131-827-6300	Sequence 6300, Ap
654	5	16.7	50	3	US-10-131-827-7788	Sequence 7788, Ap
655	5	16.7	51	3	US-08-956-171E-2010	Sequence 2010, Ap
656	5	16.7	51	3	US-08-781-986A-2010	Sequence 2010, Ap
657	5	16.7	52	2	US-08-291-932A-770	Sequence 770, App
658	5	16.7	52	2	US-08-291-932A-799	Sequence 799, App
c 659	5	16.7	54	3	US-09-214-453A-29	Sequence 29, Appl
660	5	16.7	55	2	US-08-790-963-20	Sequence 20, Appl
661	5	16.7	55	2	US-08-790-963-24	Sequence 24, Appl
662	5	16.7	55	2	US-08-535-243-3	Sequence 3, Appli
663	5	16.7	55	3	US-09-371-774-20	Sequence 20, Appl
664	5	16.7	55	3	US-09-371-774-24	Sequence 24, Appl
665	5	16.7	55	3	US-09-875-082-20	Sequence 20, Appl
666	5	16.7	55	3	US-09-875-082-24	Sequence 24, Appl

667	5	16.7	55	8	US-09-636-771-3	Sequence 3, Appli
668	5	16.7	61	3	US-08-569-147-65	Sequence 65, Appl
c 669	5	16.7	67	3	US-09-121-286-7	Sequence 7, Appli
c 670	5	16.7	67	3	US-09-275-850-314	Sequence 314, App
c 671	5	16.7	67	3	US-09-907-111-314	Sequence 314, App
c 672	5	16.7	76	2	US-08-442-572-34	Sequence 34, Appl
673	5	16.7	76	2	US-08-178-476A-3	Sequence 3, Appli
c 674	5	16.7	76	2	US-08-361-795-34	Sequence 34, Appl
675	5	16.7	76	2	US-08-257-073-121	Sequence 121, App
676	5	16.7	76	3	US-09-083-366-3	Sequence 3, Appli
c 677	5	16.7	76	6	PCT-US95-05600-117	Sequence 117, App
678	5	16.7	81	3	US-09-513-999C-34012	Sequence 34012, A
679	5	16.7	83	3	US-08-862-337-2	Sequence 2, Appli
680	5	16.7	83	3	US-08-862-337-3	Sequence 3, Appli
c 681	5	16.7	84	2	US-08-257-073-122	Sequence 122, App
682	5	16.7	85	2	US-08-477-527A-153	Sequence 153, App
683	5	16.7	85	3	US-08-481-710-153	Sequence 153, App
684	5	16.7	85	6	PCT-US96-09537-153	Sequence 153, App
685	5	16.7	88	2	US-07-915-247A-31	Sequence 31, Appl
686	5	16.7	88	2	US-08-443-863-31	Sequence 31, Appl
687	5	16.7	88	2	US-08-448-070-31	Sequence 31, Appl
688	5	16.7	88	2	US-08-449-500-31	Sequence 31, Appl
689	5	16.7	88	2	US-08-449-317A-31	Sequence 31, Appl
690	5	16.7	88	2	US-08-477-022-31	Sequence 31, Appl
691	5	16.7	88	2	US-08-449-447-31	Sequence 31, Appl
692	5	16.7	88	2	US-08-184-328-31	Sequence 31, Appl
693	5	16.7	88	2	US-08-521-097-31	Sequence 31, Appl
694	5	16.7	88	3	US-09-670-075A-4	Sequence 4, Appli
c 695	5	16.7	90	2	US-07-915-247A-32	Sequence 32, Appl
c 696	5	16.7	90	2	US-08-443-863-32	Sequence 32, Appl
c 697	5	16.7	90	2	US-08-448-070-32	Sequence 32, Appl
c 698	5	16.7	90	2	US-08-449-500-32	Sequence 32, Appl
c 699	5	16.7	90	2	US-08-449-317A-32	Sequence 32, Appl
c 700	5	16.7	90	2	US-08-477-022-32	Sequence 32, Appl
c 701	5	16.7	90	2	US-08-449-447-32	Sequence 32, Appl
c 702	5	16.7	90	2	US-08-184-328-32	Sequence 32, Appl
c 703	5	16.7	90	2	US-08-521-097-32	Sequence 32, Appl
704	5	16.7	90	3	US-09-866-108A-15688	Sequence 15688, A
c 705	5	16.7	98	2	US-08-210-222-23	Sequence 23, Appl
706	5	16.7	100	3	US-08-956-171E-1932	Sequence 1932, Ap
707	5	16.7	100	3	US-08-781-986A-1932	Sequence 1932, Ap
708	5	16.7	101	3	US-09-621-976-12392	Sequence 12392, A
709	5	16.7	103	3	US-08-956-171E-1566	Sequence 1566, Ap
710	5	16.7	103	3	US-09-621-976-12007	Sequence 12007, A
711	5	16.7	103	3	US-08-781-986A-1566	Sequence 1566, Ap
712	5	16.7	104	3	US-09-621-976-12251	Sequence 12251, A
713	5	16.7	104	3	US-09-917-330-16	Sequence 16, Appl
714	5	16.7	106	3	US-09-513-999C-17939	Sequence 17939, A
715	5	16.7	106	3	US-09-513-999C-19435	Sequence 19435, A
716	5	16.7	108	3	US-10-340-484-1	Sequence 1, Appli
717	5	16.7	109	3	US-09-621-976-11645	Sequence 11645, A
c 718	5	16.7	109	3	US-09-513-999C-20650	Sequence 20650, A
719	5	16.7	111	3	US-09-621-976-13332	Sequence 13332, A
720	5	16.7	114	3	US-08-956-171E-2168	Sequence 2168, Ap
721	5	16.7	114	3	US-08-781-986A-2168	Sequence 2168, Ap
722	5	16.7	118	3	US-09-621-976-11692	Sequence 11692, A
723	5	16.7	118	3	US-09-621-976-11800	Sequence 11800, A
724	5	16.7	118	3	US-09-621-976-11962	Sequence 11962, A
725	5	16.7	118	3	US-09-621-976-12204	Sequence 12204, A
726	5	16.7	119	3	US-09-621-976-11955	Sequence 11955, A
727	5	16.7	121	3	US-08-862-337-1	Sequence 1, Appli
728	5	16.7	122	3	US-08-956-171E-3250	Sequence 3250, Ap
729	5	16.7	122	3	US-08-781-986A-3250	Sequence 3250, Ap
c 730	5	16.7	123	3	US-09-513-999C-21076	Sequence 21076, A
731	5	16.7	127	3	US-09-270-767-30906	Sequence 30906, A
c 732	5	16.7	129	3	US-09-513-999C-28248	Sequence 28248, A
c 733	5	16.7	134	3	US-09-513-999C-36425	Sequence 36425, A
734	5	16.7	137	3	US-09-621-976-11950	Sequence 11950, A
735	5	16.7	138	3	US-09-513-999C-28625	Sequence 28625, A
c 736	5	16.7	139	3	US-09-513-999C-14319	Sequence 14319, A
737	5	16.7	140	3	US-09-621-976-12422	Sequence 12422, A
c 738	5	16.7	141	3	US-09-513-999C-28947	Sequence 28947, A
739	5	16.7	145	3	US-09-621-976-12053	Sequence 12053, A
c 740	5	16.7	145	3	US-09-513-999C-24159	Sequence 24159, A
741	5	16.7	146	3	US-09-513-999C-20840	Sequence 20840, A
742	5	16.7	146	3	US-09-513-999C-24731	Sequence 24731, A
c 743	5	16.7	148	3	US-09-513-999C-13767	Sequence 13767, A
744	5	16.7	152	3	US-09-621-976-11624	Sequence 11624, A
745	5	16.7	152	3	US-09-621-976-11957	Sequence 11957, A
c 746	5	16.7	155	3	US-09-313-294A-3677	Sequence 3677, Ap
747	5	16.7	156	3	US-09-621-976-12157	Sequence 12157, A
748	5	16.7	156	3	US-09-621-976-12406	Sequence 12406, A
749	5	16.7	157	3	US-09-621-976-12187	Sequence 12187, A
750	5	16.7	157	3	US-09-621-976-13600	Sequence 13600, A
751	5	16.7	158	3	US-09-621-976-11870	Sequence 11870, A
752	5	16.7	158	3	US-09-621-976-12431	Sequence 12431, A
753	5	16.7	158	3	US-09-621-976-12438	Sequence 12438, A
754	5	16.7	159	3	US-09-270-767-1846	Sequence 1846, Ap
755	5	16.7	159	3	US-09-270-767-17128	Sequence 17128, A
756	5	16.7	163	3	US-09-702-705-1491	Sequence 1491, Ap
757	5	16.7	163	3	US-09-736-457-1491	Sequence 1491, Ap
758	5	16.7	163	3	US-09-614-124B-1491	Sequence 1491, Ap
759	5	16.7	163	3	US-09-671-325-1491	Sequence 1491, Ap
760	5	16.7	163	3	US-09-658-824-1491	Sequence 1491, Ap
761	5	16.7	163	3	US-10-017-754-1491	Sequence 1491, Ap
762	5	16.7	163	3	US-09-651-563-1491	Sequence 1491, Ap
c 763	5	16.7	166	3	US-09-702-705-1393	Sequence 1393, Ap
764	5	16.7	166	3	US-09-702-705-1442	Sequence 1442, Ap
c 765	5	16.7	166	3	US-09-736-457-1393	Sequence 1393, Ap
766	5	16.7	166	3	US-09-736-457-1442	Sequence 1442, Ap
c 767	5	16.7	166	3	US-09-614-124B-1393	Sequence 1393, Ap
768	5	16.7	166	3	US-09-614-124B-1442	Sequence 1442, Ap
c 769	5	16.7	166	3	US-09-671-325-1393	Sequence 1393, Ap
770	5	16.7	166	3	US-09-671-325-1442	Sequence 1442, Ap
c 771	5	16.7	166	3	US-09-658-824-1393	Sequence 1393, Ap
772	5	16.7	166	3	US-09-658-824-1442	Sequence 1442, Ap
c 773	5	16.7	166	3	US-10-017-754-1393	Sequence 1393, Ap
774	5	16.7	166	3	US-10-017-754-1442	Sequence 1442, Ap
c 775	5	16.7	166	3	US-09-651-563-1393	Sequence 1393, Ap
776	5	16.7	166	3	US-09-651-563-1442	Sequence 1442, Ap
777	5	16.7	168	3	US-09-513-999C-30218	Sequence 30218, A
778	5	16.7	170	3	US-09-270-767-25856	Sequence 25856, A
779	5	16.7	172	3	US-09-513-999C-10185	Sequence 10185, A
c 780	5	16.7	176	3	US-09-513-999C-21005	Sequence 21005, A
c 781	5	16.7	179	3	US-09-513-999C-33110	Sequence 33110, A
782	5	16.7	180	3	US-09-419-212-1	Sequence 1, Appli
c 783	5	16.7	182	3	US-09-513-999C-14148	Sequence 14148, A
784	5	16.7	183	3	US-09-071-035-199	Sequence 199, App
785	5	16.7	183	3	US-09-134-000C-405	Sequence 405, App
c 786	5	16.7	183	3	US-09-540-236-1805	Sequence 1805, Ap
787	5	16.7	183	3	US-10-206-576-199	Sequence 199, App
788	5	16.7	185	2	US-08-090-523-33	Sequence 33, Appl
789	5	16.7	185	2	US-08-398-627-33	Sequence 33, Appl
790	5	16.7	185	3	US-08-399-023-33	Sequence 33, Appl
791	5	16.7	186	3	US-09-328-352-176	Sequence 176, App
c 792	5	16.7	189	3	US-09-248-796A-12217	Sequence 12217, A
793	5	16.7	189	3	US-09-513-999C-31929	Sequence 31929, A
794	5	16.7	190	3	US-09-270-767-25512	Sequence 25512, A
c 795	5	16.7	192	3	US-09-322-478-15	Sequence 15, Appl
c 796	5	16.7	192	3	US-09-540-236-666	Sequence 666, App
c 797	5	16.7	192	3	US-09-586-106D-15	Sequence 15, Appl
c 798	5	16.7	192	3	US-09-513-999C-14202	Sequence 14202, A
c 799	5	16.7	192	3	US-10-799-870-15	Sequence 15, Appl
c 800	5	16.7	195	3	US-09-583-110-916	Sequence 916, App
801	5	16.7	195	3	US-09-248-796A-13637	Sequence 13637, A
802	5	16.7	196	3	US-09-702-705-125	Sequence 125, App
803	5	16.7	196	3	US-09-736-457-125	Sequence 125, App
804	5	16.7	196	3	US-09-614-124B-125	Sequence 125, App
805	5	16.7	196	3	US-09-671-325-125	Sequence 125, App
806	5	16.7	196	3	US-09-589-184-125	Sequence 125, App
807	5	16.7	196	3	US-09-658-824-125	Sequence 125, App
808	5	16.7	196	3	US-09-513-999C-25953	Sequence 25953, A
809	5	16.7	196	3	US-10-017-754-125	Sequence 125, App
810	5	16.7	196	3	US-09-651-563-125	Sequence 125, App
811	5	16.7	196	3	US-09-519-642-125	Sequence 125, App
c 812	5	16.7	197	3	US-09-513-999C-34949	Sequence 34949, A

813	5	16.7	198	3	US-09-248-796A-14011	Sequence 14011, A
c 814	5	16.7	198	3	US-09-107-433-1752	Sequence 1752, Ap
815	5	16.7	201	3	US-09-513-999C-24685	Sequence 24685, A
816	5	16.7	201	3	US-09-513-999C-24690	Sequence 24690, A
817	5	16.7	203	3	US-09-513-999C-23089	Sequence 23089, A
c 818	5	16.7	204	2	US-08-507-431-40	Sequence 40, Appl
c 819	5	16.7	204	2	US-08-902-655A-40	Sequence 40, Appl
c 820	5	16.7	204	3	US-09-116-622-40	Sequence 40, Appl
c 821	5	16.7	204	3	US-09-219-277-40	Sequence 40, Appl
c 822	5	16.7	204	3	US-09-599-661-40	Sequence 40, Appl
c 823	5	16.7	204	3	US-09-248-796A-7921	Sequence 7921, Ap
824	5	16.7	204	3	US-09-248-796A-12714	Sequence 12714, A
825	5	16.7	204	3	US-09-513-999C-16727	Sequence 16727, A
c 826	5	16.7	206	3	US-09-513-999C-11446	Sequence 11446, A
827	5	16.7	207	3	US-09-476-124-8	Sequence 8, Appli
c 828	5	16.7	208	2	US-08-090-523-36	Sequence 36, Appl
c 829	5	16.7	208	2	US-08-398-627-36	Sequence 36, Appl
830	5	16.7	208	3	US-09-476-124-43	Sequence 43, Appl
831	5	16.7	208	3	US-09-270-542-106	Sequence 106, App
c 832	5	16.7	208	3	US-08-399-023-36	Sequence 36, Appl
c 833	5	16.7	213	3	US-09-248-796A-6105	Sequence 6105, Ap
c 834	5	16.7	216	3	US-09-107-532A-729	Sequence 729, App
835	5	16.7	216	3	US-09-583-110-2496	Sequence 2496, Ap
836	5	16.7	216	3	US-09-248-796A-7236	Sequence 7236, Ap
837	5	16.7	216	3	US-09-248-796A-9258	Sequence 9258, Ap
838	5	16.7	218	3	US-09-817-318-6	Sequence 6, Appli
839	5	16.7	219	3	US-09-248-796A-8757	Sequence 8757, Ap
840	5	16.7	220	3	US-09-270-767-1817	Sequence 1817, Ap
841	5	16.7	220	3	US-09-270-767-17099	Sequence 17099, A
c 842	5	16.7	221	3	US-09-313-294A-6429	Sequence 6429, Ap
c 843	5	16.7	221	3	US-09-513-999C-29252	Sequence 29252, A
844	5	16.7	222	3	US-09-313-294A-6937	Sequence 6937, Ap
c 845	5	16.7	225	3	US-09-328-352-2567	Sequence 2567, Ap
c 846	5	16.7	225	3	US-09-583-110-586	Sequence 586, App
c 847	5	16.7	225	3	US-09-513-999C-21210	Sequence 21210, A
c 848	5	16.7	228	3	US-09-016-434-567	Sequence 567, App
c 849	5	16.7	228	3	US-09-248-796A-8144	Sequence 8144, Ap
850	5	16.7	231	3	US-09-313-294A-1381	Sequence 1381, Ap
851	5	16.7	231	3	US-09-248-796A-12308	Sequence 12308, A
c 852	5	16.7	232	3	US-09-513-999C-17993	Sequence 17993, A
853	5	16.7	234	3	US-09-513-999C-29712	Sequence 29712, A
854	5	16.7	234	3	US-09-107-433-858	Sequence 858, App
855	5	16.7	235	3	US-09-513-999C-23275	Sequence 23275, A
856	5	16.7	236	3	US-09-513-999C-34417	Sequence 34417, A
c 857	5	16.7	236	3	US-09-092-297A-2	Sequence 2, Appli
c 858	5	16.7	240	3	US-09-016-434-96	Sequence 96, Appl
c 859	5	16.7	245	3	US-09-270-767-7375	Sequence 7375, Ap
c 860	5	16.7	245	3	US-09-270-767-22657	Sequence 22657, A
861	5	16.7	247	3	US-09-513-999C-22956	Sequence 22956, A
c 862	5	16.7	249	3	US-09-580-497B-45	Sequence 45, Appl
c 863	5	16.7	249	3	US-09-328-352-3062	Sequence 3062, Ap
c 864	5	16.7	249	3	US-09-489-039A-3570	Sequence 3570, Ap
c 865	5	16.7	249	3	US-09-248-796A-3368	Sequence 3368, Ap
866	5	16.7	249	3	US-09-107-433-1683	Sequence 1683, Ap
c 867	5	16.7	251	3	US-09-313-294A-567	Sequence 567, App
c 868	5	16.7	252	3	US-09-621-976-10238	Sequence 10238, A
c 869	5	16.7	252	3	US-09-513-999C-21400	Sequence 21400, A
c 870	5	16.7	252	3	US-10-197-220-51	Sequence 51, Appl
c 871	5	16.7	253	3	US-09-621-976-17794	Sequence 17794, A
872	5	16.7	254	3	US-09-702-705-611	Sequence 611, App
873	5	16.7	254	3	US-09-736-457-611	Sequence 611, App
874	5	16.7	254	3	US-09-614-124B-611	Sequence 611, App
875	5	16.7	254	3	US-09-671-325-611	Sequence 611, App
876	5	16.7	254	3	US-09-589-184-611	Sequence 611, App
877	5	16.7	254	3	US-09-658-824-611	Sequence 611, App
878	5	16.7	254	3	US-09-513-999C-26627	Sequence 26627, A
879	5	16.7	254	3	US-10-017-754-611	Sequence 611, App
880	5	16.7	254	3	US-09-651-563-611	Sequence 611, App
881	5	16.7	254	3	US-09-519-642-611	Sequence 611, App
882	5	16.7	255	3	US-09-134-001C-540	Sequence 540, App
c 883	5	16.7	255	3	US-09-252-991A-12226	Sequence 12226, A
c 884	5	16.7	255	3	US-09-248-796A-10561	Sequence 10561, A
c 885	5	16.7	256	3	US-10-116-993A-16	Sequence 16, Appl
886	5	16.7	257	3	US-09-513-999C-18136	Sequence 18136, A
887	5	16.7	258	3	US-09-583-110-762	Sequence 762, App
888	5	16.7	261	3	US-09-328-352-3213	Sequence 3213, Ap
889	5	16.7	261	3	US-09-248-796A-13338	Sequence 13338, A
890	5	16.7	261	3	US-09-902-540-4469	Sequence 4469, Ap
891	5	16.7	262	3	US-09-513-999C-21437	Sequence 21437, A
c 892	5	16.7	264	3	US-09-134-001C-856	Sequence 856, App
893	5	16.7	264	3	US-09-328-352-1619	Sequence 1619, Ap
894	5	16.7	264	3	US-09-248-796A-13396	Sequence 13396, A
c 895	5	16.7	264	3	US-09-513-999C-8870	Sequence 8870, Ap
c 896	5	16.7	264	3	US-09-513-999C-8914	Sequence 8914, Ap
897	5	16.7	267	3	US-09-313-294A-2513	Sequence 2513, Ap
c 898	5	16.7	267	3	US-09-328-352-1284	Sequence 1284, Ap
899	5	16.7	268	3	US-09-313-294A-3597	Sequence 3597, Ap
c 900	5	16.7	269	3	US-09-313-294A-214	Sequence 214, App
901	5	16.7	270	3	US-09-404-879A-130	Sequence 130, App
902	5	16.7	270	3	US-09-338-933-130	Sequence 130, App
903	5	16.7	270	3	US-09-215-681-130	Sequence 130, App
c 904	5	16.7	270	3	US-09-107-532A-27	Sequence 27, Appl
905	5	16.7	270	3	US-09-216-003A-130	Sequence 130, App
906	5	16.7	270	3	US-09-667-857-130	Sequence 130, App
c 907	5	16.7	270	3	US-09-513-999C-23673	Sequence 23673, A
c 908	5	16.7	270	3	US-09-513-999C-31737	Sequence 31737, A
909	5	16.7	270	3	US-10-198-053-130	Sequence 130, App
910	5	16.7	270	3	US-09-827-271-130	Sequence 130, App
911	5	16.7	271	3	US-09-973-278-715	Sequence 715, App
912	5	16.7	271	3	US-09-973-278-717	Sequence 717, App
913	5	16.7	271	3	US-09-973-278-720	Sequence 720, App
914	5	16.7	272	2	US-08-454-557C-100	Sequence 100, App
915	5	16.7	272	2	US-08-340-426D-100	Sequence 100, App
916	5	16.7	272	2	US-08-450-673C-100	Sequence 100, App
917	5	16.7	272	3	US-09-313-294A-1947	Sequence 1947, Ap
c 918	5	16.7	272	3	US-09-270-767-25638	Sequence 25638, A
919	5	16.7	272	6	PCT-US95-17111A-100	Sequence 100, App
920	5	16.7	275	3	US-09-313-294A-855	Sequence 855, App
921	5	16.7	275	3	US-09-513-999C-28408	Sequence 28408, A
c 922	5	16.7	276	3	US-09-313-294A-4549	Sequence 4549, Ap
c 923	5	16.7	277	3	US-09-621-976-2134	Sequence 2134, Ap
c 924	5	16.7	277	3	US-09-513-999C-12303	Sequence 12303, A
c 925	5	16.7	277	3	US-09-513-999C-26407	Sequence 26407, A
926	5	16.7	279	3	US-09-313-294A-24	Sequence 24, Appl
c 927	5	16.7	279	3	US-09-107-532A-487	Sequence 487, App
928	5	16.7	280	3	US-09-313-294A-3955	Sequence 3955, Ap
929	5	16.7	280	3	US-09-313-294A-5278	Sequence 5278, Ap
c 930	5	16.7	281	3	US-09-313-294A-4243	Sequence 4243, Ap
c 931	5	16.7	282	3	US-09-313-294A-2197	Sequence 2197, Ap
c 932	5	16.7	282	3	US-09-313-294A-5764	Sequence 5764, Ap
933	5	16.7	282	3	US-09-270-767-30954	Sequence 30954, A
c 934	5	16.7	282	3	US-09-248-796A-7811	Sequence 7811, Ap
935	5	16.7	282	3	US-09-248-796A-9539	Sequence 9539, Ap
936	5	16.7	285	3	US-09-313-294A-92	Sequence 92, Appl
937	5	16.7	285	3	US-09-313-294A-1150	Sequence 1150, Ap
938	5	16.7	285	3	US-09-252-991A-6909	Sequence 6909, Ap
c 939	5	16.7	286	3	US-09-157-177-108	Sequence 108, App
c 940	5	16.7	286	3	US-09-541-210-108	Sequence 108, App
941	5	16.7	286	3	US-09-513-999C-32480	Sequence 32480, A
c 942	5	16.7	287	3	US-09-513-999C-36246	Sequence 36246, A
943	5	16.7	288	3	US-09-270-767-8293	Sequence 8293, Ap
944	5	16.7	288	3	US-09-270-767-23575	Sequence 23575, A
945	5	16.7	288	3	US-09-513-999C-11082	Sequence 11082, A
c 946	5	16.7	293	3	US-09-313-294A-7280	Sequence 7280, Ap
947	5	16.7	294	3	US-09-489-039A-2368	Sequence 2368, Ap
948	5	16.7	296	3	US-09-313-294A-1348	Sequence 1348, Ap
c 949	5	16.7	297	2	US-08-894-526-57	Sequence 57, Appl
c 950	5	16.7	297	3	US-09-313-294A-5954	Sequence 5954, Ap
c 951	5	16.7	297	3	US-09-313-294A-6878	Sequence 6878, Ap
952	5	16.7	297	3	US-09-583-110-917	Sequence 917, App
c 953	5	16.7	297	3	US-09-248-796A-510	Sequence 510, App
c 954	5	16.7	297	3	US-09-513-999C-27349	Sequence 27349, A
955	5	16.7	300	3	US-09-252-991A-4211	Sequence 4211, Ap
956	5	16.7	300	3	US-09-583-110-1664	Sequence 1664, Ap
957	5	16.7	300	3	US-09-248-796A-5683	Sequence 5683, Ap
958	5	16.7	300	3	US-09-513-999C-31099	Sequence 31099, A

959	5	16.7	300	3	US-09-107-433-235	Sequence 235, App
c 960	5	16.7	301	3	US-09-439-313-281	Sequence 281, App
c 961	5	16.7	301	3	US-09-352-616A-281	Sequence 281, App
c 962	5	16.7	301	3	US-09-232-149A-281	Sequence 281, App
c 963	5	16.7	301	3	US-09-159-812-281	Sequence 281, App
c 964	5	16.7	301	3	US-09-636-215-281	Sequence 281, App
c 965	5	16.7	301	3	US-09-685-166A-281	Sequence 281, App
c 966	5	16.7	301	3	US-09-688-489-281	Sequence 281, App
c 967	5	16.7	301	3	US-09-679-426-281	Sequence 281, App
c 968	5	16.7	301	3	US-09-513-999C-13202	Sequence 13202, A
c 969	5	16.7	301	3	US-09-759-143-281	Sequence 281, App
c 970	5	16.7	301	3	US-09-651-236-281	Sequence 281, App
c 971	5	16.7	301	3	US-09-657-279-281	Sequence 281, App
c 972	5	16.7	301	3	US-10-012-896-281	Sequence 281, App
c 973	5	16.7	303	3	US-09-252-991A-7608	Sequence 7608, Ap
974	5	16.7	303	3	US-09-543-681A-641	Sequence 641, App
975	5	16.7	303	3	US-09-107-433-1184	Sequence 1184, Ap
c 976	5	16.7	304	3	US-09-270-767-4814	Sequence 4814, Ap
c 977	5	16.7	304	3	US-09-270-767-20096	Sequence 20096, A
c 978	5	16.7	306	3	US-09-313-294A-7582	Sequence 7582, Ap
979	5	16.7	306	3	US-09-543-681A-121	Sequence 121, App
c 980	5	16.7	306	3	US-09-248-796A-7701	Sequence 7701, Ap
c 981	5	16.7	307	3	US-08-956-171E-4488	Sequence 4488, Ap
c 982	5	16.7	307	3	US-08-781-986A-4488	Sequence 4488, Ap
c 983	5	16.7	307	3	US-09-513-999C-25394	Sequence 25394, A
c 984	5	16.7	308	3	US-09-533-559-3502	Sequence 3502, Ap
985	5	16.7	310	3	US-09-513-999C-16759	Sequence 16759, A
986	5	16.7	310	3	US-09-640-211A-141	Sequence 141, App
987	5	16.7	310	3	US-09-533-559-3393	Sequence 3393, Ap
988	5	16.7	311	3	US-09-313-294A-3900	Sequence 3900, Ap
c 989	5	16.7	315	3	US-09-543-681A-1317	Sequence 1317, Ap
990	5	16.7	315	3	US-09-710-279-1725	Sequence 1725, Ap
991	5	16.7	315	3	US-09-513-999C-26968	Sequence 26968, A
992	5	16.7	315	3	US-09-640-211A-1511	Sequence 1511, Ap
c 993	5	16.7	316	3	US-09-513-999C-3596	Sequence 3596, Ap
994	5	16.7	318	3	US-08-444-818-5	Sequence 5, Appli
995	5	16.7	318	3	US-09-252-991A-13823	Sequence 13823, A
c 996	5	16.7	318	3	US-09-621-976-12577	Sequence 12577, A
c 997	5	16.7	318	3	US-09-248-796A-10481	Sequence 10481, A
998	5	16.7	318	3	US-09-513-999C-2959	Sequence 2959, Ap
999	5	16.7	319	3	US-09-328-111-38	Sequence 38, Appl
c1000	5	16.7	321	3	US-09-107-532A-2069	Sequence 2069, Ap

ALIGNMENTS

```
RESULT 1
US-09-445-160B-5
; Sequence 5, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 5
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;  PUBLICATION INFORMATION:
US-09-445-160B-5

Alignment Scores:
Pred. No.:              5.06e-17      Length:          65
Score:                  21.00         Matches:         21
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            70.0%         Indels:          0
DB:                     3             Gaps:            0

US-10-758-902-1 (1-30) x US-09-445-160B-5 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 2
US-09-445-160B-8
; Sequence 8, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;  PUBLICATION INFORMATION:
US-09-445-160B-8

Alignment Scores:
Pred. No.:              5.22e-08      Length:          363
Score:                  14.00         Matches:         14
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            46.7%         Indels:          0
DB:                     3             Gaps:            0

US-10-758-902-1 (1-30) x US-09-445-160B-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 3
US-09-445-160B-3
; Sequence 3, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
```

; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Bougainvillea spectrabilis
; NAME/KEY:
; LOCATION: 3, 9, 21
; OTHER INFORMATION: a, c, g or t
; PUBLICATION INFORMATION:
US-09-445-160B-3

Alignment Scores:

Pred. No.:	0.858	Length:	23
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-445-160B-3 (1-23)

```
Qy          9 GlyGluAlaTyrGluTyrPro 15
              |||||||||||||||||||
Db          1 GGNGARGCNTAYGARTAYCCN 21
```

RESULT 4
US-09-445-160B-4/c
; Sequence 4, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenza
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
; FILE REFERENCE: Stirpe
; CURRENT APPLICATION NUMBER: US/09/445,160B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/NL98/00336
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 4
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Bougainvillea spectrabilis
; NAME/KEY:
; LOCATION: 3, 6, 12, 15
; OTHER INFORMATION: a, c, g or t
; PUBLICATION INFORMATION:
US-09-445-160B-4

Alignment Scores:

Pred. No.:	0.858	Length:	23
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-445-160B-4 (1-23)

```
Qy         23 AsnGluLeuAlaLysGlyThr 29
              |||||||||||||||||||
Db         23 AAYGARCTNGCNAARGGNACN 3
```

RESULT 5
US-09-445-160B-6
; Sequence 6, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenza
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
; FILE REFERENCE: Stirpe
; CURRENT APPLICATION NUMBER: US/09/445,160B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/NL98/00336
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Bougainvillea spectrabilis
; PUBLICATION INFORMATION:
US-09-445-160B-6

Alignment Scores:

Pred. No.:	0.927	Length:	25
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-445-160B-6 (1-25)

```
Qy         17 PheIleGlnAspLeuArgAsn 23
              |||||||||||||||||||
Db          3 TTTATACAAGATTTGCGCAAC 23
```

RESULT 6
US-09-060-756-98
; Sequence 98, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-060-756-98

Alignment Scores:

Pred. No.:	13.1	Length:	439
Score:	7.00	Matches:	7

```
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            23.3%           Indels:        0
DB:                     3               Gaps:          0

US-10-758-902-1 (1-30) x US-09-060-756-98 (1-439)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              ||||||||||||||||||||||
Db        364 CAGGATCTCAGAAACGAGCTG 384

RESULT 7
US-09-670-314-98
; Sequence 98, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
;  APPLICANT: Cole, Stewart
;  APPLICANT:  Buchrieser-Brosch, Roland
;  APPLICANT:  Gordon, Stephen
;  APPLICANT:  Billault, Alain
;  TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;  TITLE OF INVENTION:  THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;  TITLE OF INVENTION:  LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;  FILE REFERENCE: 3495-0169
;  CURRENT APPLICATION NUMBER: US/09/670,314
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 09/060,756
;  PRIOR FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 743
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
;   LENGTH: 439
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-670-314-98

Alignment Scores:
Pred. No.:              13.1            Length:        439
Score:                  7.00            Matches:       7
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            23.3%           Indels:        0
DB:                     3               Gaps:          0

US-10-758-902-1 (1-30) x US-09-670-314-98 (1-439)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              ||||||||||||||||||||||
Db        364 CAGGATCTCAGAAACGAGCTG 384

RESULT 8
US-09-949-016-124164/c
; Sequence 124164, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124164
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-124164

Alignment Scores:
Pred. No.:              17.5            Length:        601
Score:                  7.00            Matches:       7
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            23.3%           Indels:        0
DB:                     3               Gaps:          0

US-10-758-902-1 (1-30) x US-09-949-016-124164 (1-601)

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||||||||||||||
Db        289 CTGAGAAACGAGCTGGCCAAA 269

RESULT 9
US-09-949-016-124165/c
; Sequence 124165, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124165
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-124165

Alignment Scores:
Pred. No.:              17.5            Length:        601
Score:                  7.00            Matches:       7
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            23.3%           Indels:        0
DB:                     3               Gaps:          0

US-10-758-902-1 (1-30) x US-09-949-016-124165 (1-601)

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||||||||||||||
Db        494 CTGAGAAACGAGCTGGCCAAA 474

RESULT 10
US-09-949-016-146880
; Sequence 146880, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 146880
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-146880

Alignment Scores:
Pred. No.:                17.5          Length:         601
Score:                    7.00          Matches:        7
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              23.3%         Indels:         0
DB:                       3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-146880 (1-601)

Qy          18 IleGlnAspLeuArgAsnGlu 24
               ||||||||||||||||||||
Db         384 ATACAGGATCTAAGGAATGAG 404

RESULT 11
US-09-949-016-148868
; Sequence 148868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148868
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-148868

Alignment Scores:
Pred. No.:                17.5          Length:         601
Score:                    7.00          Matches:        7
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              23.3%         Indels:         0
DB:                       3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-148868 (1-601)

Qy          15 ProThrPheIleGlnAspLeu 21
               |||||||||||||||||||||
Db         190 CCAACCTTCATCCAGGATCTG 210

RESULT 12
US-09-134-000C-5
; Sequence 5, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 651
;   TYPE: DNA
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-5

Alignment Scores:
Pred. No.:                18.9          Length:         651
Score:                    7.00          Matches:        7
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              23.3%         Indels:         0
DB:                       3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-134-000C-5 (1-651)

Qy          24 GluLeuAlaLysGlyThrPro 30
               ||||||||||||||||||||||
Db         496 GAATTAGCAAAAGGTACGCCG 516

RESULT 13
US-09-831-683B-13
; Sequence 13, Application US/09831683B
; Patent No. 6891083
; GENERAL INFORMATION:
;  APPLICANT: E. I. du Pont de Nemours and Company
;  TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetases
;  FILE REFERENCE: BB1270
;  CURRENT APPLICATION NUMBER: US/09/831,683B
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/107,789
;  PRIOR FILING DATE: 1998-11-10
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
;   LENGTH: 731
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-831-683B-13

Alignment Scores:
Pred. No.:                21            Length:         731
Score:                    7.00          Matches:        7
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              23.3%         Indels:         0
DB:                       3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-831-683B-13 (1-731)

Qy          24 GluLeuAlaLysGlyThrPro 30
               ||||||||||||||||||||||
Db         582 GAGCTAGCAAAAGGAACTCCT 602

RESULT 14
US-09-949-016-2364/c
; Sequence 2364, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
```

```
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2364
;   LENGTH: 1414
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2364

Alignment Scores:
Pred. No.:              38.6          Length:         1414
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.3%         Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-2364 (1-1414)

Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db        858 AGTTTCAATCTGGGTGAGGCC 838

RESULT 15
US-09-018-760-3/c
; Sequence 3, Application US/09018760
; Patent No. 5981249
;  GENERAL INFORMATION:
;    APPLICANT:  Shi, Qinwei
;    APPLICANT:  Tobias, Rowel
;    TITLE OF INVENTION:  A SINGLE CHAIN CREATINE KINASE MB
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue, 4th Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/018,760
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1112-1-050
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2343 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
US-09-018-760-3

Alignment Scores:
Pred. No.:              61.6          Length:         2343
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.3%         Indels:         0
DB:                     2             Gaps:           0

US-10-758-902-1 (1-30) x US-09-018-760-3 (1-2343)

Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db       1983 AGTTTCAATCTGGGTGAGGCC 1963

RESULT 16
US-08-811-682-18
; Sequence 18, Application US/08811682
; Patent No. 6331616
;  GENERAL INFORMATION:
;    APPLICANT:  Tompkins, Wayne A.F.
;    APPLICANT:  Tompkins, Mary B.
;    APPLICANT:  Yang, Joo-Sung
;    TITLE OF INVENTION:  Feline Immunodeficiency Virus Clone
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson
;      STREET:  PO Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 6331616th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/811,682
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Virginia C.
;      REGISTRATION NUMBER:  37,092
;      REFERENCE/DOCKET NUMBER:  5051-332
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2556 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-811-682-18

Alignment Scores:
Pred. No.:              66.8          Length:         2556
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.3%         Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-1 (1-30) x US-08-811-682-18 (1-2556)

Qy          19 GlnAspLeuArgAsnGluLeu 25
               |||||||||||||||||||||
Db         190 CAAGATTTACGGAATGAACTT 210

RESULT 17
US-09-023-655-259/c
; Sequence 259, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  259:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3016 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGNOT03
;      CLONE:  1242547
US-09-023-655-259

Alignment Scores:
Pred. No.:              77.8          Length:         3016
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.3%         Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-023-655-259 (1-3016)

Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||
Db       2449 AGTTTCAATCTGGGTGAGGCC 2429

RESULT 18
US-08-482-090-14
; Sequence 14, Application US/08482090
; Patent No. 5820869
;  GENERAL INFORMATION:
;    APPLICANT:  Wasmoen, Terri
;    APPLICANT:  Chu, Hsien-Jue
;    APPLICANT:  Chavez, Lloyd
;    TITLE OF INVENTION:  Recombinant Raccoon Pox Viruses and
;    TITLE OF INVENTION:  Their Use as an Effective Vaccine Against Feline
;    TITLE OF INVENTION:  Immunodeficiency Virus Infection
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,090
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schaffer, Robert
;      REGISTRATION NUMBER:  31,194
;      REFERENCE/DOCKET NUMBER:  0632/0B170
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)527-7700
;      TELEFAX:  (212)753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3225 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  feline immunodeficiency virus
;      INDIVIDUAL ISOLATE:  NCSU-1
;    POSITION IN GENOME:
;      MAP POSITION:  1-3225
;      UNITS:  bp
US-08-482-090-14

Alignment Scores:
Pred. No.:              82.8          Length:         3225
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.3%         Indels:         0
DB:                     2             Gaps:           0

US-10-758-902-1 (1-30) x US-08-482-090-14 (1-3225)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db        206 CAAGATTTACGGAATGAACTT 226

RESULT 19
US-08-481-700B-7
; Sequence 7, Application US/08481700B
; Patent No. 5849303
;  GENERAL INFORMATION:
;    APPLICANT:  Wasmoen, Terri
;    APPLICANT:  Chu, Hsien-Jue
;    TITLE OF INVENTION:  Recombinant Feline Immunodeficiency
;    TITLE OF INVENTION:  Vaccines Produced in Baculovirus and Their Use Agsinst
;    TITLE OF INVENTION:  Feline Immunodeficiency Virus Infection
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,700B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schaffer, Robert
```

```
;      REGISTRATION NUMBER:  31,194
;      REFERENCE/DOCKET NUMBER:  0623/0B168
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)527-7700
;      TELEFAX:  (212)753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3225 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  feline immunodeficiency virus
;      INDIVIDUAL ISOLATE:  NCSU-1
;    POSITION IN GENOME:
;      MAP POSITION:  1-3225
;      UNITS:  bp
US-08-481-700B-7

Alignment Scores:
Pred. No.:              82.8          Length:        3225
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x US-08-481-700B-7 (1-3225)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db        206 CAAGATTTACGGAATGAACTT 226

RESULT 20
US-09-007-383-14
; Sequence 14, Application US/09007383A
; Patent No. 5989562
; GENERAL INFORMATION:
;  APPLICANT: Wasmoen, Terri
;  APPLICANT: Chu, Hsien-Jue
;  APPLICANT: Chavez, Lloyd
;  TITLE OF INVENTION: Recombinant Raccoon Pox Viruses And
;  TITLE OF INVENTION: Their Use As An Effective Vaccine Against Feline
;  TITLE OF INVENTION: Immunodeficiency Virus Infection
;  FILE REFERENCE: 0632/1B170 US1
;  CURRENT APPLICATION NUMBER: US/09/007,383A
;  CURRENT FILING DATE: 1998-01-15
;  EARLIER APPLICATION NUMBER: 08/482,090
;  EARLIER FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 3225
;   TYPE: DNA
;   ORGANISM: Feline Immunodeficiency Virus
US-09-007-383-14

Alignment Scores:
Pred. No.:              82.8          Length:        3225
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x US-09-007-383-14 (1-3225)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db        206 CAAGATTTACGGAATGAACTT 226

RESULT 21
US-08-811-682-1
; Sequence 1, Application US/08811682
; Patent No. 6331616
; GENERAL INFORMATION:
;   APPLICANT:  Tompkins, Wayne A.F.
;   APPLICANT:  Tompkins, Mary B.
;   APPLICANT:  Yang, Joo-Sung
;   TITLE OF INVENTION:  Feline Immunodeficiency Virus Clone
;   NUMBER OF SEQUENCES:  33
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Bell Seltzer Park & Gibson
;     STREET:  PO Drawer 34009
;     CITY:  Charlotte
;     STATE:  No. 6331616th Carolina
;     COUNTRY:  USA
;     ZIP:  28234
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/811,682
;     FILING DATE:
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bennett, Virginia C.
;     REGISTRATION NUMBER:  37,092
;     REFERENCE/DOCKET NUMBER:  5051-332
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  919-420-2200
;     TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  9471 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  631..1980
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  6269..8824
US-08-811-682-1

Alignment Scores:
Pred. No.:              224           Length:        9471
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-08-811-682-1 (1-9471)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db       6458 CAAGATTTACGGAATGAACTT 6478

RESULT 22
US-09-949-016-15928/c
; Sequence 15928, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
```

```
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15928
;   LENGTH: 10713
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15928

Alignment Scores:
Pred. No.:                251             Length:         10713
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              23.3%           Indels:         0
DB:                       3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-15928 (1-10713)

Qy          15 ProThrPheIleGlnAspLeu 21
               |||||||||||||||||||||
Db        3110 CCAACCTTCATCCAGGATCTG 3090

RESULT 23
US-08-680-327-2/c
; Sequence 2, Application US/08680327
; Patent No. 5859321
;  GENERAL INFORMATION:
;    APPLICANT:  Staskawicz, Brian S., Oldroyd, Giles Edward,
;    APPLICANT:  Salmeron, John M., Rommens, Caius
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR PLANT
;    TITLE OF INVENTION:  PATHOGEN RESISTANCE
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/680,327
;      FILING DATE:  July 11, 1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/310,912
;      FILING DATE:  September 22, 1994
;      CLASSIFICATION:  800
;      APPLICATION NUMBER:  08/227,360
;      FILING DATE:  April 13, 1994
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Alan. E.
;      REGISTRATION NUMBER:  35,123
;      REFERENCE/DOCKET NUMBER:  5151-45038
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10968 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double stranded
;      TOPOLOGY:  linear
US-08-680-327-2

Alignment Scores:
Pred. No.:                257             Length:         10968
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              23.3%           Indels:         0
DB:                       2               Gaps:           0

US-10-758-902-1 (1-30) x US-08-680-327-2 (1-10968)

Qy          20 AspLeuArgAsnGluLeuAla 26
               ||||||||||||||||||||
Db        3775 GATCTACGAAATGAACTGGCT 3755

RESULT 24
US-09-228-246-1/c
; Sequence 1, Application US/09228246
; Patent No. 6245510
; GENERAL INFORMATION:
;  APPLICANT: Staskawicz, B. S. et al.
;  TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences:  Compositions
;  TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
;  FILE REFERENCE: 51700
;  CURRENT APPLICATION NUMBER: US/09/228,246
;  CURRENT FILING DATE: 1999-01-11
;  EARLIER APPLICATION NUMBER: 08/680,327
;  EARLIER FILING DATE: 1996-07-11
;  EARLIER APPLICATION NUMBER: 08/310,912
;  EARLIER FILING DATE: 1994-09-22
;  EARLIER APPLICATION NUMBER: 08/227,360
;  EARLIER FILING DATE: 1994-04-13
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 10968
;   TYPE: DNA
;   ORGANISM: Lycopersicon esculentum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3879)..(8186)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (8300)..(9466)
US-09-228-246-1

Alignment Scores:
Pred. No.:                257             Length:         10968
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              23.3%           Indels:         0
DB:                       3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-228-246-1 (1-10968)

Qy          20 AspLeuArgAsnGluLeuAla 26
               ||||||||||||||||||||
Db        3775 GATCTACGAAATGAACTGGCT 3755

RESULT 25
US-09-949-016-15865
; Sequence 15865, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

```
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15865
;   LENGTH: 37059
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(37059)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15865

Alignment Scores:
Pred. No.:              791             Length:         37059
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-15865 (1-37059)

Qy         18 IleGlnAspLeuArgAsnGlu 24
              ||||||||||||||||||||
Db       9755 ATACAGGATCTAAGGAATGAG 9775

RESULT 26
US-09-949-016-12140
; Sequence 12140, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12140
;   LENGTH: 68529
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(68529)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12140

Alignment Scores:
Pred. No.:              1.4e+03         Length:         68529
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-12140 (1-68529)

Qy         20 AspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||
Db      67755 GATCTTCGGAATGAATTGGCT 67775

RESULT 27
US-09-949-016-15671
; Sequence 15671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15671
;   LENGTH: 68529
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(68529)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15671

Alignment Scores:
Pred. No.:              1.4e+03         Length:         68529
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-15671 (1-68529)

Qy         20 AspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||
Db      67755 GATCTTCGGAATGAATTGGCT 67775

RESULT 28
US-09-949-016-13629/c
; Sequence 13629, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13629
;   LENGTH: 93894
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
```

```
;   LOCATION: (1)...(93894)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13629

Alignment Scores:
Pred. No.:              1.87e+03        Length:         93894
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-13629 (1-93894)

Qy         22 ArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||
Db      11341 AGGAACGAGCTTGCCAAGGGA 11321

RESULT 29
US-09-949-016-13698/c
; Sequence 13698, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13698
;   LENGTH: 110243
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(110243)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13698

Alignment Scores:
Pred. No.:              2.17e+03        Length:         110243
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-13698 (1-110243)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db      33962 AATACAGTTTCCTTCAATTTA 33942

RESULT 30
US-09-949-016-16329
; Sequence 16329, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16329
;   LENGTH: 113538
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(113538)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16329

Alignment Scores:
Pred. No.:              2.23e+03        Length:         113538
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-16329 (1-113538)

Qy         20 AspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||
Db      81499 GACCTAAGAAATGAGCTGGCC 81519

RESULT 31
US-09-949-016-15238
; Sequence 15238, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15238
;   LENGTH: 143644
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(143644)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15238

Alignment Scores:
Pred. No.:              2.77e+03        Length:         143644
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-15238 (1-143644)

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||||||||||||
Db      74270 CTGAGAAACGAGCTGGCCAAA 74290
```

RESULT 32
US-09-949-016-17394/c
; Sequence 17394, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17394
; LENGTH: 145241
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17394

Alignment Scores:

Pred. No.:	2.8e+03	Length:	145241
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-949-016-17394 (1-145241)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db      87718 TCATTCAACCTGGGAGAAGCC 87698
```

RESULT 33
US-09-949-016-17395/c
; Sequence 17395, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17395
; LENGTH: 145241
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17395

Alignment Scores:

Pred. No.:	2.8e+03	Length:	145241
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-949-016-17395 (1-145241)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db      87718 TCATTCAACCTGGGAGAAGCC 87698
```

RESULT 34
US-09-949-016-12111
; Sequence 12111, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12111
; LENGTH: 187848
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(187848)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12111

Alignment Scores:

Pred. No.:	3.55e+03	Length:	187848
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-949-016-12111 (1-187848)

```
Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||||||||||||||
Db      70474 CTGAGAAACGAGCTGGCCAAA 70494
```

RESULT 35
US-10-131-827-7466
; Sequence 7466, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7466
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Human cytomegalovirus

US-10-131-827-7466

Alignment Scores:

Pred. No.:	27.2	Length:	50
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	20.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-10-131-827-7466 (1-50)

```
Qy         18 IleGlnAspLeuArgAsn 23
              |||||||||||||||||
Db         25 ATCCAGGACCTGAGGAAC 42
```

RESULT 36
US-09-121-286-4
; Sequence 4, Application US/09121286
; Patent No. 6146848
; GENERAL INFORMATION:
; APPLICANT: WONG, Wan K
; APPLICANT: LAM, Kat H
; TITLE OF INVENTION: Bacterial Expression System
; FILE REFERENCE: M98/0273/US
; CURRENT APPLICATION NUMBER: US/09/121,286
; CURRENT FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: oligonucleotide encoding Veg cassette
US-09-121-286-4

Alignment Scores:

Pred. No.:	37.1	Length:	70
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	20.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-121-286-4 (1-70)

```
Qy          2 AsnThrValSerPheAsn 7
              |||||||||||||||||
Db          5 AACACGGTCAGTTTCAAC 22
```

RESULT 37
US-09-121-286-19
; Sequence 19, Application US/09121286
; Patent No. 6146848
; GENERAL INFORMATION:
; APPLICANT: WONG, Wan K
; APPLICANT: LAM, Kat H
; TITLE OF INVENTION: Bacterial Expression System
; FILE REFERENCE: M98/0273/US
; CURRENT APPLICATION NUMBER: US/09/121,286
; CURRENT FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-121-286-19

Alignment Scores:

Pred. No.:	37.1	Length:	70
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	20.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-121-286-19 (1-70)

```
Qy          2 AsnThrValSerPheAsn 7
              |||||||||||||||||
Db         15 AACACGGTCAGTTTCAAC 32
```

RESULT 38
US-09-513-999C-18774
; Sequence 18774, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 18774
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-18774

Alignment Scores:

Pred. No.:	48.2	Length:	93
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	20.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-513-999C-18774 (1-93)

```
Qy         22 ArgAsnGluLeuAlaLys 27
              |||||||||||||||||
Db         19 AGGAATGAGCTTGCAAAA 36
```

RESULT 39
US-08-611-757-84/c
; Sequence 84, Application US/08611757
; Patent No. 5859230
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Reyes, Gregory R.
; APPLICANT: Wages, John
; APPLICANT: Zhang-Keck, Zhen-Yang
; APPLICANT: Young, LaVonne
; TITLE OF INVENTION: No. 5859230-A/No. 5859230-B/No. 5859230-C/No. 5859230-D/No. 5
; TITLE OF INVENTION: Agents and Molecular Cloning Thereof
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/611,757
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/246,985
;      FILING DATE:  20-MAY-1994
;      APPLICATION NUMBER:  US 025,396
;      FILING DATE:  24-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/922,493
;      FILING DATE:  30-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  105 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  SCH Clone SC1-2
US-08-611-757-84

Alignment Scores:
Pred. No.:              54              Length:         105
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            20.0%           Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-1 (1-30) x US-08-611-757-84 (1-105)

Qy          8 LeuGlyGluAlaTyrGlu 13
              |||||||||||||||||
Db         80 CTTGGAGAAGCGTATGAA 63

RESULT 40
PCT-US95-05980-84/c
; Sequence 84, Application PC/TUS9505980
;  GENERAL INFORMATION:
;    APPLICANT:
;    APPLICANT:
;    TITLE OF INVENTION:  Non-A/Non-B/Non-C/Non-D/Non-E Hepatitis
;    TITLE OF INVENTION:  Agents and Molecular Cloning Thereof
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05980
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/246,986
;      FILING DATE:  20-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0201.49
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  105 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  SCH Clone SC1-2
PCT-US95-05980-84

Alignment Scores:
Pred. No.:              54              Length:         105
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            20.0%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x PCT-US95-05980-84 (1-105)

Qy          8 LeuGlyGluAlaTyrGlu 13
              |||||||||||||||||
Db         80 CTTGGAGAAGCGTATGAA 63


Search completed: February 20, 2006, 03:08:54
Job time : 86.5866 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 01:12:01 ; Search time 223.408 Seconds
(without alignments)
1110.442 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 30
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 1

Total number of hits satisfying chosen parameters: 19572471

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160840_4165/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=oligo.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05p
-USER=US10758902_@CGN_1_1_2064_@runat_17022006_160840_4165 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30	100.0	2404	10	US-11-084-080-15	Sequence 15, Appl
2	30	100.0	2404	10	US-11-084-080-19	Sequence 19, Appl
3	30	100.0	2404	10	US-11-084-080-21	Sequence 21, Appl
4	30	100.0	2404	10	US-11-084-080-23	Sequence 23, Appl
5	30	100.0	2431	10	US-11-084-080-27	Sequence 27, Appl
6	21	70.0	65	8	US-10-758-902-5	Sequence 5, Appli
7	14	46.7	363	8	US-10-758-902-8	Sequence 8, Appli
8	8	26.7	416	4	US-09-925-065A-47024	Sequence 47024, A
9	8	26.7	622	4	US-09-925-065A-787599	Sequence 787599,
c 10	8	26.7	2443	4	US-09-925-065A-694362	Sequence 694362,
11	8	26.7	2772	6	US-10-252-157-398	Sequence 398, App
c 12	8	26.7	12648	7	US-10-741-601-5652	Sequence 5652, Ap
13	8	26.7	31657	7	US-10-741-601-5690	Sequence 5690, Ap
14	8	26.7	41309	7	US-10-741-601-5771	Sequence 5771, Ap
c 15	7	23.3	23	8	US-10-758-902-3	Sequence 3, Appli
16	7	23.3	25	8	US-10-758-902-6	Sequence 6, Appli
c 17	7	23.3	25	10	US-11-036-317-212714	Sequence 212714,
c 18	7	23.3	25	10	US-11-036-317-329781	Sequence 329781,
c 19	7	23.3	25	10	US-11-036-317-381661	Sequence 381661,
c 20	7	23.3	25	10	US-11-036-317-484022	Sequence 484022,
21	7	23.3	36	10	US-11-084-080-125	Sequence 125, App
c 22	7	23.3	254	7	US-10-424-599-18718	Sequence 18718, A
c 23	7	23.3	431	8	US-10-357-930-18350	Sequence 18350, A
24	7	23.3	439	6	US-10-259-678-98	Sequence 98, Appl
c 25	7	23.3	471	3	US-09-732-627A-4376	Sequence 4376, Ap
c 26	7	23.3	472	3	US-09-764-869-187	Sequence 187, App
c 27	7	23.3	472	5	US-10-091-504-187	Sequence 187, App
c 28	7	23.3	472	6	US-10-227-577-187	Sequence 187, App
c 29	7	23.3	498	8	US-10-357-930-48164	Sequence 48164, A
30	7	23.3	524	4	US-09-925-065A-455365	Sequence 455365,
31	7	23.3	548	4	US-09-925-065A-810826	Sequence 810826,
32	7	23.3	551	4	US-09-925-065A-123248	Sequence 123248,
c 33	7	23.3	555	3	US-09-918-995-26126	Sequence 26126, A
c 34	7	23.3	561	4	US-09-925-065A-760512	Sequence 760512,
35	7	23.3	565	4	US-09-925-065A-761519	Sequence 761519,
36	7	23.3	566	4	US-09-925-065A-771199	Sequence 771199,
37	7	23.3	571	4	US-09-925-065A-762385	Sequence 762385,
38	7	23.3	588	3	US-09-974-300-4903	Sequence 4903, Ap
39	7	23.3	588	8	US-10-357-930-55024	Sequence 55024, A
c 40	7	23.3	600	9	US-10-972-079-881	Sequence 881, App
c 41	7	23.3	600	9	US-10-972-079-882	Sequence 882, App
42	7	23.3	600	9	US-10-972-079-21980	Sequence 21980, A
43	7	23.3	617	4	US-09-925-065A-305608	Sequence 305608,
44	7	23.3	617	4	US-09-925-065A-305609	Sequence 305609,
45	7	23.3	688	5	US-10-027-632-147761	Sequence 147761,
46	7	23.3	688	6	US-10-027-632-147761	Sequence 147761,
47	7	23.3	693	3	US-09-974-300-4910	Sequence 4910, Ap
c 48	7	23.3	726	7	US-10-424-599-95499	Sequence 95499, A
49	7	23.3	755	5	US-10-027-632-18840	Sequence 18840, A
50	7	23.3	755	6	US-10-027-632-18840	Sequence 18840, A
c 51	7	23.3	1143	6	US-10-412-222-4	Sequence 4, Appli
c 52	7	23.3	1143	6	US-10-412-233-4	Sequence 4, Appli
c 53	7	23.3	1167	7	US-10-282-122A-36977	Sequence 36977, A
c 54	7	23.3	1360	3	US-09-880-107-2269	Sequence 2269, Ap
c 55	7	23.3	1360	3	US-09-873-367C-707	Sequence 707, App
c 56	7	23.3	1360	9	US-10-843-641A-707	Sequence 707, App
57	7	23.3	1390	6	US-10-264-049-261	Sequence 261, App
c 58	7	23.3	1431	7	US-10-764-425-7	Sequence 7, Appli
c 59	7	23.3	1431	9	US-10-887-553A-184	Sequence 184, App
c 60	7	23.3	1431	10	US-11-019-829-5	Sequence 5, Appli
c 61	7	23.3	1432	6	US-10-133-937-3	Sequence 3, Appli
c 62	7	23.3	1432	6	US-10-159-563-3	Sequence 3, Appli
c 63	7	23.3	1432	6	US-10-159-563-191	Sequence 191, App
c 64	7	23.3	1432	7	US-10-755-889-271	Sequence 271, App
c 65	7	23.3	1539	7	US-10-282-122A-39529	Sequence 39529, A
66	7	23.3	1554	7	US-10-398-221-3281	Sequence 3281, Ap
c 67	7	23.3	1659	3	US-09-815-242-9963	Sequence 9963, Ap
68	7	23.3	1818	6	US-10-369-493-42594	Sequence 42594, A
c 69	7	23.3	2371	7	US-10-437-963-58240	Sequence 58240, A
70	7	23.3	2493	7	US-10-437-963-95638	Sequence 95638, A
71	7	23.3	2523	7	US-10-437-963-95641	Sequence 95641, A
72	7	23.3	2645	4	US-09-925-065A-89593	Sequence 89593, A
c 73	7	23.3	3016	7	US-10-641-643-259	Sequence 259, App
74	7	23.3	4962	10	US-11-097-143-25819	Sequence 25819, A
75	7	23.3	4995	10	US-11-097-143-25816	Sequence 25816, A
76	7	23.3	5862	3	US-09-764-891-7363	Sequence 7363, Ap
c 77	7	23.3	7893	3	US-09-070-927A-228	Sequence 228, App
78	7	23.3	9804	10	US-11-097-143-25813	Sequence 25813, A
c 79	7	23.3	10476	3	US-09-964-824A-98	Sequence 98, Appl
c 80	7	23.3	10476	3	US-09-964-824A-552	Sequence 552, App

c	81	7	23.3	10476	9	US-10-843-641A-5401	Sequence 5401, Ap
c	82	7	23.3	10476	9	US-10-843-641A-5855	Sequence 5855, Ap
c	83	7	23.3	10476	9	US-10-756-149-839	Sequence 839, App
	84	7	23.3	32249	3	US-09-764-891-7364	Sequence 7364, Ap
c	85	7	23.3	96597	3	US-09-997-722-73	Sequence 73, Appl
	86	7	23.3	383432	9	US-10-737-082-34	Sequence 34, Appl
	87	7	23.3	383432	9	US-10-765-790-34	Sequence 34, Appl
	88	6	20.0	20	8	US-10-758-902-4	Sequence 4, Appli
	89	6	20.0	22	9	US-10-708-204-2734	Sequence 2734, Ap
	90	6	20.0	25	7	US-10-719-956-517116	Sequence 517116,
	91	6	20.0	25	7	US-10-719-956-611354	Sequence 611354,
	92	6	20.0	25	8	US-10-719-900-79080	Sequence 79080, A
	93	6	20.0	25	8	US-10-719-900-324355	Sequence 324355,
	94	6	20.0	25	8	US-10-719-900-758066	Sequence 758066,
c	95	6	20.0	25	8	US-10-719-900-820711	Sequence 820711,
c	96	6	20.0	25	9	US-10-956-157-264976	Sequence 264976,
	97	6	20.0	25	10	US-11-036-317-185006	Sequence 185006,
	98	6	20.0	25	10	US-11-036-317-238501	Sequence 238501,
c	99	6	20.0	25	10	US-11-036-317-280518	Sequence 280518,
	100	6	20.0	25	10	US-11-036-317-281167	Sequence 281167,
	101	6	20.0	25	10	US-11-036-317-306590	Sequence 306590,
c	102	6	20.0	25	10	US-11-036-317-318443	Sequence 318443,
	103	6	20.0	25	10	US-11-036-317-375107	Sequence 375107,
c	104	6	20.0	25	10	US-11-036-317-392233	Sequence 392233,
	105	6	20.0	25	10	US-11-036-317-394184	Sequence 394184,
	106	6	20.0	25	10	US-11-036-317-412013	Sequence 412013,
	107	6	20.0	25	10	US-11-036-317-804998	Sequence 804998,
	108	6	20.0	25	10	US-11-036-317-807090	Sequence 807090,
c	109	6	20.0	25	10	US-11-036-317-878521	Sequence 878521,
c	110	6	20.0	25	10	US-11-036-317-948577	Sequence 948577,
	111	6	20.0	50	6	US-10-131-827-7466	Sequence 7466, Ap
c	112	6	20.0	55	6	US-10-199-957A-139	Sequence 139, App
	113	6	20.0	60	3	US-09-908-975-15504	Sequence 15504, A
	114	6	20.0	60	3	US-09-908-975-23106	Sequence 23106, A
	115	6	20.0	60	8	US-10-786-445A-23	Sequence 23, Appl
	116	6	20.0	96	6	US-10-199-957A-53	Sequence 53, Appl
	117	6	20.0	96	6	US-10-199-957A-80	Sequence 80, Appl
c	118	6	20.0	138	6	US-10-293-086-122	Sequence 122, App
	119	6	20.0	163	8	US-10-674-124A-14660	Sequence 14660, A
c	120	6	20.0	183	3	US-09-864-761-28554	Sequence 28554, A
c	121	6	20.0	196	3	US-09-924-035A-716	Sequence 716, App
	122	6	20.0	197	7	US-10-424-599-12570	Sequence 12570, A
c	123	6	20.0	201	7	US-10-741-601-25255	Sequence 25255, A
c	124	6	20.0	201	8	US-10-719-993-14171	Sequence 14171, A
	125	6	20.0	201	8	US-10-719-993-15496	Sequence 15496, A
c	126	6	20.0	201	8	US-10-741-600-19782	Sequence 19782, A
	127	6	20.0	201	8	US-10-741-600-37814	Sequence 37814, A
c	128	6	20.0	201	8	US-10-741-600-69134	Sequence 69134, A
c	129	6	20.0	207	3	US-09-783-590-7628	Sequence 7628, Ap
	130	6	20.0	210	7	US-10-282-122A-968	Sequence 968, App
c	131	6	20.0	217	7	US-10-430-201-4498	Sequence 4498, Ap
c	132	6	20.0	217	7	US-10-430-201-4499	Sequence 4499, Ap
	133	6	20.0	218	7	US-10-424-599-77160	Sequence 77160, A
	134	6	20.0	219	7	US-10-424-599-125652	Sequence 125652,
	135	6	20.0	221	8	US-10-425-115-134612	Sequence 134612,
	136	6	20.0	224	8	US-10-425-115-30048	Sequence 30048, A
	137	6	20.0	233	7	US-10-424-599-59193	Sequence 59193, A
	138	6	20.0	234	8	US-10-425-115-151187	Sequence 151187,
	139	6	20.0	242	7	US-10-424-599-11886	Sequence 11886, A
c	140	6	20.0	249	3	US-09-783-590-8082	Sequence 8082, Ap
c	141	6	20.0	251	7	US-10-242-535A-53108	Sequence 53108, A
c	142	6	20.0	251	7	US-10-085-783A-53108	Sequence 53108, A
	143	6	20.0	253	8	US-10-425-115-108237	Sequence 108237,
c	144	6	20.0	260	7	US-10-424-599-28050	Sequence 28050, A
c	145	6	20.0	261	7	US-10-242-535A-3436	Sequence 3436, Ap
c	146	6	20.0	261	7	US-10-085-783A-3436	Sequence 3436, Ap
c	147	6	20.0	262	7	US-10-424-599-113999	Sequence 113999,
	148	6	20.0	265	7	US-10-425-114-12432	Sequence 12432, A
c	149	6	20.0	268	7	US-10-424-599-89805	Sequence 89805, A
c	150	6	20.0	269	5	US-10-040-739-400	Sequence 400, App
	151	6	20.0	269	7	US-10-424-599-142147	Sequence 142147,
c	152	6	20.0	270	7	US-10-469-285-29	Sequence 29, Appl
c	153	6	20.0	272	8	US-10-425-115-125168	Sequence 125168,
c	154	6	20.0	275	7	US-10-424-599-129104	Sequence 129104,
c	155	6	20.0	277	7	US-10-424-599-7684	Sequence 7684, Ap
c	156	6	20.0	280	7	US-10-424-599-62857	Sequence 62857, A
c	157	6	20.0	285	3	US-09-294-093B-1968	Sequence 1968, Ap
c	158	6	20.0	286	3	US-09-864-761-27903	Sequence 27903, A
c	159	6	20.0	288	9	US-10-501-282-357	Sequence 357, App
	160	6	20.0	291	5	US-10-260-877-121	Sequence 121, App
c	161	6	20.0	292	7	US-10-242-535A-15558	Sequence 15558, A
c	162	6	20.0	292	7	US-10-085-783A-15558	Sequence 15558, A
c	163	6	20.0	293	6	US-10-341-961A-378	Sequence 378, App
c	164	6	20.0	300	7	US-10-242-535A-5666	Sequence 5666, Ap
c	165	6	20.0	300	7	US-10-085-783A-5666	Sequence 5666, Ap
c	166	6	20.0	302	7	US-10-767-701-17696	Sequence 17696, A
c	167	6	20.0	305	7	US-10-242-535A-18347	Sequence 18347, A
c	168	6	20.0	305	7	US-10-085-783A-18347	Sequence 18347, A
c	169	6	20.0	306	6	US-10-341-961A-98	Sequence 98, Appl
c	170	6	20.0	310	7	US-10-437-963-69652	Sequence 69652, A
	171	6	20.0	314	6	US-10-263-828-48	Sequence 48, Appl
c	172	6	20.0	319	8	US-10-425-115-183105	Sequence 183105,
	173	6	20.0	332	3	US-09-866-050A-83	Sequence 83, Appl
	174	6	20.0	332	5	US-10-152-661-83	Sequence 83, Appl
c	175	6	20.0	333	3	US-09-764-891-1393	Sequence 1393, Ap
	176	6	20.0	334	8	US-10-425-115-60704	Sequence 60704, A
	177	6	20.0	336	7	US-10-424-599-139621	Sequence 139621,
c	178	6	20.0	337	8	US-10-425-115-117253	Sequence 117253,
c	179	6	20.0	343	8	US-10-425-115-13128	Sequence 13128, A
	180	6	20.0	347	3	US-09-938-842A-3465	Sequence 3465, Ap
	181	6	20.0	347	3	US-09-938-842A-3465	Sequence 3465, Ap
	182	6	20.0	350	3	US-09-918-995-10843	Sequence 10843, A
	183	6	20.0	354	5	US-10-027-632-274374	Sequence 274374,
	184	6	20.0	354	6	US-10-027-632-274374	Sequence 274374,
	185	6	20.0	355	8	US-10-357-930-46976	Sequence 46976, A
	186	6	20.0	359	8	US-10-425-115-119151	Sequence 119151,
c	187	6	20.0	360	3	US-09-918-995-30118	Sequence 30118, A
	188	6	20.0	360	7	US-10-424-599-31487	Sequence 31487, A
	189	6	20.0	361	3	US-09-803-719-87	Sequence 87, Appl
	190	6	20.0	361	9	US-10-779-543-13357	Sequence 13357, A
	191	6	20.0	362	7	US-10-424-599-102367	Sequence 102367,
	192	6	20.0	363	8	US-10-425-115-137581	Sequence 137581,
	193	6	20.0	364	8	US-10-674-124A-1754	Sequence 1754, Ap
c	194	6	20.0	365	3	US-09-918-995-30155	Sequence 30155, A
c	195	6	20.0	367	3	US-09-864-761-20541	Sequence 20541, A
c	196	6	20.0	368	8	US-10-674-124A-8623	Sequence 8623, Ap
c	197	6	20.0	368	8	US-10-425-115-87031	Sequence 87031, A
	198	6	20.0	369	7	US-10-424-599-79409	Sequence 79409, A
c	199	6	20.0	370	7	US-10-424-599-141385	Sequence 141385,
c	200	6	20.0	372	3	US-09-983-965-3636	Sequence 3636, Ap
	201	6	20.0	374	8	US-10-674-124A-20229	Sequence 20229, A
	202	6	20.0	376	7	US-10-425-114-35754	Sequence 35754, A
c	203	6	20.0	380	4	US-09-925-065A-228927	Sequence 228927,
	204	6	20.0	384	8	US-10-357-930-17153	Sequence 17153, A
	205	6	20.0	387	5	US-10-027-632-96558	Sequence 96558, A
	206	6	20.0	387	6	US-10-027-632-96558	Sequence 96558, A
c	207	6	20.0	388	4	US-09-925-065A-247522	Sequence 247522,
	208	6	20.0	389	9	US-10-779-543-12556	Sequence 12556, A
c	209	6	20.0	390	3	US-09-738-626-124	Sequence 124, App
	210	6	20.0	390	7	US-10-437-963-46481	Sequence 46481, A
	211	6	20.0	390	7	US-10-437-963-95670	Sequence 95670, A
c	212	6	20.0	392	8	US-10-425-115-51130	Sequence 51130, A
c	213	6	20.0	394	6	US-10-007-926A-315	Sequence 315, App
	214	6	20.0	394	7	US-10-767-701-26525	Sequence 26525, A
c	215	6	20.0	395	7	US-10-424-599-137709	Sequence 137709,
c	216	6	20.0	396	8	US-10-425-115-124312	Sequence 124312,
	217	6	20.0	398	4	US-09-925-065A-124209	Sequence 124209,
	218	6	20.0	400	7	US-10-767-701-16823	Sequence 16823, A
c	219	6	20.0	402	4	US-09-925-065A-585353	Sequence 585353,
	220	6	20.0	402	9	US-10-756-149-4643	Sequence 4643, Ap
c	221	6	20.0	403	3	US-09-960-352-11738	Sequence 11738, A
c	222	6	20.0	404	3	US-09-918-995-6089	Sequence 6089, Ap
c	223	6	20.0	404	4	US-09-925-065A-379589	Sequence 379589,
	224	6	20.0	404	8	US-10-425-115-93367	Sequence 93367, A
c	225	6	20.0	405	7	US-10-424-599-98948	Sequence 98948, A
c	226	6	20.0	407	4	US-09-925-065A-607552	Sequence 607552,

	227	6	20.0	407	4	US-09-925-065A-613438	Sequence 613438,
	228	6	20.0	407	4	US-09-925-065A-613439	Sequence 613439,
c	229	6	20.0	408	5	US-10-027-632-19321	Sequence 19321, A
c	230	6	20.0	408	6	US-10-027-632-19321	Sequence 19321, A
	231	6	20.0	408	7	US-10-424-599-15634	Sequence 15634, A
c	232	6	20.0	409	8	US-10-425-115-48838	Sequence 48838, A
	233	6	20.0	410	4	US-09-925-065A-508381	Sequence 508381,
c	234	6	20.0	412	3	US-09-960-352-4655	Sequence 4655, Ap
	235	6	20.0	413	3	US-09-864-761-2007	Sequence 2007, Ap
c	236	6	20.0	413	9	US-10-972-079-21599	Sequence 21599, A
c	237	6	20.0	414	3	US-09-960-352-8959	Sequence 8959, Ap
c	238	6	20.0	414	4	US-09-925-065A-125919	Sequence 125919,
c	239	6	20.0	414	9	US-10-756-149-604	Sequence 604, App
	240	6	20.0	416	4	US-09-925-065A-912468	Sequence 912468,
c	241	6	20.0	417	3	US-09-960-352-1297	Sequence 1297, Ap
	242	6	20.0	417	5	US-10-027-632-274373	Sequence 274373,
	243	6	20.0	417	5	US-10-027-632-274375	Sequence 274375,
	244	6	20.0	417	6	US-10-027-632-274373	Sequence 274373,
	245	6	20.0	417	6	US-10-027-632-274375	Sequence 274375,
	246	6	20.0	418	8	US-10-425-115-67548	Sequence 67548, A
	247	6	20.0	419	3	US-09-864-408A-7641	Sequence 7641, Ap
	248	6	20.0	422	4	US-09-925-065A-116233	Sequence 116233,
c	249	6	20.0	423	4	US-09-925-065A-95695	Sequence 95695, A
c	250	6	20.0	423	4	US-09-925-065A-130218	Sequence 130218,
c	251	6	20.0	424	3	US-09-960-352-5610	Sequence 5610, Ap
c	252	6	20.0	424	4	US-09-925-065A-217393	Sequence 217393,
	253	6	20.0	425	7	US-10-437-963-50043	Sequence 50043, A
	254	6	20.0	426	5	US-10-027-632-181716	Sequence 181716,
	255	6	20.0	426	6	US-10-027-632-181716	Sequence 181716,
	256	6	20.0	428	8	US-10-357-930-58950	Sequence 58950, A
c	257	6	20.0	429	4	US-09-925-065A-130219	Sequence 130219,
	258	6	20.0	433	3	US-09-918-995-16601	Sequence 16601, A
	259	6	20.0	433	4	US-09-925-065A-639620	Sequence 639620,
	260	6	20.0	433	4	US-09-925-065A-639621	Sequence 639621,
c	261	6	20.0	435	5	US-10-027-632-175160	Sequence 175160,
	262	6	20.0	435	5	US-10-027-632-182885	Sequence 182885,
c	263	6	20.0	435	6	US-10-027-632-175160	Sequence 175160,
	264	6	20.0	435	6	US-10-027-632-182885	Sequence 182885,
c	265	6	20.0	439	8	US-10-674-124A-17384	Sequence 17384, A
	266	6	20.0	440	3	US-09-983-965-217	Sequence 217, App
	267	6	20.0	440	7	US-10-437-963-36129	Sequence 36129, A
c	268	6	20.0	441	3	US-09-764-891-415	Sequence 415, App
c	269	6	20.0	441	4	US-09-925-065A-142089	Sequence 142089,
c	270	6	20.0	441	5	US-10-205-428-49	Sequence 49, Appl
	271	6	20.0	442	7	US-10-425-114-14195	Sequence 14195, A
c	272	6	20.0	446	3	US-09-864-761-10909	Sequence 10909, A
	273	6	20.0	446	6	US-10-029-386-22378	Sequence 22378, A
c	274	6	20.0	447	4	US-09-925-065A-200046	Sequence 200046,
c	275	6	20.0	449	3	US-09-864-761-11272	Sequence 11272, A
c	276	6	20.0	449	4	US-09-925-065A-172316	Sequence 172316,
c	277	6	20.0	451	7	US-10-424-599-103487	Sequence 103487,
	278	6	20.0	453	7	US-10-437-963-81724	Sequence 81724, A
c	279	6	20.0	454	4	US-09-925-065A-778596	Sequence 778596,
c	280	6	20.0	454	4	US-09-925-065A-840036	Sequence 840036,
c	281	6	20.0	454	7	US-10-437-963-92218	Sequence 92218, A
c	282	6	20.0	455	7	US-10-425-114-18767	Sequence 18767, A
c	283	6	20.0	456	5	US-10-027-632-195920	Sequence 195920,
c	284	6	20.0	456	6	US-10-027-632-195920	Sequence 195920,
	285	6	20.0	457	4	US-09-925-065A-233071	Sequence 233071,
	286	6	20.0	460	4	US-09-925-065A-153845	Sequence 153845,
	287	6	20.0	460	7	US-10-424-599-113889	Sequence 113889,
c	288	6	20.0	462	4	US-09-925-065A-222562	Sequence 222562,
	289	6	20.0	462	4	US-09-925-065A-738876	Sequence 738876,
	290	6	20.0	462	9	US-10-501-282-351	Sequence 351, App
	291	6	20.0	462	9	US-10-501-282-353	Sequence 353, App
c	292	6	20.0	464	3	US-09-732-627A-3827	Sequence 3827, Ap
c	293	6	20.0	464	8	US-10-425-115-20478	Sequence 20478, A
c	294	6	20.0	465	3	US-09-864-761-3775	Sequence 3775, Ap
	295	6	20.0	465	3	US-09-864-761-10217	Sequence 10217, A
c	296	6	20.0	466	3	US-09-864-761-11279	Sequence 11279, A
	297	6	20.0	466	3	US-09-918-995-12712	Sequence 12712, A
c	298	6	20.0	466	7	US-10-424-599-28596	Sequence 28596, A
c	299	6	20.0	468	6	US-10-029-386-15076	Sequence 15076, A
c	300	6	20.0	469	5	US-10-078-770-119	Sequence 119, App
c	301	6	20.0	473	7	US-10-242-535A-40874	Sequence 40874, A
c	302	6	20.0	473	7	US-10-424-599-58909	Sequence 58909, A
c	303	6	20.0	473	7	US-10-085-783A-40874	Sequence 40874, A
	304	6	20.0	475	4	US-09-925-065A-956935	Sequence 956935,
	305	6	20.0	475	5	US-10-027-632-88147	Sequence 88147, A
	306	6	20.0	475	5	US-10-027-632-88148	Sequence 88148, A
	307	6	20.0	475	5	US-10-027-632-303458	Sequence 303458,
	308	6	20.0	475	5	US-10-027-632-303459	Sequence 303459,
	309	6	20.0	475	6	US-10-027-632-88147	Sequence 88147, A
	310	6	20.0	475	6	US-10-027-632-88148	Sequence 88148, A
	311	6	20.0	475	6	US-10-027-632-303458	Sequence 303458,
	312	6	20.0	475	6	US-10-027-632-303459	Sequence 303459,
	313	6	20.0	475	7	US-10-430-201-4282	Sequence 4282, Ap
	314	6	20.0	475	7	US-10-430-201-4283	Sequence 4283, Ap
c	315	6	20.0	476	9	US-10-972-079-26828	Sequence 26828, A
c	316	6	20.0	479	8	US-10-425-115-160203	Sequence 160203,
c	317	6	20.0	480	4	US-09-925-065A-440878	Sequence 440878,
c	318	6	20.0	480	5	US-10-027-632-46365	Sequence 46365, A
c	319	6	20.0	480	6	US-10-027-632-46365	Sequence 46365, A
	320	6	20.0	480	7	US-10-424-599-128964	Sequence 128964,
	321	6	20.0	481	4	US-09-925-065A-337499	Sequence 337499,
c	322	6	20.0	481	8	US-10-425-115-157854	Sequence 157854,
c	323	6	20.0	482	4	US-09-925-065A-442678	Sequence 442678,
c	324	6	20.0	482	7	US-10-242-535A-26414	Sequence 26414, A
c	325	6	20.0	482	7	US-10-085-783A-26414	Sequence 26414, A
c	326	6	20.0	483	3	US-09-821-687-1	Sequence 1, Appli
c	327	6	20.0	483	10	US-11-097-143-31082	Sequence 31082, A
	328	6	20.0	486	5	US-10-027-632-308321	Sequence 308321,
	329	6	20.0	486	6	US-10-027-632-308321	Sequence 308321,
	330	6	20.0	487	4	US-09-925-065A-844720	Sequence 844720,
	331	6	20.0	488	3	US-09-814-353-18107	Sequence 18107, A
c	332	6	20.0	488	4	US-09-925-065A-319278	Sequence 319278,
	333	6	20.0	488	5	US-10-027-632-84685	Sequence 84685, A
	334	6	20.0	488	6	US-10-027-632-84685	Sequence 84685, A
c	335	6	20.0	489	5	US-10-027-632-188282	Sequence 188282,
c	336	6	20.0	489	6	US-10-027-632-188282	Sequence 188282,
c	337	6	20.0	489	7	US-10-424-599-27458	Sequence 27458, A
c	338	6	20.0	490	3	US-09-764-891-6267	Sequence 6267, Ap
c	339	6	20.0	490	3	US-09-764-891-6268	Sequence 6268, Ap
c	340	6	20.0	490	3	US-09-764-891-6269	Sequence 6269, Ap
c	341	6	20.0	490	5	US-10-205-428-583	Sequence 583, App
c	342	6	20.0	490	5	US-10-205-428-584	Sequence 584, App
c	343	6	20.0	490	5	US-10-205-428-585	Sequence 585, App
c	344	6	20.0	491	7	US-10-424-599-124213	Sequence 124213,
c	345	6	20.0	492	3	US-09-918-995-9034	Sequence 9034, Ap
c	346	6	20.0	492	4	US-09-925-065A-500374	Sequence 500374,
c	347	6	20.0	492	4	US-09-925-065A-500375	Sequence 500375,
c	348	6	20.0	492	9	US-10-972-079-21598	Sequence 21598, A
	349	6	20.0	493	4	US-09-925-065A-323291	Sequence 323291,
	350	6	20.0	493	7	US-10-424-599-128071	Sequence 128071,
	351	6	20.0	494	4	US-09-925-065A-192427	Sequence 192427,
	352	6	20.0	495	8	US-10-357-930-14573	Sequence 14573, A
c	353	6	20.0	497	7	US-10-437-963-94501	Sequence 94501, A
c	354	6	20.0	498	4	US-09-925-065A-152941	Sequence 152941,
	355	6	20.0	498	5	US-10-027-632-37315	Sequence 37315, A
	356	6	20.0	498	6	US-10-027-632-37315	Sequence 37315, A
	357	6	20.0	500	3	US-09-783-590-818	Sequence 818, App
c	358	6	20.0	500	7	US-10-621-901-178	Sequence 178, App
	359	6	20.0	502	4	US-09-925-065A-279603	Sequence 279603,
c	360	6	20.0	502	7	US-10-424-599-1368	Sequence 1368, Ap
	361	6	20.0	503	4	US-09-925-065A-579244	Sequence 579244,
	362	6	20.0	503	4	US-09-925-065A-579245	Sequence 579245,
	363	6	20.0	503	4	US-09-925-065A-579246	Sequence 579246,
	364	6	20.0	503	4	US-09-925-065A-579247	Sequence 579247,
c	365	6	20.0	503	4	US-09-925-065A-893208	Sequence 893208,
c	366	6	20.0	505	3	US-09-783-590-7288	Sequence 7288, Ap
	367	6	20.0	505	5	US-10-027-632-299844	Sequence 299844,
	368	6	20.0	505	5	US-10-027-632-299845	Sequence 299845,
	369	6	20.0	505	6	US-10-027-632-299844	Sequence 299844,
	370	6	20.0	505	6	US-10-027-632-299845	Sequence 299845,
	371	6	20.0	505	7	US-10-424-599-141539	Sequence 141539,
	372	6	20.0	505	7	US-10-152-319A-1981	Sequence 1981, Ap

c 373	6	20.0	508	3	US-09-864-761-13389	Sequence 13389, A
c 374	6	20.0	508	8	US-10-425-115-18523	Sequence 18523, A
c 375	6	20.0	509	9	US-10-779-543-19209	Sequence 19209, A
c 376	6	20.0	510	3	US-09-864-761-8598	Sequence 8598, Ap
c 377	6	20.0	513	8	US-10-781-014-625	Sequence 625, App
378	6	20.0	513	8	US-10-425-115-155832	Sequence 155832,
379	6	20.0	514	4	US-09-925-065A-279604	Sequence 279604,
380	6	20.0	514	4	US-09-925-065A-350331	Sequence 350331,
c 381	6	20.0	515	3	US-09-998-598-1418	Sequence 1418, Ap
382	6	20.0	515	4	US-09-925-065A-516567	Sequence 516567,
383	6	20.0	515	7	US-10-437-963-74621	Sequence 74621, A
384	6	20.0	515	9	US-10-779-543-16798	Sequence 16798, A
c 385	6	20.0	516	3	US-09-998-598-1076	Sequence 1076, Ap
c 386	6	20.0	516	4	US-09-925-065A-186109	Sequence 186109,
c 387	6	20.0	516	9	US-10-779-543-21074	Sequence 21074, A
c 388	6	20.0	517	3	US-09-880-192-3	Sequence 3, Appli
389	6	20.0	517	4	US-09-925-065A-551046	Sequence 551046,
c 390	6	20.0	517	6	US-10-427-348-3	Sequence 3, Appli
391	6	20.0	519	4	US-09-925-065A-758150	Sequence 758150,
392	6	20.0	519	5	US-10-027-632-6820	Sequence 6820, Ap
393	6	20.0	519	6	US-10-027-632-6820	Sequence 6820, Ap
c 394	6	20.0	520	5	US-10-027-632-182747	Sequence 182747,
c 395	6	20.0	520	6	US-10-027-632-182747	Sequence 182747,
c 396	6	20.0	520	7	US-10-424-599-114892	Sequence 114892,
c 397	6	20.0	521	5	US-10-027-632-6650	Sequence 6650, Ap
c 398	6	20.0	521	6	US-10-027-632-6650	Sequence 6650, Ap
c 399	6	20.0	522	4	US-09-925-065A-152275	Sequence 152275,
c 400	6	20.0	522	4	US-09-925-065A-152276	Sequence 152276,
c 401	6	20.0	522	4	US-09-925-065A-152277	Sequence 152277,
402	6	20.0	522	4	US-09-925-065A-551104	Sequence 551104,
403	6	20.0	523	4	US-09-925-065A-98650	Sequence 98650, A
c 404	6	20.0	523	4	US-09-925-065A-178735	Sequence 178735,
405	6	20.0	524	4	US-09-925-065A-16218	Sequence 16218, A
c 406	6	20.0	524	5	US-10-027-632-193942	Sequence 193942,
c 407	6	20.0	524	6	US-10-027-632-193942	Sequence 193942,
408	6	20.0	524	8	US-10-357-930-35678	Sequence 35678, A
409	6	20.0	524	8	US-10-357-930-43948	Sequence 43948, A
410	6	20.0	524	8	US-10-357-930-44484	Sequence 44484, A
c 411	6	20.0	526	4	US-09-925-065A-813340	Sequence 813340,
c 412	6	20.0	527	6	US-10-029-386-10314	Sequence 10314, A
413	6	20.0	527	7	US-10-242-535A-2751	Sequence 2751, Ap
414	6	20.0	527	7	US-10-085-783A-2751	Sequence 2751, Ap
c 415	6	20.0	527	7	US-10-115-635-347	Sequence 347, App
c 416	6	20.0	528	9	US-10-779-543-21876	Sequence 21876, A
c 417	6	20.0	529	4	US-09-925-065A-11267	Sequence 11267, A
c 418	6	20.0	529	4	US-09-925-065A-176620	Sequence 176620,
419	6	20.0	529	4	US-09-925-065A-358936	Sequence 358936,
420	6	20.0	529	4	US-09-925-065A-358937	Sequence 358937,
c 421	6	20.0	529	4	US-09-925-065A-841645	Sequence 841645,
c 422	6	20.0	530	4	US-09-925-065A-553100	Sequence 553100,
c 423	6	20.0	530	7	US-10-242-535A-20744	Sequence 20744, A
c 424	6	20.0	530	7	US-10-085-783A-20744	Sequence 20744, A
c 425	6	20.0	531	9	US-10-972-079-59799	Sequence 59799, A
426	6	20.0	532	4	US-09-925-065A-153827	Sequence 153827,
427	6	20.0	532	4	US-09-925-065A-956909	Sequence 956909,
428	6	20.0	532	8	US-10-425-115-137046	Sequence 137046,
429	6	20.0	532	8	US-10-363-345A-18229	Sequence 18229, A
c 430	6	20.0	532	8	US-10-363-345A-18230	Sequence 18230, A
431	6	20.0	532	9	US-10-363-483A-18229	Sequence 18229, A
c 432	6	20.0	532	9	US-10-363-483A-18230	Sequence 18230, A
433	6	20.0	533	4	US-09-925-065A-593647	Sequence 593647,
434	6	20.0	533	4	US-09-925-065A-653939	Sequence 653939,
435	6	20.0	535	4	US-09-925-065A-758204	Sequence 758204,
436	6	20.0	537	4	US-09-925-065A-220036	Sequence 220036,
437	6	20.0	537	4	US-09-925-065A-220037	Sequence 220037,
438	6	20.0	537	4	US-09-925-065A-220038	Sequence 220038,
439	6	20.0	537	4	US-09-925-065A-338232	Sequence 338232,
440	6	20.0	537	4	US-09-925-065A-790763	Sequence 790763,
441	6	20.0	537	4	US-09-925-065A-790764	Sequence 790764,
442	6	20.0	537	4	US-09-925-065A-848118	Sequence 848118,
c 443	6	20.0	537	6	US-10-029-386-1374	Sequence 1374, Ap
444	6	20.0	537	6	US-10-029-386-8650	Sequence 8650, Ap
c 445	6	20.0	537	9	US-10-972-079-21597	Sequence 21597, A
446	6	20.0	538	4	US-09-925-065A-31796	Sequence 31796, A
447	6	20.0	538	4	US-09-925-065A-238437	Sequence 238437,
448	6	20.0	538	4	US-09-925-065A-663712	Sequence 663712,
449	6	20.0	538	4	US-09-925-065A-663713	Sequence 663713,
c 450	6	20.0	538	5	US-10-001-857-21	Sequence 21, Appl
c 451	6	20.0	539	3	US-09-814-353-17896	Sequence 17896, A
c 452	6	20.0	539	5	US-10-027-632-240730	Sequence 240730,
c 453	6	20.0	539	6	US-10-027-632-240730	Sequence 240730,
c 454	6	20.0	540	4	US-09-925-065A-569621	Sequence 569621,
c 455	6	20.0	542	4	US-09-925-065A-496817	Sequence 496817,
c 456	6	20.0	542	4	US-09-925-065A-496818	Sequence 496818,
c 457	6	20.0	543	4	US-09-925-065A-176891	Sequence 176891,
c 458	6	20.0	543	4	US-09-925-065A-176892	Sequence 176892,
c 459	6	20.0	543	4	US-09-925-065A-376881	Sequence 376881,
c 460	6	20.0	543	4	US-09-925-065A-570031	Sequence 570031,
c 461	6	20.0	543	4	US-09-925-065A-904983	Sequence 904983,
462	6	20.0	543	4	US-09-925-065A-906601	Sequence 906601,
463	6	20.0	543	7	US-10-437-963-78378	Sequence 78378, A
c 464	6	20.0	544	4	US-09-925-065A-563608	Sequence 563608,
c 465	6	20.0	545	4	US-09-925-065A-470129	Sequence 470129,
c 466	6	20.0	545	4	US-09-925-065A-806504	Sequence 806504,
c 467	6	20.0	545	4	US-09-925-065A-858396	Sequence 858396,
c 468	6	20.0	545	5	US-10-027-632-280342	Sequence 280342,
c 469	6	20.0	545	6	US-10-027-632-280342	Sequence 280342,
470	6	20.0	546	3	US-09-864-761-26855	Sequence 26855, A
c 471	6	20.0	546	5	US-10-027-632-199119	Sequence 199119,
472	6	20.0	546	5	US-10-027-632-235945	Sequence 235945,
c 473	6	20.0	546	6	US-10-027-632-199119	Sequence 199119,
474	6	20.0	546	6	US-10-027-632-235945	Sequence 235945,
475	6	20.0	547	4	US-09-925-065A-118913	Sequence 118913,
c 476	6	20.0	547	8	US-10-425-115-97874	Sequence 97874, A
c 477	6	20.0	547	8	US-10-357-930-55738	Sequence 55738, A
478	6	20.0	548	4	US-09-925-065A-564994	Sequence 564994,
479	6	20.0	548	4	US-09-925-065A-564995	Sequence 564995,
480	6	20.0	548	4	US-09-925-065A-564996	Sequence 564996,
c 481	6	20.0	548	4	US-09-925-065A-596237	Sequence 596237,
c 482	6	20.0	548	4	US-09-925-065A-596238	Sequence 596238,
c 483	6	20.0	549	3	US-09-560-863-190	Sequence 190, App
484	6	20.0	549	3	US-09-769-736-93	Sequence 93, Appl
485	6	20.0	549	4	US-09-925-065A-608016	Sequence 608016,
486	6	20.0	549	4	US-09-925-065A-648127	Sequence 648127,
487	6	20.0	549	4	US-09-925-065A-736858	Sequence 736858,
488	6	20.0	549	4	US-09-925-065A-814331	Sequence 814331,
c 489	6	20.0	549	4	US-09-925-065A-900891	Sequence 900891,
c 490	6	20.0	549	7	US-10-621-901-10	Sequence 10, Appl
491	6	20.0	550	4	US-09-925-065A-114001	Sequence 114001,
492	6	20.0	550	4	US-09-925-065A-193021	Sequence 193021,
493	6	20.0	550	4	US-09-925-065A-694846	Sequence 694846,
c 494	6	20.0	550	4	US-09-925-065A-891651	Sequence 891651,
495	6	20.0	551	4	US-09-925-065A-25630	Sequence 25630, A
c 496	6	20.0	552	4	US-09-925-065A-107183	Sequence 107183,
497	6	20.0	554	3	US-09-918-995-14171	Sequence 14171, A
498	6	20.0	554	4	US-09-925-065A-112249	Sequence 112249,
499	6	20.0	554	4	US-09-925-065A-194744	Sequence 194744,
500	6	20.0	554	4	US-09-925-065A-194745	Sequence 194745,
c 501	6	20.0	554	4	US-09-925-065A-270236	Sequence 270236,
c 502	6	20.0	554	5	US-10-027-632-270524	Sequence 270524,
c 503	6	20.0	554	6	US-10-027-632-270524	Sequence 270524,
504	6	20.0	555	4	US-09-925-065A-316283	Sequence 316283,
c 505	6	20.0	555	6	US-10-369-493-46693	Sequence 46693, A
506	6	20.0	556	4	US-09-925-065A-181661	Sequence 181661,
507	6	20.0	556	4	US-09-925-065A-181662	Sequence 181662,
c 508	6	20.0	557	3	US-09-991-936-1538	Sequence 1538, Ap
c 509	6	20.0	557	4	US-09-925-065A-448753	Sequence 448753,
510	6	20.0	557	5	US-10-027-632-32504	Sequence 32504, A
511	6	20.0	557	6	US-10-027-632-32504	Sequence 32504, A
c 512	6	20.0	557	9	US-10-978-245-1538	Sequence 1538, Ap
513	6	20.0	558	3	US-09-796-692-7854	Sequence 7854, Ap
c 514	6	20.0	558	4	US-09-925-065A-180764	Sequence 180764,
515	6	20.0	558	4	US-09-925-065A-828604	Sequence 828604,
516	6	20.0	558	5	US-10-040-862-7854	Sequence 7854, Ap
517	6	20.0	558	6	US-10-057-475B-7854	Sequence 7854, Ap
518	6	20.0	558	6	US-10-154-884B-7854	Sequence 7854, Ap

519	6	20.0	558	8	US-10-764-324-7854	Sequence 7854, Ap
520	6	20.0	559	4	US-09-925-065A-152119	Sequence 152119,
521	6	20.0	559	4	US-09-925-065A-621721	Sequence 621721,
c 522	6	20.0	559	6	US-10-029-386-11232	Sequence 11232, A
523	6	20.0	559	7	US-10-021-323-2946	Sequence 2946, Ap
c 524	6	20.0	560	4	US-09-925-065A-103434	Sequence 103434,
c 525	6	20.0	560	4	US-09-925-065A-156687	Sequence 156687,
c 526	6	20.0	560	4	US-09-925-065A-240219	Sequence 240219,
c 527	6	20.0	560	5	US-10-027-632-206354	Sequence 206354,
c 528	6	20.0	560	6	US-10-027-632-206354	Sequence 206354,
c 529	6	20.0	561	4	US-09-925-065A-103433	Sequence 103433,
c 530	6	20.0	561	4	US-09-925-065A-399749	Sequence 399749,
531	6	20.0	561	4	US-09-925-065A-611942	Sequence 611942,
c 532	6	20.0	561	4	US-09-925-065A-748713	Sequence 748713,
c 533	6	20.0	561	5	US-10-027-632-283307	Sequence 283307,
c 534	6	20.0	561	6	US-10-027-632-283307	Sequence 283307,
535	6	20.0	562	4	US-09-925-065A-649469	Sequence 649469,
c 536	6	20.0	562	4	US-09-925-065A-782342	Sequence 782342,
c 537	6	20.0	562	4	US-09-925-065A-843127	Sequence 843127,
538	6	20.0	562	8	US-10-425-115-169600	Sequence 169600,
539	6	20.0	563	4	US-09-925-065A-449368	Sequence 449368,
c 540	6	20.0	564	4	US-09-925-065A-404422	Sequence 404422,
541	6	20.0	564	4	US-09-925-065A-814414	Sequence 814414,
542	6	20.0	565	4	US-09-925-065A-212333	Sequence 212333,
543	6	20.0	565	4	US-09-925-065A-657373	Sequence 657373,
544	6	20.0	567	5	US-10-027-632-272184	Sequence 272184,
545	6	20.0	567	6	US-10-027-632-272184	Sequence 272184,
546	6	20.0	568	5	US-10-027-632-82635	Sequence 82635, A
c 547	6	20.0	568	5	US-10-027-632-247242	Sequence 247242,
548	6	20.0	568	6	US-10-027-632-82635	Sequence 82635, A
c 549	6	20.0	568	6	US-10-027-632-247242	Sequence 247242,
c 550	6	20.0	568	7	US-10-437-963-59248	Sequence 59248, A
551	6	20.0	569	4	US-09-925-065A-649886	Sequence 649886,
552	6	20.0	569	4	US-09-925-065A-649887	Sequence 649887,
553	6	20.0	569	4	US-09-925-065A-734209	Sequence 734209,
554	6	20.0	569	4	US-09-925-065A-734210	Sequence 734210,
555	6	20.0	569	9	US-10-779-543-16402	Sequence 16402, A
556	6	20.0	570	6	US-10-156-761-5029	Sequence 5029, Ap
c 557	6	20.0	570	9	US-10-972-079-40880	Sequence 40880, A
c 558	6	20.0	571	4	US-09-925-065A-166372	Sequence 166372,
c 559	6	20.0	572	4	US-09-925-065A-397503	Sequence 397503,
560	6	20.0	572	5	US-10-027-632-219687	Sequence 219687,
561	6	20.0	572	5	US-10-027-632-219688	Sequence 219688,
562	6	20.0	572	5	US-10-198-846-11050	Sequence 11050, A
563	6	20.0	572	6	US-10-027-632-219687	Sequence 219687,
564	6	20.0	572	6	US-10-027-632-219688	Sequence 219688,
c 565	6	20.0	573	4	US-09-925-065A-429737	Sequence 429737,
566	6	20.0	574	4	US-09-925-065A-378726	Sequence 378726,
c 567	6	20.0	574	4	US-09-925-065A-733492	Sequence 733492,
568	6	20.0	575	4	US-09-925-065A-165240	Sequence 165240,
c 569	6	20.0	575	4	US-09-925-065A-492813	Sequence 492813,
c 570	6	20.0	575	4	US-09-925-065A-492814	Sequence 492814,
571	6	20.0	575	4	US-09-925-065A-938868	Sequence 938868,
572	6	20.0	575	4	US-09-925-065A-938869	Sequence 938869,
c 573	6	20.0	575	8	US-10-425-115-184457	Sequence 184457,
574	6	20.0	576	4	US-09-925-065A-328566	Sequence 328566,
c 575	6	20.0	576	4	US-09-925-065A-632034	Sequence 632034,
c 576	6	20.0	576	4	US-09-925-065A-632035	Sequence 632035,
c 577	6	20.0	576	4	US-09-925-065A-632036	Sequence 632036,
578	6	20.0	577	4	US-09-925-065A-416541	Sequence 416541,
c 579	6	20.0	577	4	US-09-925-065A-869925	Sequence 869925,
580	6	20.0	577	4	US-09-925-065A-882171	Sequence 882171,
c 581	6	20.0	577	4	US-09-925-065A-901449	Sequence 901449,
c 582	6	20.0	577	4	US-09-925-065A-901450	Sequence 901450,
583	6	20.0	577	4	US-09-925-065A-909431	Sequence 909431,
584	6	20.0	577	4	US-09-925-065A-909432	Sequence 909432,
c 585	6	20.0	577	4	US-09-925-065A-936019	Sequence 936019,
586	6	20.0	578	4	US-09-925-065A-223701	Sequence 223701,
c 587	6	20.0	578	7	US-10-767-701-23869	Sequence 23869, A
588	6	20.0	578	8	US-10-653-047-1570	Sequence 1570, Ap
c 589	6	20.0	580	4	US-09-925-065A-277200	Sequence 277200,
c 590	6	20.0	580	4	US-09-925-065A-277201	Sequence 277201,
591	6	20.0	580	4	US-09-925-065A-440891	Sequence 440891,
c 592	6	20.0	580	4	US-09-925-065A-557305	Sequence 557305,
593	6	20.0	580	4	US-09-925-065A-922811	Sequence 922811,
594	6	20.0	581	4	US-09-925-065A-119754	Sequence 119754,
c 595	6	20.0	581	4	US-09-925-065A-190489	Sequence 190489,
c 596	6	20.0	581	4	US-09-925-065A-190490	Sequence 190490,
c 597	6	20.0	581	4	US-09-925-065A-874458	Sequence 874458,
c 598	6	20.0	581	4	US-09-925-065A-874459	Sequence 874459,
c 599	6	20.0	581	4	US-09-925-065A-904300	Sequence 904300,
600	6	20.0	582	4	US-09-925-065A-297555	Sequence 297555,
c 601	6	20.0	582	4	US-09-925-065A-334112	Sequence 334112,
c 602	6	20.0	582	4	US-09-925-065A-334113	Sequence 334113,
c 603	6	20.0	582	4	US-09-925-065A-469456	Sequence 469456,
604	6	20.0	582	4	US-09-925-065A-626318	Sequence 626318,
605	6	20.0	582	4	US-09-925-065A-710163	Sequence 710163,
606	6	20.0	582	4	US-09-925-065A-710164	Sequence 710164,
607	6	20.0	582	4	US-09-925-065A-710165	Sequence 710165,
608	6	20.0	582	5	US-10-027-632-88852	Sequence 88852, A
609	6	20.0	582	5	US-10-027-632-88853	Sequence 88853, A
610	6	20.0	582	6	US-10-027-632-88852	Sequence 88852, A
611	6	20.0	582	6	US-10-027-632-88853	Sequence 88853, A
612	6	20.0	582	7	US-10-424-599-43709	Sequence 43709, A
c 613	6	20.0	583	4	US-09-925-065A-152564	Sequence 152564,
c 614	6	20.0	583	4	US-09-925-065A-152565	Sequence 152565,
c 615	6	20.0	583	4	US-09-925-065A-152566	Sequence 152566,
c 616	6	20.0	583	4	US-09-925-065A-152567	Sequence 152567,
617	6	20.0	583	4	US-09-925-065A-250481	Sequence 250481,
618	6	20.0	583	4	US-09-925-065A-299836	Sequence 299836,
c 619	6	20.0	584	4	US-09-925-065A-941617	Sequence 941617,
c 620	6	20.0	584	4	US-09-925-065A-941618	Sequence 941618,
c 621	6	20.0	585	4	US-09-925-065A-753296	Sequence 753296,
622	6	20.0	585	4	US-09-925-065A-896177	Sequence 896177,
c 623	6	20.0	585	9	US-10-972-079-40879	Sequence 40879, A
624	6	20.0	586	4	US-09-925-065A-429909	Sequence 429909,
625	6	20.0	586	4	US-09-925-065A-429910	Sequence 429910,
c 626	6	20.0	586	7	US-10-021-323-15504	Sequence 15504, A
c 627	6	20.0	586	9	US-10-450-763-22194	Sequence 22194, A
c 628	6	20.0	587	4	US-09-925-065A-652296	Sequence 652296,
c 629	6	20.0	588	4	US-09-925-065A-21277	Sequence 21277, A
630	6	20.0	588	5	US-10-027-632-228764	Sequence 228764,
631	6	20.0	588	6	US-10-027-632-228764	Sequence 228764,
c 632	6	20.0	589	3	US-09-864-761-13612	Sequence 13612, A
633	6	20.0	589	5	US-10-027-632-128684	Sequence 128684,
634	6	20.0	589	6	US-10-027-632-128684	Sequence 128684,
635	6	20.0	589	7	US-10-424-599-114794	Sequence 114794,
636	6	20.0	589	8	US-10-767-795-776	Sequence 776, App
637	6	20.0	590	5	US-10-027-632-125984	Sequence 125984,
c 638	6	20.0	590	6	US-10-029-386-5859	Sequence 5859, Ap
639	6	20.0	590	6	US-10-027-632-125984	Sequence 125984,
c 640	6	20.0	591	4	US-09-925-065A-650784	Sequence 650784,
c 641	6	20.0	591	4	US-09-925-065A-650785	Sequence 650785,
c 642	6	20.0	591	4	US-09-925-065A-713026	Sequence 713026,
c 643	6	20.0	591	4	US-09-925-065A-713027	Sequence 713027,
c 644	6	20.0	591	4	US-09-925-065A-713028	Sequence 713028,
645	6	20.0	591	6	US-10-029-386-1788	Sequence 1788, Ap
646	6	20.0	591	7	US-10-021-323-9235	Sequence 9235, Ap
647	6	20.0	591	8	US-10-363-345A-18315	Sequence 18315, A
c 648	6	20.0	591	8	US-10-363-345A-18316	Sequence 18316, A
649	6	20.0	591	9	US-10-363-483A-18315	Sequence 18315, A
c 650	6	20.0	591	9	US-10-363-483A-18316	Sequence 18316, A
651	6	20.0	592	4	US-09-925-065A-570114	Sequence 570114,
c 652	6	20.0	594	4	US-09-925-065A-549928	Sequence 549928,
c 653	6	20.0	594	4	US-09-925-065A-712739	Sequence 712739,
654	6	20.0	594	4	US-09-925-065A-921288	Sequence 921288,
655	6	20.0	594	4	US-09-925-065A-930365	Sequence 930365,
656	6	20.0	595	4	US-09-925-065A-122755	Sequence 122755,
657	6	20.0	595	4	US-09-925-065A-122756	Sequence 122756,
658	6	20.0	595	4	US-09-925-065A-122757	Sequence 122757,
c 659	6	20.0	595	4	US-09-925-065A-623586	Sequence 623586,
660	6	20.0	595	4	US-09-925-065A-667951	Sequence 667951,
c 661	6	20.0	595	5	US-10-027-632-270493	Sequence 270493,
c 662	6	20.0	595	6	US-10-027-632-270493	Sequence 270493,
663	6	20.0	596	4	US-09-925-065A-534821	Sequence 534821,
664	6	20.0	596	9	US-10-915-740A-331	Sequence 331, App

c 665	6	20.0	597	3	US-09-770-149-998	Sequence 998, App
c 666	6	20.0	597	4	US-09-925-065A-275874	Sequence 275874,
667	6	20.0	597	4	US-09-925-065A-357220	Sequence 357220,
c 668	6	20.0	598	5	US-10-027-632-194345	Sequence 194345,
c 669	6	20.0	598	5	US-10-027-632-194346	Sequence 194346,
c 670	6	20.0	598	6	US-10-027-632-194345	Sequence 194345,
c 671	6	20.0	598	6	US-10-027-632-194346	Sequence 194346,
c 672	6	20.0	599	9	US-10-972-079-2993	Sequence 2993, Ap
c 673	6	20.0	599	9	US-10-972-079-23472	Sequence 23472, A
674	6	20.0	599	9	US-10-972-079-24521	Sequence 24521, A
c 675	6	20.0	599	9	US-10-972-079-85535	Sequence 85535, A
c 676	6	20.0	599	9	US-10-972-079-91598	Sequence 91598, A
677	6	20.0	599	9	US-10-972-079-94065	Sequence 94065, A
c 678	6	20.0	600	3	US-09-864-761-11974	Sequence 11974, A
c 679	6	20.0	600	9	US-10-956-157-7858	Sequence 7858, Ap
680	6	20.0	600	9	US-10-972-079-3190	Sequence 3190, Ap
681	6	20.0	600	9	US-10-972-079-17750	Sequence 17750, A
682	6	20.0	600	9	US-10-972-079-24522	Sequence 24522, A
683	6	20.0	600	9	US-10-972-079-32863	Sequence 32863, A
684	6	20.0	600	9	US-10-972-079-34451	Sequence 34451, A
685	6	20.0	600	9	US-10-972-079-34452	Sequence 34452, A
686	6	20.0	600	9	US-10-972-079-34453	Sequence 34453, A
c 687	6	20.0	600	9	US-10-972-079-45369	Sequence 45369, A
c 688	6	20.0	600	9	US-10-972-079-45370	Sequence 45370, A
c 689	6	20.0	600	9	US-10-972-079-45371	Sequence 45371, A
690	6	20.0	600	9	US-10-972-079-49435	Sequence 49435, A
c 691	6	20.0	600	9	US-10-972-079-55547	Sequence 55547, A
c 692	6	20.0	600	9	US-10-972-079-59798	Sequence 59798, A
c 693	6	20.0	600	9	US-10-972-079-61975	Sequence 61975, A
694	6	20.0	600	9	US-10-972-079-64990	Sequence 64990, A
c 695	6	20.0	600	9	US-10-972-079-65320	Sequence 65320, A
696	6	20.0	600	9	US-10-972-079-69990	Sequence 69990, A
697	6	20.0	600	9	US-10-972-079-74773	Sequence 74773, A
698	6	20.0	600	9	US-10-972-079-74774	Sequence 74774, A
699	6	20.0	600	9	US-10-972-079-74775	Sequence 74775, A
700	6	20.0	600	9	US-10-972-079-74776	Sequence 74776, A
701	6	20.0	600	9	US-10-972-079-74777	Sequence 74777, A
c 702	6	20.0	600	9	US-10-972-079-91402	Sequence 91402, A
703	6	20.0	600	9	US-10-972-079-94564	Sequence 94564, A
704	6	20.0	600	9	US-10-972-079-94565	Sequence 94565, A
c 705	6	20.0	601	4	US-09-925-065A-431857	Sequence 431857,
c 706	6	20.0	601	6	US-10-388-934-417	Sequence 417, App
c 707	6	20.0	601	8	US-10-425-115-11849	Sequence 11849, A
708	6	20.0	602	3	US-09-764-853-891	Sequence 891, App
709	6	20.0	602	3	US-09-764-853-934	Sequence 934, App
710	6	20.0	602	5	US-10-091-438-247	Sequence 247, App
711	6	20.0	602	5	US-10-091-438-260	Sequence 260, App
712	6	20.0	603	4	US-09-925-065A-81159	Sequence 81159, A
713	6	20.0	603	4	US-09-925-065A-81160	Sequence 81160, A
714	6	20.0	603	4	US-09-925-065A-81161	Sequence 81161, A
715	6	20.0	603	4	US-09-925-065A-588934	Sequence 588934,
c 716	6	20.0	603	4	US-09-925-065A-622145	Sequence 622145,
c 717	6	20.0	603	4	US-09-925-065A-622146	Sequence 622146,
c 718	6	20.0	604	4	US-09-925-065A-146201	Sequence 146201,
c 719	6	20.0	604	4	US-09-925-065A-355307	Sequence 355307,
c 720	6	20.0	604	4	US-09-925-065A-355308	Sequence 355308,
721	6	20.0	604	4	US-09-925-065A-357158	Sequence 357158,
c 722	6	20.0	605	8	US-10-357-930-39259	Sequence 39259, A
c 723	6	20.0	606	4	US-09-925-065A-48331	Sequence 48331, A
c 724	6	20.0	606	4	US-09-925-065A-258100	Sequence 258100,
c 725	6	20.0	606	4	US-09-925-065A-258101	Sequence 258101,
c 726	6	20.0	606	4	US-09-925-065A-258102	Sequence 258102,
727	6	20.0	606	4	US-09-925-065A-543797	Sequence 543797,
728	6	20.0	606	4	US-09-925-065A-543798	Sequence 543798,
c 729	6	20.0	606	4	US-09-925-065A-575932	Sequence 575932,
c 730	6	20.0	606	4	US-09-925-065A-834694	Sequence 834694,
731	6	20.0	606	8	US-10-357-930-35088	Sequence 35088, A
732	6	20.0	606	8	US-10-357-930-43935	Sequence 43935, A
733	6	20.0	607	4	US-09-925-065A-254618	Sequence 254618,
734	6	20.0	609	4	US-09-925-065A-760518	Sequence 760518,
c 735	6	20.0	609	4	US-09-925-065A-891938	Sequence 891938,
c 736	6	20.0	609	4	US-09-925-065A-891939	Sequence 891939,
c 737	6	20.0	609	4	US-09-925-065A-914766	Sequence 914766,
738	6	20.0	610	4	US-09-925-065A-215370	Sequence 215370,
c 739	6	20.0	610	4	US-09-925-065A-244058	Sequence 244058,
c 740	6	20.0	610	4	US-09-925-065A-609920	Sequence 609920,
c 741	6	20.0	610	4	US-09-925-065A-609921	Sequence 609921,
c 742	6	20.0	610	4	US-09-925-065A-609922	Sequence 609922,
743	6	20.0	610	4	US-09-925-065A-798636	Sequence 798636,
744	6	20.0	610	4	US-09-925-065A-852772	Sequence 852772,
745	6	20.0	610	6	US-10-312-162-14	Sequence 14, Appl
c 746	6	20.0	611	4	US-09-925-065A-102390	Sequence 102390,
c 747	6	20.0	612	4	US-09-925-065A-116514	Sequence 116514,
748	6	20.0	612	4	US-09-925-065A-391944	Sequence 391944,
749	6	20.0	612	5	US-10-027-632-291873	Sequence 291873,
750	6	20.0	612	6	US-10-027-632-291873	Sequence 291873,
751	6	20.0	613	4	US-09-925-065A-265418	Sequence 265418,
c 752	6	20.0	613	4	US-09-925-065A-924293	Sequence 924293,
753	6	20.0	615	4	US-09-925-065A-85201	Sequence 85201, A
754	6	20.0	615	4	US-09-925-065A-85202	Sequence 85202, A
755	6	20.0	615	4	US-09-925-065A-85203	Sequence 85203, A
c 756	6	20.0	615	4	US-09-925-065A-334165	Sequence 334165,
c 757	6	20.0	615	4	US-09-925-065A-334167	Sequence 334167,
c 758	6	20.0	615	4	US-09-925-065A-878206	Sequence 878206,
c 759	6	20.0	615	4	US-09-925-065A-878207	Sequence 878207,
c 760	6	20.0	615	4	US-09-925-065A-878208	Sequence 878208,
c 761	6	20.0	615	4	US-09-925-065A-878209	Sequence 878209,
c 762	6	20.0	616	4	US-09-925-065A-279639	Sequence 279639,
763	6	20.0	616	4	US-09-925-065A-384912	Sequence 384912,
c 764	6	20.0	616	4	US-09-925-065A-393932	Sequence 393932,
765	6	20.0	616	4	US-09-925-065A-532579	Sequence 532579,
c 766	6	20.0	616	4	US-09-925-065A-556565	Sequence 556565,
767	6	20.0	617	4	US-09-925-065A-395194	Sequence 395194,
768	6	20.0	617	4	US-09-925-065A-851221	Sequence 851221,
c 769	6	20.0	617	8	US-10-357-930-59164	Sequence 59164, A
770	6	20.0	619	4	US-09-925-065A-453134	Sequence 453134,
c 771	6	20.0	619	4	US-09-925-065A-642412	Sequence 642412,
c 772	6	20.0	619	4	US-09-925-065A-642413	Sequence 642413,
c 773	6	20.0	619	4	US-09-925-065A-830191	Sequence 830191,
c 774	6	20.0	619	8	US-10-767-795-4991	Sequence 4991, Ap
775	6	20.0	620	4	US-09-925-065A-126975	Sequence 126975,
776	6	20.0	620	4	US-09-925-065A-136004	Sequence 136004,
c 777	6	20.0	620	4	US-09-925-065A-399750	Sequence 399750,
c 778	6	20.0	620	4	US-09-925-065A-399751	Sequence 399751,
c 779	6	20.0	621	4	US-09-925-065A-389520	Sequence 389520,
c 780	6	20.0	621	4	US-09-925-065A-389521	Sequence 389521,
c 781	6	20.0	621	4	US-09-925-065A-389522	Sequence 389522,
c 782	6	20.0	621	4	US-09-925-065A-415707	Sequence 415707,
783	6	20.0	621	8	US-10-357-930-5569	Sequence 5569, Ap
784	6	20.0	622	4	US-09-925-065A-405915	Sequence 405915,
785	6	20.0	622	4	US-09-925-065A-642411	Sequence 642411,
786	6	20.0	622	4	US-09-925-065A-684894	Sequence 684894,
c 787	6	20.0	623	4	US-09-925-065A-277199	Sequence 277199,
788	6	20.0	623	4	US-09-925-065A-343588	Sequence 343588,
789	6	20.0	623	4	US-09-925-065A-449084	Sequence 449084,
790	6	20.0	623	4	US-09-925-065A-639364	Sequence 639364,
791	6	20.0	623	4	US-09-925-065A-658800	Sequence 658800,
792	6	20.0	624	5	US-10-027-632-197365	Sequence 197365,
793	6	20.0	624	5	US-10-027-632-215182	Sequence 215182,
c 794	6	20.0	624	5	US-10-027-632-231034	Sequence 231034,
795	6	20.0	624	6	US-10-027-632-197365	Sequence 197365,
796	6	20.0	624	6	US-10-027-632-215182	Sequence 215182,
c 797	6	20.0	624	6	US-10-027-632-231034	Sequence 231034,
798	6	20.0	624	8	US-10-363-345A-29975	Sequence 29975, A
c 799	6	20.0	624	8	US-10-363-345A-29976	Sequence 29976, A
800	6	20.0	624	9	US-10-363-483A-29975	Sequence 29975, A
c 801	6	20.0	624	9	US-10-363-483A-29976	Sequence 29976, A
802	6	20.0	628	4	US-09-925-065A-524870	Sequence 524870,
803	6	20.0	628	4	US-09-925-065A-524871	Sequence 524871,
804	6	20.0	628	4	US-09-925-065A-741720	Sequence 741720,
805	6	20.0	628	5	US-10-027-632-90693	Sequence 90693, A
806	6	20.0	628	5	US-10-027-632-317490	Sequence 317490,
807	6	20.0	628	6	US-10-027-632-90693	Sequence 90693, A
808	6	20.0	628	6	US-10-027-632-317490	Sequence 317490,
809	6	20.0	628	8	US-10-425-115-126792	Sequence 126792,
c 810	6	20.0	629	4	US-09-925-065A-789500	Sequence 789500,

811	6	20.0	630	4	US-09-925-065A-247810	Sequence 247810,
c 812	6	20.0	630	7	US-10-021-323-1225	Sequence 1225, Ap
c 813	6	20.0	630	8	US-10-425-115-150842	Sequence 150842,
814	6	20.0	631	4	US-09-925-065A-774513	Sequence 774513,
815	6	20.0	631	5	US-10-027-632-270334	Sequence 270334,
816	6	20.0	631	6	US-10-027-632-270334	Sequence 270334,
817	6	20.0	633	4	US-09-925-065A-534342	Sequence 534342,
c 818	6	20.0	633	4	US-09-925-065A-790937	Sequence 790937,
819	6	20.0	634	4	US-09-925-065A-668969	Sequence 668969,
c 820	6	20.0	634	4	US-09-925-065A-899217	Sequence 899217,
c 821	6	20.0	634	4	US-09-925-065A-899218	Sequence 899218,
c 822	6	20.0	635	9	US-10-487-901-1955	Sequence 1955, Ap
823	6	20.0	636	4	US-09-925-065A-554580	Sequence 554580,
824	6	20.0	636	4	US-09-925-065A-901667	Sequence 901667,
c 825	6	20.0	637	4	US-09-925-065A-75347	Sequence 75347, A
826	6	20.0	637	4	US-09-925-065A-479888	Sequence 479888,
c 827	6	20.0	637	4	US-09-925-065A-670197	Sequence 670197,
c 828	6	20.0	637	4	US-09-925-065A-777277	Sequence 777277,
829	6	20.0	637	5	US-10-027-632-14966	Sequence 14966, A
c 830	6	20.0	637	5	US-10-027-632-185994	Sequence 185994,
c 831	6	20.0	637	5	US-10-027-632-185995	Sequence 185995,
832	6	20.0	637	6	US-10-027-632-14966	Sequence 14966, A
c 833	6	20.0	637	6	US-10-027-632-185994	Sequence 185994,
c 834	6	20.0	637	6	US-10-027-632-185995	Sequence 185995,
c 835	6	20.0	639	7	US-10-260-238-964	Sequence 964, App
836	6	20.0	640	4	US-09-925-065A-885237	Sequence 885237,
837	6	20.0	640	5	US-10-027-632-237247	Sequence 237247,
838	6	20.0	640	6	US-10-027-632-237247	Sequence 237247,
839	6	20.0	640	8	US-10-425-115-19491	Sequence 19491, A
840	6	20.0	641	4	US-09-925-065A-722902	Sequence 722902,
841	6	20.0	641	4	US-09-925-065A-722903	Sequence 722903,
c 842	6	20.0	642	4	US-09-925-065A-492701	Sequence 492701,
c 843	6	20.0	642	4	US-09-925-065A-760449	Sequence 760449,
c 844	6	20.0	642	4	US-09-925-065A-829354	Sequence 829354,
845	6	20.0	642	7	US-10-424-599-65830	Sequence 65830, A
846	6	20.0	643	3	US-09-764-853-243	Sequence 243, App
847	6	20.0	643	4	US-09-925-065A-424383	Sequence 424383,
848	6	20.0	643	4	US-09-925-065A-424384	Sequence 424384,
849	6	20.0	643	4	US-09-925-065A-424385	Sequence 424385,
c 850	6	20.0	643	4	US-09-925-065A-583886	Sequence 583886,
c 851	6	20.0	643	4	US-09-925-065A-583887	Sequence 583887,
c 852	6	20.0	643	4	US-09-925-065A-583888	Sequence 583888,
c 853	6	20.0	643	4	US-09-925-065A-856425	Sequence 856425,
854	6	20.0	643	5	US-10-091-438-35	Sequence 35, Appl
c 855	6	20.0	644	4	US-09-925-065A-179456	Sequence 179456,
856	6	20.0	644	4	US-09-925-065A-744282	Sequence 744282,
c 857	6	20.0	644	5	US-10-027-632-291861	Sequence 291861,
c 858	6	20.0	644	5	US-10-198-846-7892	Sequence 7892, Ap
c 859	6	20.0	644	6	US-10-027-632-291861	Sequence 291861,
860	6	20.0	648	4	US-09-925-065A-815816	Sequence 815816,
c 861	6	20.0	648	4	US-09-925-065A-896418	Sequence 896418,
c 862	6	20.0	648	4	US-09-925-065A-916987	Sequence 916987,
c 863	6	20.0	648	8	US-10-653-047-4497	Sequence 4497, Ap
c 864	6	20.0	649	4	US-09-925-065A-1368	Sequence 1368, Ap
865	6	20.0	649	4	US-09-925-065A-56971	Sequence 56971, A
866	6	20.0	649	5	US-10-027-632-126435	Sequence 126435,
867	6	20.0	649	5	US-10-027-632-126436	Sequence 126436,
868	6	20.0	649	6	US-10-027-632-126435	Sequence 126435,
869	6	20.0	649	6	US-10-027-632-126436	Sequence 126436,
c 870	6	20.0	649	8	US-10-425-115-157874	Sequence 157874,
c 871	6	20.0	650	3	US-09-991-936-1617	Sequence 1617, Ap
872	6	20.0	650	4	US-09-925-065A-954664	Sequence 954664,
873	6	20.0	650	5	US-10-027-632-190184	Sequence 190184,
874	6	20.0	650	5	US-10-027-632-213922	Sequence 213922,
875	6	20.0	650	6	US-10-027-632-190184	Sequence 190184,
876	6	20.0	650	6	US-10-027-632-213922	Sequence 213922,
c 877	6	20.0	650	9	US-10-978-245-1617	Sequence 1617, Ap
878	6	20.0	652	4	US-09-925-065A-498800	Sequence 498800,
879	6	20.0	652	4	US-09-925-065A-827548	Sequence 827548,
c 880	6	20.0	652	7	US-10-767-701-2812	Sequence 2812, Ap
c 881	6	20.0	653	7	US-10-424-599-3535	Sequence 3535, Ap
c 882	6	20.0	654	5	US-10-027-632-288287	Sequence 288287,
c 883	6	20.0	654	6	US-10-027-632-288287	Sequence 288287,
884	6	20.0	655	9	US-10-764-420-2301	Sequence 2301, Ap
c 885	6	20.0	656	4	US-09-925-065A-99276	Sequence 99276, A
c 886	6	20.0	658	4	US-09-925-065A-267724	Sequence 267724,
887	6	20.0	658	4	US-09-925-065A-740040	Sequence 740040,
888	6	20.0	658	4	US-09-925-065A-740041	Sequence 740041,
889	6	20.0	658	4	US-09-925-065A-816271	Sequence 816271,
890	6	20.0	658	4	US-09-925-065A-896349	Sequence 896349,
c 891	6	20.0	658	8	US-10-425-115-146137	Sequence 146137,
c 892	6	20.0	659	4	US-09-925-065A-717553	Sequence 717553,
c 893	6	20.0	659	4	US-09-925-065A-717554	Sequence 717554,
c 894	6	20.0	662	4	US-09-925-065A-672274	Sequence 672274,
c 895	6	20.0	662	4	US-09-925-065A-672275	Sequence 672275,
896	6	20.0	662	4	US-09-925-065A-879284	Sequence 879284,
897	6	20.0	665	4	US-09-925-065A-88995	Sequence 88995, A
c 898	6	20.0	665	5	US-10-027-632-126434	Sequence 126434,
c 899	6	20.0	665	6	US-10-027-632-126434	Sequence 126434,
c 900	6	20.0	665	6	US-10-242-355-269	Sequence 269, App
901	6	20.0	666	5	US-10-065-200A-11	Sequence 11, Appl
c 902	6	20.0	666	5	US-10-065-200A-12	Sequence 12, Appl
903	6	20.0	666	8	US-10-855-541-11	Sequence 11, Appl
c 904	6	20.0	666	8	US-10-855-541-12	Sequence 12, Appl
c 905	6	20.0	667	3	US-09-974-300-4963	Sequence 4963, Ap
c 906	6	20.0	668	3	US-09-974-300-4970	Sequence 4970, Ap
c 907	6	20.0	669	4	US-09-925-065A-687871	Sequence 687871,
c 908	6	20.0	669	4	US-09-925-065A-687872	Sequence 687872,
c 909	6	20.0	671	4	US-09-925-065A-885097	Sequence 885097,
c 910	6	20.0	674	4	US-09-925-065A-539560	Sequence 539560,
c 911	6	20.0	674	4	US-09-925-065A-539561	Sequence 539561,
c 912	6	20.0	674	7	US-10-767-701-1485	Sequence 1485, Ap
913	6	20.0	676	5	US-10-027-632-186780	Sequence 186780,
c 914	6	20.0	676	5	US-10-027-632-243721	Sequence 243721,
915	6	20.0	676	6	US-10-027-632-186780	Sequence 186780,
c 916	6	20.0	676	6	US-10-027-632-243721	Sequence 243721,
c 917	6	20.0	677	4	US-09-925-065A-199686	Sequence 199686,
c 918	6	20.0	677	4	US-09-925-065A-199687	Sequence 199687,
c 919	6	20.0	679	7	US-10-767-701-9753	Sequence 9753, Ap
c 920	6	20.0	680	7	US-10-424-599-41994	Sequence 41994, A
921	6	20.0	684	8	US-10-653-047-7530	Sequence 7530, Ap
922	6	20.0	686	7	US-10-260-238-4379	Sequence 4379, Ap
c 923	6	20.0	689	4	US-09-925-065A-265048	Sequence 265048,
924	6	20.0	690	5	US-10-027-632-103381	Sequence 103381,
925	6	20.0	690	6	US-10-027-632-103381	Sequence 103381,
c 926	6	20.0	690	7	US-10-724-972A-108	Sequence 108, App
927	6	20.0	693	7	US-10-282-122A-29226	Sequence 29226, A
c 928	6	20.0	694	5	US-10-001-843-26	Sequence 26, Appl
c 929	6	20.0	694	10	US-11-005-609-26	Sequence 26, Appl
930	6	20.0	696	7	US-10-282-122A-29452	Sequence 29452, A
c 931	6	20.0	698	8	US-10-425-115-28004	Sequence 28004, A
c 932	6	20.0	700	5	US-10-027-632-17528	Sequence 17528, A
c 933	6	20.0	700	5	US-10-027-632-17529	Sequence 17529, A
c 934	6	20.0	700	6	US-10-027-632-17528	Sequence 17528, A
c 935	6	20.0	700	6	US-10-027-632-17529	Sequence 17529, A
936	6	20.0	705	8	US-10-425-115-75222	Sequence 75222, A
937	6	20.0	707	5	US-10-027-632-136068	Sequence 136068,
938	6	20.0	707	5	US-10-027-632-136069	Sequence 136069,
939	6	20.0	707	5	US-10-027-632-136070	Sequence 136070,
940	6	20.0	707	5	US-10-027-632-136071	Sequence 136071,
941	6	20.0	707	6	US-10-027-632-136068	Sequence 136068,
942	6	20.0	707	6	US-10-027-632-136069	Sequence 136069,
943	6	20.0	707	6	US-10-027-632-136070	Sequence 136070,
944	6	20.0	707	6	US-10-027-632-136071	Sequence 136071,
945	6	20.0	713	7	US-10-282-122A-9735	Sequence 9735, Ap
c 946	6	20.0	713	9	US-10-817-423-5	Sequence 5, Appli
c 947	6	20.0	714	7	US-10-425-114-7063	Sequence 7063, Ap
948	6	20.0	716	4	US-09-925-065A-753713	Sequence 753713,
c 949	6	20.0	719	5	US-10-027-632-145832	Sequence 145832,
c 950	6	20.0	719	5	US-10-027-632-145833	Sequence 145833,
c 951	6	20.0	719	5	US-10-027-632-145834	Sequence 145834,
c 952	6	20.0	719	6	US-10-027-632-145832	Sequence 145832,
c 953	6	20.0	719	6	US-10-027-632-145833	Sequence 145833,
c 954	6	20.0	719	6	US-10-027-632-145834	Sequence 145834,
955	6	20.0	720	7	US-10-437-963-93220	Sequence 93220, A
c 956	6	20.0	722	6	US-10-242-355-1167	Sequence 1167, Ap

c 957	6	20.0	727	4	US-09-925-065A-944125	Sequence 944125,
c 958	6	20.0	727	4	US-09-925-065A-944126	Sequence 944126,
c 959	6	20.0	727	4	US-09-925-065A-944127	Sequence 944127,
960	6	20.0	728	7	US-10-424-599-23641	Sequence 23641, A
c 961	6	20.0	732	8	US-10-425-115-120332	Sequence 120332,
c 962	6	20.0	734	4	US-09-925-065A-422894	Sequence 422894,
c 963	6	20.0	735	4	US-09-925-065A-11310	Sequence 11310, A
c 964	6	20.0	735	4	US-09-925-065A-11311	Sequence 11311, A
c 965	6	20.0	735	9	US-10-956-157-3832	Sequence 3832, Ap
c 966	6	20.0	735	9	US-10-956-157-9067	Sequence 9067, Ap
967	6	20.0	738	5	US-10-027-632-16006	Sequence 16006, A
968	6	20.0	738	5	US-10-027-632-16007	Sequence 16007, A
969	6	20.0	738	5	US-10-027-632-16008	Sequence 16008, A
970	6	20.0	738	6	US-10-027-632-16006	Sequence 16006, A
971	6	20.0	738	6	US-10-027-632-16007	Sequence 16007, A
972	6	20.0	738	6	US-10-027-632-16008	Sequence 16008, A
973	6	20.0	745	7	US-10-437-963-22092	Sequence 22092, A
974	6	20.0	746	6	US-10-029-386-20439	Sequence 20439, A
c 975	6	20.0	751	7	US-10-424-599-88211	Sequence 88211, A
976	6	20.0	755	7	US-10-767-701-9469	Sequence 9469, Ap
c 977	6	20.0	756	6	US-10-369-493-41779	Sequence 41779, A
c 978	6	20.0	758	5	US-10-066-543-106	Sequence 106, App
979	6	20.0	760	8	US-10-653-047-7777	Sequence 7777, Ap
c 980	6	20.0	761	5	US-10-027-632-18728	Sequence 18728, A
c 981	6	20.0	761	6	US-10-027-632-18728	Sequence 18728, A
982	6	20.0	764	5	US-10-027-632-13239	Sequence 13239, A
983	6	20.0	764	6	US-10-027-632-13239	Sequence 13239, A
c 984	6	20.0	768	3	US-09-738-626-2888	Sequence 2888, Ap
985	6	20.0	776	5	US-10-027-632-28652	Sequence 28652, A
986	6	20.0	776	6	US-10-027-632-28652	Sequence 28652, A
c 987	6	20.0	779	8	US-10-425-115-123427	Sequence 123427,
988	6	20.0	780	6	US-10-369-493-28835	Sequence 28835, A
989	6	20.0	780	6	US-10-369-493-28836	Sequence 28836, A
c 990	6	20.0	780	8	US-10-357-930-3985	Sequence 3985, Ap
c 991	6	20.0	781	5	US-10-108-605-360	Sequence 360, App
992	6	20.0	783	4	US-09-925-065A-9117	Sequence 9117, Ap
c 993	6	20.0	787	3	US-09-989-920-145	Sequence 145, App
994	6	20.0	787	4	US-09-925-065A-930523	Sequence 930523,
995	6	20.0	788	8	US-10-425-115-105957	Sequence 105957,
996	6	20.0	793	5	US-10-027-632-161337	Sequence 161337,
997	6	20.0	793	6	US-10-027-632-161337	Sequence 161337,
c 998	6	20.0	794	4	US-09-925-065A-927510	Sequence 927510,
999	6	20.0	796	4	US-09-925-065A-78429	Sequence 78429, A
1000	6	20.0	796	4	US-09-925-065A-78430	Sequence 78430, A

ALIGNMENTS

```
RESULT 1
US-11-084-080-15
; Sequence 15, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-15

Alignment Scores:
Pred. No.:                1.46e-23        Length:          2404
Score:                    30.00           Matches:         30
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       10              Gaps:            0

US-10-758-902-1 (1-30) x US-11-084-080-15 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 884

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        885 TTGCGCAATGAATTGGCTAAGGGCACACCA 914

RESULT 2
US-11-084-080-19
; Sequence 19, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Alignment Scores:
Pred. No.:                1.46e-23        Length:          2404
Score:                    30.00           Matches:         30
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       10              Gaps:            0

US-10-758-902-1 (1-30) x US-11-084-080-19 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1643 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1702

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
```

```
Db       1703 TTGCGCAATGAATTGGCTAAGGGCACACCA 1732

RESULT 3
US-11-084-080-21
; Sequence 21, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-21

Alignment Scores:
Pred. No.:              1.46e-23       Length:          2404
Score:                  30.00          Matches:         30
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     10             Gaps:            0

US-10-758-902-1 (1-30) x US-11-084-080-21 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 191

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        192 TTGCGCAATGAATTGGCTAAGGGCACACCA 221

RESULT 4
US-11-084-080-23
; Sequence 23, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Alignment Scores:
Pred. No.:              1.46e-23       Length:          2404
Score:                  30.00          Matches:         30
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     10             Gaps:            0

US-10-758-902-1 (1-30) x US-11-084-080-23 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        950 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1009

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db       1010 TTGCGCAATGAATTGGCTAAGGGCACACCA 1039

RESULT 5
US-11-084-080-27
; Sequence 27, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 2431
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-011
US-11-084-080-27

Alignment Scores:
Pred. No.:              1.48e-23       Length:          2431
Score:                  30.00          Matches:         30
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     10             Gaps:            0

US-10-758-902-1 (1-30) x US-11-084-080-27 (1-2431)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        852 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 911

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        912 TTGCGCAATGAATTGGCTAAGGGCACACCA 941

RESULT 6
US-10-758-902-5
; Sequence 5, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-5

Alignment Scores:
Pred. No.:              7.34e-15       Length:         65
Score:                  21.00          Matches:        21
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            70.0%          Indels:         0
DB:                     8              Gaps:           0

US-10-758-902-1 (1-30) x US-10-758-902-5 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 7
US-10-758-902-8
; Sequence 8, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)...(361)
US-10-758-902-8

Alignment Scores:
Pred. No.:              2.44e-06       Length:         363
Score:                  14.00          Matches:        14
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            46.7%          Indels:         0
DB:                     8              Gaps:           0

US-10-758-902-1 (1-30) x US-10-758-902-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 8
US-09-925-065A-47024
; Sequence 47024, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47024
;   LENGTH: 416
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-47024

Alignment Scores:
Pred. No.:              15             Length:         416
Score:                  8.00           Matches:        8
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            26.7%          Indels:         0
DB:                     4              Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-47024 (1-416)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        303 ACAGTGTCATTTAATTTGGGAGAG 326

RESULT 9
US-09-925-065A-787599
; Sequence 787599, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
```

```
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 787599
;   LENGTH: 622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-787599

Alignment Scores:
Pred. No.:              21.4          Length:         622
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-787599 (1-622)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db         17 ACAGTGTCATTTAATTTGGGAGAG 40

RESULT 10
US-09-925-065A-694362/c
; Sequence 694362, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 694362
;   LENGTH: 2443
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352,
;   LOCATION: 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362,
;   LOCATION: 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372,
;   LOCATION: 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391,
;   LOCATION: 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401,
;   LOCATION: 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411,
;   LOCATION: 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430,
;   LOCATION: 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440,
;   LOCATION: 2441, 2442
;   OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-694362

Alignment Scores:
Pred. No.:              72.6          Length:         2443
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-694362 (1-2443)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db       2040 ACAGTGTCATTTAATTTGGGAGAG 2017

RESULT 11
US-10-252-157-398
; Sequence 398, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
;  APPLICANT: Faris, Mary
;  APPLICANT:  Pearson, Cecelia I.
;  TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
;  FILE REFERENCE: PA-0027-1 US
;  CURRENT APPLICATION NUMBER: US/10/252,157
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/295,048
;  PRIOR FILING DATE: 2001-05-31
;  NUMBER OF SEQ ID NOS: 501
;  SOFTWARE: PERL Program
; SEQ ID NO 398
;   LENGTH: 2772
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030190640A1 040057.2
US-10-252-157-398

Alignment Scores:
Pred. No.:              81.3          Length:         2772
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x US-10-252-157-398 (1-2772)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db       2634 ACAGTGTCATTTAATTTGGGAGAG 2657

RESULT 12
US-10-741-601-5652/c
; Sequence 5652, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5652
```

```
;   LENGTH: 12648
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5652

Alignment Scores:
Pred. No.:              315          Length:        12648
Score:                  8.00         Matches:       8
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            26.7%        Indels:        0
DB:                     7            Gaps:          0

US-10-758-902-1 (1-30) x US-10-741-601-5652 (1-12648)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db      12509 ACAGTGTCATTTAATTTGGGAGAG 12486

RESULT 13
US-10-741-601-5690
; Sequence 5690, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5690
;   LENGTH: 31657
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5690

Alignment Scores:
Pred. No.:              715          Length:        31657
Score:                  8.00         Matches:       8
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            26.7%        Indels:        0
DB:                     7            Gaps:          0

US-10-758-902-1 (1-30) x US-10-741-601-5690 (1-31657)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        190 ACAGTGTCATTTAATTTGGGAGAG 213

RESULT 14
US-10-741-601-5771
; Sequence 5771, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5771
;   LENGTH: 41309
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5771

Alignment Scores:
Pred. No.:              906          Length:        41309
Score:                  8.00         Matches:       8
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            26.7%        Indels:        0
DB:                     7            Gaps:          0

US-10-758-902-1 (1-30) x US-10-741-601-5771 (1-41309)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db      34625 ACAGTGTCATTTAATTTGGGAGAG 34648

RESULT 15
US-10-758-902-3/c
; Sequence 3, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR primer 116 for Ribosome-inactivating protein,
;   OTHER INFORMATION: bouganin.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 3, 6, 12, 15
;   OTHER INFORMATION: n = A,T,C or G
US-10-758-902-3

Alignment Scores:
Pred. No.:              15           Length:        23
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     8            Gaps:          0

US-10-758-902-1 (1-30) x US-10-758-902-3 (1-23)

Qy          23 AsnGluLeuAlaLysGlyThr 29
               |||||||||||||||||||
Db          23 AAYGARCTNGCNAARGGNACN 3

RESULT 16
US-10-758-902-6
; Sequence 6, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
```

; PRIOR APPLICATION NUMBER: PCT/NL98/0336
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer 125 for Ribosome-inactivating protein,
; OTHER INFORMATION: bouganin.
US-10-758-902-6

Alignment Scores:

Pred. No.:	16.1	Length:	25
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-10-758-902-6 (1-25)

```
Qy         17 PheIleGlnAspLeuArgAsn 23
              |||||||||||||||||||||
Db          3 TTTATACAAGATTTGCGCAAC 23
```

RESULT 17
US-11-036-317-212714/c
; Sequence 212714, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 212714
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-212714

Alignment Scores:

Pred. No.:	16.1	Length:	25
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-1 (1-30) x US-11-036-317-212714 (1-25)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db         23 TCATTTAATTTGGGAGAAGCC 3
```

RESULT 18
US-11-036-317-329781/c
; Sequence 329781, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 329781
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-329781

Alignment Scores:

Pred. No.:	16.1	Length:	25
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-1 (1-30) x US-11-036-317-329781 (1-25)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db         21 TCATTTAATTTGGGAGAAGCC 1
```

RESULT 19
US-11-036-317-381661/c
; Sequence 381661, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 381661
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-381661

Alignment Scores:

Pred. No.:	16.1	Length:	25
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-1 (1-30) x US-11-036-317-381661 (1-25)

```
Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db         22 TCATTTAATTTGGGAGAAGCC 2
```

RESULT 20
US-11-036-317-484022/c
; Sequence 484022, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174

```
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 484022
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-484022

Alignment Scores:
Pred. No.:              16.1          Length:         25
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.3%         Indels:         0
DB:                     10            Gaps:           0

US-10-758-902-1 (1-30) x US-11-036-317-484022 (1-25)

Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db         21 AGCTTTAACCTCGGAGAGGCA 1

RESULT 21
US-11-084-080-125
; Sequence 125, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125
;   LENGTH: 36
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer OL1068
US-11-084-080-125

Alignment Scores:
Pred. No.:              22.3          Length:         36
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.3%         Indels:         0
DB:                     10            Gaps:           0

US-10-758-902-1 (1-30) x US-11-084-080-125 (1-36)

Qy          1 TyrAsnThrValSerPheAsn 7
              |||||||||||||||||||||
Db         16 TACAACACTGTGTCATTTAAC 36

RESULT 22
US-10-424-599-18718/c
; Sequence 18718, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 18718
;   LENGTH: 254
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_116906C.1
US-10-424-599-18718

Alignment Scores:
Pred. No.:              128           Length:         254
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.3%         Indels:         0
DB:                     7             Gaps:           0

US-10-758-902-1 (1-30) x US-10-424-599-18718 (1-254)

Qy          5 SerPheAsnLeuGlyGluAla 11
              |||||||||||||||||||||
Db        241 AGTTTCAATCTGGGTGAGGCC 221

RESULT 23
US-10-357-930-18350/c
; Sequence 18350, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18350
;   LENGTH: 431
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 51, 296
;   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-18350

Alignment Scores:
Pred. No.:              205           Length:         431
```

```
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x US-10-357-930-18350 (1-431)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        253 AATACAGTTTCCTTCAATTTA 233

RESULT 24
US-10-259-678-98
; Sequence 98, Application US/10259678
; Publication No. US20030198974A1
; GENERAL INFORMATION:
;  APPLICANT: Cole, Stewart
;  APPLICANT:  Buchrieser-Brosch, Roland
;  APPLICANT:  Gordon, Stephen
;  APPLICANT:  Billault, Alain
;  TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;  TITLE OF INVENTION:  THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;  TITLE OF INVENTION:  LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;  FILE REFERENCE: 3495-0169
;  CURRENT APPLICATION NUMBER: US/10/259,678
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: US/09/060,756
;  PRIOR FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 743
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
;   LENGTH: 439
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-10-259-678-98

Alignment Scores:
Pred. No.:              208           Length:        439
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-1 (1-30) x US-10-259-678-98 (1-439)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db        364 CAGGATCTCAGAAACGAGCTG 384

RESULT 25
US-09-732-627A-4376/c
; Sequence 4376, Application US/09732627A
; Publication No. US20040123338A1
; GENERAL INFORMATION:
;  APPLICANT: Fincher, Karen L.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(51770)B
;  CURRENT APPLICATION NUMBER: US/09/732,627A
;  CURRENT FILING DATE:  2000-12-08
;  NUMBER OF SEQ ID NOS: 4930
; SEQ ID NO 4376
;   LENGTH: 471
;   TYPE: DNA
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(471)
;   OTHER INFORMATION: unsure at all n locations
;   OTHER INFORMATION: Clone ID: LIB3493-033-P1-M1-G11
US-09-732-627A-4376

Alignment Scores:
Pred. No.:              221           Length:        471
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-09-732-627A-4376 (1-471)

Qy          4 ValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||
Db        379 GTGAGCTTTAATTTGGGGGAA 359

RESULT 26
US-09-764-869-187/c
; Sequence 187, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC007
;  CURRENT APPLICATION NUMBER: US/09/764,869
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2442
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 187
;   LENGTH: 472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (357)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (378)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (432)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-187

Alignment Scores:
Pred. No.:              222           Length:        472
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-09-764-869-187 (1-472)

Qy          4 ValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||
Db        245 GTTTCCTTCAAYCTAGGAGAA 225

RESULT 27
US-10-091-504-187/c
; Sequence 187, Application US/10091504
; Publication No. US20030059908A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC007C1
;  CURRENT APPLICATION NUMBER: US/10/091,504
;  CURRENT FILING DATE:  2002-03-07
;  NUMBER OF SEQ ID NOS: 2442
;  Prior Application removed - See File Wrapper or Palm
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 187
;   LENGTH: 472
```

```
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (357)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (378)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (432)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-091-504-187

Alignment Scores:
Pred. No.:              222           Length:        472
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     5             Gaps:          0

US-10-758-902-1 (1-30) x US-10-091-504-187 (1-472)

Qy          4 ValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||
Db        245 GTTTCCTTCAAYCTAGGAGAA 225

RESULT 28
US-10-227-577-187/c
; Sequence 187, Application US/10227577
; Publication No. US20040005575A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC007C2
;  CURRENT APPLICATION NUMBER: US/10/227,577
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: 10/091,504
;  PRIOR FILING DATE: 2002-03-07
;  PRIOR APPLICATION NUMBER: 09/764,869
;  PRIOR FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: 60/179,065
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/180,628
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: 60/214,886
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/217,487
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,758
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/220,963
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/217,496
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,447
;  PRIOR FILING DATE: 2000-08-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2442
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 187
;   LENGTH: 472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (357)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (378)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (432)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-227-577-187

Alignment Scores:
Pred. No.:              222           Length:        472
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-1 (1-30) x US-10-227-577-187 (1-472)

Qy          4 ValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||
Db        245 GTTTCCTTCAAYCTAGGAGAA 225

RESULT 29
US-10-357-930-48164/c
; Sequence 48164, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48164
;   LENGTH: 498
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-357-930-48164

Alignment Scores:
Pred. No.:              233           Length:        498
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.3%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x US-10-357-930-48164 (1-498)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        305 AATACAGTTTCCTTCAATTTA 285

RESULT 30
US-09-925-065A-455365
; Sequence 455365, Application US/09925065A
```

; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 455365
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-455365

Alignment Scores:

Pred. No.:	244	Length:	524
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-1 (1-30) x US-09-925-065A-455365 (1-524)

```
Qy          2 AsnThrValSerPheAsnLeu 8
              |||||||||||||||||||||
Db        247 AACACTGTTTCCTTCAATCTA 267
```

RESULT 31
US-09-925-065A-810826
; Sequence 810826, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 810826
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-810826

Alignment Scores:

Pred. No.:	253	Length:	548
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-1 (1-30) x US-09-925-065A-810826 (1-548)

```
Qy          1 TyrAsnThrValSerPheAsn 7
              |||||||||||||||||||||
Db        358 TATAACACCGTATCATTTAAT 378
```

RESULT 32
US-09-925-065A-123248
; Sequence 123248, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 123248
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-123248

Alignment Scores:

Pred. No.:	255	Length:	551
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-1 (1-30) x US-09-925-065A-123248 (1-551)

```
Qy          2 AsnThrValSerPheAsnLeu 8
              |||||||||||||||||||||
Db        344 AACACCGTCTCATTTAATCTT 364
```

RESULT 33
US-09-918-995-26126/c
; Sequence 26126, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26126
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(555)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-26126

Alignment Scores:
Pred. No.:              256          Length:        555
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     3            Gaps:          0

US-10-758-902-1 (1-30) x US-09-918-995-26126 (1-555)

Qy          5 SerPheAsnLeuGlyGluAla 11
              ||||||||||||||||||||||
Db        184 AGTTTCAATCTGGGTGAGGCC 164

RESULT 34
US-09-925-065A-760512/c
; Sequence 760512, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 760512
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-760512

Alignment Scores:
Pred. No.:              259          Length:        561
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     4            Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-760512 (1-561)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||||
Db        283 AATACGGTCTCTTTTAATTTG 263

RESULT 35
US-09-925-065A-761519
; Sequence 761519, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 761519
;   LENGTH: 565
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-761519

Alignment Scores:
Pred. No.:              260          Length:        565
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     4            Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-761519 (1-565)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||||
Db        279 AATACGGTCTCTTTTAATTTG 299

RESULT 36
US-09-925-065A-771199
; Sequence 771199, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 771199
;   LENGTH: 566
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-771199

Alignment Scores:
Pred. No.:              261          Length:        566
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     4            Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-771199 (1-566)

Qy          1 TyrAsnThrValSerPheAsn 7
              |||||||||||||||||||||
```

```
Db        190 TATAACACTGTTAGTTTTAAT 210

RESULT 37
US-09-925-065A-762385
; Sequence 762385, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 08827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 762385
;   LENGTH: 571
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-762385

Alignment Scores:
Pred. No.:              263          Length:         571
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            23.3%        Indels:         0
DB:                     4            Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-762385 (1-571)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        279 AATACGGTCTCTTTTAATTTG 299

RESULT 38
US-09-974-300-4903
; Sequence 4903, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
;  APPLICANT: Berka, Randy M.
;  APPLICANT:  Clausen, Ib Groth
;  TITLE OF INVENTION: Methods For Monitoring Multiple Gene
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE: 10085.500-US
;  CURRENT APPLICATION NUMBER: US/09/974,300
;  CURRENT FILING DATE:  2001-10-05
;  PRIOR APPLICATION NUMBER: 09/680,598
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: 60/279,526
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 8481
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4903
;   LENGTH: 588
;   TYPE: DNA
;   ORGANISM: Bacillus clausii
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(588)
;   OTHER INFORMATION: n = A,T,C or G
US-09-974-300-4903

Alignment Scores:
Pred. No.:              270          Length:         588
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            23.3%        Indels:         0
DB:                     3            Gaps:           0

US-10-758-902-1 (1-30) x US-09-974-300-4903 (1-588)

Qy          9 GlyGluAlaTyrGluTyrPro 15
              |||||||||||||||||||||
Db        470 GGAGAAGCATATGAGTATCCA 490

RESULT 39
US-10-357-930-55024
; Sequence 55024, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55024
;   LENGTH: 588
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-357-930-55024

Alignment Scores:
Pred. No.:              270          Length:         588
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            23.3%        Indels:         0
DB:                     8            Gaps:           0

US-10-758-902-1 (1-30) x US-10-357-930-55024 (1-588)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        120 AATACAGTTTCCTTCAATTTA 140

RESULT 40
US-10-972-079-881/c
; Sequence 881, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  KERR, Richard
```

```
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  HOLM, Tom
;  TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
;  TITLE OF INVENTION:  LIVESTOCK
;  FILE REFERENCE: MMI1110-2
;  CURRENT APPLICATION NUMBER: US/10/972,079
;  CURRENT FILING DATE:  2004-10-22
;  PRIOR APPLICATION NUMBER: US 60/514,333
;  PRIOR FILING DATE: 2003-10-24
;  NUMBER OF SEQ ID NOS: 96631
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 881
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Chicken  19866894085227_1
US-10-972-079-881

Alignment Scores:
Pred. No.:              275           Length:       600
Score:                  7.00          Matches:      7
Percent Similarity:     100.0%        Conservative: 0
Best Local Similarity:  100.0%        Mismatches:   0
Query Match:            23.3%         Indels:       0
DB:                     9             Gaps:         0

US-10-758-902-1 (1-30) x US-10-972-079-881 (1-600)

Qy          4 ValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||
Db        434 GTTTCATTTAATCTAGGCGAG 414


Search completed: February 20, 2006, 03:14:45
Job time : 241.408 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 02:03:29 ; Search time 105.251 Seconds
(without alignments)
605.048 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 30
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7204252 seqs, 1061369211 residues

Word size: 1

Total number of hits satisfying chosen parameters: 14406941

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160842_4223/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=oligo.rnpbn
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
-USER=US10758902_@CGN_1_1_380_@runat_17022006_160842_4223 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	8	26.7	416	6	US-09-925-065A-47024	Sequence 47024, A
	2	8	26.7	622	6	US-09-925-065A-787599	Sequence 787599,
c	3	8	26.7	2443	6	US-09-925-065A-694362	Sequence 694362,
c	4	8	26.7	12648	8	US-10-995-561-13271	Sequence 13271, A
c	5	8	26.7	31130	12	US-11-124-367A-5063	Sequence 5063, Ap
	6	8	26.7	31657	8	US-10-995-561-13334	Sequence 13334, A
	7	8	26.7	41309	8	US-10-995-561-13487	Sequence 13487, A
	8	7	23.3	439	8	US-10-802-796-98	Sequence 98, Appl
	9	7	23.3	524	6	US-09-925-065A-455365	Sequence 455365,
	10	7	23.3	548	6	US-09-925-065A-810826	Sequence 810826,
	11	7	23.3	551	6	US-09-925-065A-123248	Sequence 123248,
c	12	7	23.3	561	6	US-09-925-065A-760512	Sequence 760512,
	13	7	23.3	565	6	US-09-925-065A-761519	Sequence 761519,
	14	7	23.3	566	6	US-09-925-065A-771199	Sequence 771199,
	15	7	23.3	571	6	US-09-925-065A-762385	Sequence 762385,
	16	7	23.3	617	6	US-09-925-065A-305608	Sequence 305608,
	17	7	23.3	617	6	US-09-925-065A-305609	Sequence 305609,
c	18	7	23.3	1432	12	US-11-000-688-1223	Sequence 1223, Ap
	19	7	23.3	2645	6	US-09-925-065A-89593	Sequence 89593, A
c	20	7	23.3	21044	12	US-11-124-367A-5018	Sequence 5018, Ap
c	21	6	20.0	19	10	US-11-101-244-98592	Sequence 98592, A
c	22	6	20.0	19	11	US-11-083-784-98592	Sequence 98592, A
	23	6	20.0	22	8	US-10-310-914A-1135670	Sequence 1135670,
	24	6	20.0	24	8	US-10-310-914A-723268	Sequence 723268,
c	25	6	20.0	25	8	US-10-310-914A-424632	Sequence 424632,
	26	6	20.0	25	12	US-11-121-849-28958	Sequence 28958, A
	27	6	20.0	25	12	US-11-121-849-43082	Sequence 43082, A
	28	6	20.0	25	12	US-11-121-849-43083	Sequence 43083, A
	29	6	20.0	25	12	US-11-121-849-43733	Sequence 43733, A
	30	6	20.0	25	12	US-11-121-849-153896	Sequence 153896,
	31	6	20.0	25	12	US-11-121-849-287209	Sequence 287209,
	32	6	20.0	25	12	US-11-121-849-306644	Sequence 306644,
	33	6	20.0	25	12	US-11-121-849-306829	Sequence 306829,
	34	6	20.0	25	12	US-11-121-849-438584	Sequence 438584,
c	35	6	20.0	25	12	US-11-121-849-492968	Sequence 492968,
	36	6	20.0	25	12	US-11-121-849-671499	Sequence 671499,
	37	6	20.0	25	12	US-11-121-849-671500	Sequence 671500,
	38	6	20.0	25	12	US-11-121-849-671501	Sequence 671501,
	39	6	20.0	25	12	US-11-121-849-671502	Sequence 671502,
c	40	6	20.0	26	8	US-10-310-914A-1229715	Sequence 1229715,
c	41	6	20.0	29	8	US-10-514-761-18	Sequence 18, Appl
	42	6	20.0	50	12	US-11-175-859-4867	Sequence 4867, Ap
c	43	6	20.0	50	12	US-11-175-859-75879	Sequence 75879, A
	44	6	20.0	50	12	US-11-175-859-99214	Sequence 99214, A
	45	6	20.0	123	12	US-11-043-752-3342	Sequence 3342, Ap
	46	6	20.0	200	12	US-11-098-686-7963	Sequence 7963, Ap
c	47	6	20.0	201	8	US-10-995-561-16546	Sequence 16546, A
c	48	6	20.0	201	8	US-10-995-561-19238	Sequence 19238, A
c	49	6	20.0	201	8	US-10-995-561-78328	Sequence 78328, A
	50	6	20.0	201	12	US-11-124-367A-6976	Sequence 6976, Ap
	51	6	20.0	201	12	US-11-124-367A-13427	Sequence 13427, A
c	52	6	20.0	380	6	US-09-925-065A-228927	Sequence 228927,
c	53	6	20.0	388	6	US-09-925-065A-247522	Sequence 247522,
	54	6	20.0	398	6	US-09-925-065A-124209	Sequence 124209,
c	55	6	20.0	402	6	US-09-925-065A-585353	Sequence 585353,
c	56	6	20.0	404	6	US-09-925-065A-379589	Sequence 379589,
c	57	6	20.0	407	6	US-09-925-065A-607552	Sequence 607552,
	58	6	20.0	407	6	US-09-925-065A-613438	Sequence 613438,
	59	6	20.0	407	6	US-09-925-065A-613439	Sequence 613439,
	60	6	20.0	410	6	US-09-925-065A-508381	Sequence 508381,
c	61	6	20.0	414	6	US-09-925-065A-125919	Sequence 125919,
	62	6	20.0	416	6	US-09-925-065A-912468	Sequence 912468,
	63	6	20.0	422	6	US-09-925-065A-116233	Sequence 116233,
c	64	6	20.0	423	6	US-09-925-065A-95695	Sequence 95695, A
c	65	6	20.0	423	6	US-09-925-065A-130218	Sequence 130218,
c	66	6	20.0	424	6	US-09-925-065A-217393	Sequence 217393,
c	67	6	20.0	429	6	US-09-925-065A-130219	Sequence 130219,
	68	6	20.0	433	6	US-09-925-065A-639620	Sequence 639620,
	69	6	20.0	433	6	US-09-925-065A-639621	Sequence 639621,
c	70	6	20.0	441	6	US-09-925-065A-142089	Sequence 142089,
c	71	6	20.0	447	6	US-09-925-065A-200046	Sequence 200046,
c	72	6	20.0	449	6	US-09-925-065A-172316	Sequence 172316,
	73	6	20.0	453	8	US-10-750-185-32400	Sequence 32400, A
	74	6	20.0	453	8	US-10-750-623-32400	Sequence 32400, A
c	75	6	20.0	454	6	US-09-925-065A-778596	Sequence 778596,
c	76	6	20.0	454	6	US-09-925-065A-840036	Sequence 840036,
	77	6	20.0	457	6	US-09-925-065A-233071	Sequence 233071,

78	6	20.0	460	6	US-09-925-065A-153845	Sequence 153845,
c 79	6	20.0	462	6	US-09-925-065A-222562	Sequence 222562,
80	6	20.0	462	6	US-09-925-065A-738876	Sequence 738876,
c 81	6	20.0	462	9	US-11-021-492-176	Sequence 176, App
c 82	6	20.0	469	12	US-11-120-308-119	Sequence 119, App
83	6	20.0	475	6	US-09-925-065A-956935	Sequence 956935,
c 84	6	20.0	480	6	US-09-925-065A-440878	Sequence 440878,
85	6	20.0	481	6	US-09-925-065A-337499	Sequence 337499,
c 86	6	20.0	482	6	US-09-925-065A-442678	Sequence 442678,
c 87	6	20.0	483	7	US-10-943-015-1	Sequence 1, Appli
88	6	20.0	487	6	US-09-925-065A-844720	Sequence 844720,
c 89	6	20.0	488	6	US-09-925-065A-319278	Sequence 319278,
c 90	6	20.0	492	6	US-09-925-065A-500374	Sequence 500374,
c 91	6	20.0	492	6	US-09-925-065A-500375	Sequence 500375,
92	6	20.0	493	6	US-09-925-065A-323291	Sequence 323291,
93	6	20.0	494	6	US-09-925-065A-192427	Sequence 192427,
c 94	6	20.0	498	6	US-09-925-065A-152941	Sequence 152941,
95	6	20.0	502	6	US-09-925-065A-279603	Sequence 279603,
96	6	20.0	503	6	US-09-925-065A-579244	Sequence 579244,
97	6	20.0	503	6	US-09-925-065A-579245	Sequence 579245,
98	6	20.0	503	6	US-09-925-065A-579246	Sequence 579246,
99	6	20.0	503	6	US-09-925-065A-579247	Sequence 579247,
c 100	6	20.0	503	6	US-09-925-065A-893208	Sequence 893208,
101	6	20.0	514	6	US-09-925-065A-279604	Sequence 279604,
102	6	20.0	514	6	US-09-925-065A-350331	Sequence 350331,
103	6	20.0	515	6	US-09-925-065A-516567	Sequence 516567,
c 104	6	20.0	516	6	US-09-925-065A-186109	Sequence 186109,
105	6	20.0	517	6	US-09-925-065A-551046	Sequence 551046,
106	6	20.0	519	6	US-09-925-065A-758150	Sequence 758150,
c 107	6	20.0	522	6	US-09-925-065A-152275	Sequence 152275,
c 108	6	20.0	522	6	US-09-925-065A-152276	Sequence 152276,
c 109	6	20.0	522	6	US-09-925-065A-152277	Sequence 152277,
110	6	20.0	522	6	US-09-925-065A-551104	Sequence 551104,
111	6	20.0	523	6	US-09-925-065A-98650	Sequence 98650, A
c 112	6	20.0	523	6	US-09-925-065A-178735	Sequence 178735,
113	6	20.0	524	6	US-09-925-065A-16218	Sequence 16218, A
c 114	6	20.0	526	6	US-09-925-065A-813340	Sequence 813340,
c 115	6	20.0	529	6	US-09-925-065A-11267	Sequence 11267, A
c 116	6	20.0	529	6	US-09-925-065A-176620	Sequence 176620,
117	6	20.0	529	6	US-09-925-065A-358936	Sequence 358936,
118	6	20.0	529	6	US-09-925-065A-358937	Sequence 358937,
c 119	6	20.0	529	6	US-09-925-065A-841645	Sequence 841645,
c 120	6	20.0	530	6	US-09-925-065A-553100	Sequence 553100,
121	6	20.0	532	6	US-09-925-065A-153827	Sequence 153827,
122	6	20.0	532	6	US-09-925-065A-956909	Sequence 956909,
123	6	20.0	533	6	US-09-925-065A-593647	Sequence 593647,
124	6	20.0	533	6	US-09-925-065A-653939	Sequence 653939,
125	6	20.0	535	6	US-09-925-065A-758204	Sequence 758204,
126	6	20.0	537	6	US-09-925-065A-220036	Sequence 220036,
127	6	20.0	537	6	US-09-925-065A-220037	Sequence 220037,
128	6	20.0	537	6	US-09-925-065A-220038	Sequence 220038,
129	6	20.0	537	6	US-09-925-065A-338232	Sequence 338232,
130	6	20.0	537	6	US-09-925-065A-790763	Sequence 790763,
131	6	20.0	537	6	US-09-925-065A-790764	Sequence 790764,
132	6	20.0	537	6	US-09-925-065A-848118	Sequence 848118,
133	6	20.0	538	6	US-09-925-065A-31796	Sequence 31796, A
134	6	20.0	538	6	US-09-925-065A-238437	Sequence 238437,
135	6	20.0	538	6	US-09-925-065A-663712	Sequence 663712,
136	6	20.0	538	6	US-09-925-065A-663713	Sequence 663713,
c 137	6	20.0	540	6	US-09-925-065A-569621	Sequence 569621,
c 138	6	20.0	542	6	US-09-925-065A-496817	Sequence 496817,
c 139	6	20.0	542	6	US-09-925-065A-496818	Sequence 496818,
c 140	6	20.0	543	6	US-09-925-065A-176891	Sequence 176891,
c 141	6	20.0	543	6	US-09-925-065A-176892	Sequence 176892,
c 142	6	20.0	543	6	US-09-925-065A-376881	Sequence 376881,
c 143	6	20.0	543	6	US-09-925-065A-570031	Sequence 570031,
c 144	6	20.0	543	6	US-09-925-065A-904983	Sequence 904983,
145	6	20.0	543	6	US-09-925-065A-906601	Sequence 906601,
c 146	6	20.0	544	6	US-09-925-065A-563608	Sequence 563608,
c 147	6	20.0	545	6	US-09-925-065A-470129	Sequence 470129,
c 148	6	20.0	545	6	US-09-925-065A-806504	Sequence 806504,
c 149	6	20.0	545	6	US-09-925-065A-858396	Sequence 858396,
150	6	20.0	547	6	US-09-925-065A-118913	Sequence 118913,
151	6	20.0	548	6	US-09-925-065A-564994	Sequence 564994,
152	6	20.0	548	6	US-09-925-065A-564995	Sequence 564995,
153	6	20.0	548	6	US-09-925-065A-564996	Sequence 564996,
c 154	6	20.0	548	6	US-09-925-065A-596237	Sequence 596237,
c 155	6	20.0	548	6	US-09-925-065A-596238	Sequence 596238,
156	6	20.0	549	6	US-09-925-065A-608016	Sequence 608016,
157	6	20.0	549	6	US-09-925-065A-648127	Sequence 648127,
158	6	20.0	549	6	US-09-925-065A-736858	Sequence 736858,
159	6	20.0	549	6	US-09-925-065A-814331	Sequence 814331,
c 160	6	20.0	549	6	US-09-925-065A-900891	Sequence 900891,
161	6	20.0	550	6	US-09-925-065A-114001	Sequence 114001,
162	6	20.0	550	6	US-09-925-065A-193021	Sequence 193021,
163	6	20.0	550	6	US-09-925-065A-694846	Sequence 694846,
c 164	6	20.0	550	6	US-09-925-065A-891651	Sequence 891651,
165	6	20.0	551	6	US-09-925-065A-25630	Sequence 25630, A
c 166	6	20.0	552	6	US-09-925-065A-107183	Sequence 107183,
167	6	20.0	554	6	US-09-925-065A-112249	Sequence 112249,
168	6	20.0	554	6	US-09-925-065A-194744	Sequence 194744,
169	6	20.0	554	6	US-09-925-065A-194745	Sequence 194745,
c 170	6	20.0	554	6	US-09-925-065A-270236	Sequence 270236,
171	6	20.0	555	6	US-09-925-065A-316283	Sequence 316283,
172	6	20.0	556	6	US-09-925-065A-181661	Sequence 181661,
173	6	20.0	556	6	US-09-925-065A-181662	Sequence 181662,
c 174	6	20.0	557	6	US-09-925-065A-448753	Sequence 448753,
c 175	6	20.0	558	6	US-09-925-065A-180764	Sequence 180764,
176	6	20.0	558	6	US-09-925-065A-828604	Sequence 828604,
177	6	20.0	559	6	US-09-925-065A-152119	Sequence 152119,
178	6	20.0	559	6	US-09-925-065A-621721	Sequence 621721,
c 179	6	20.0	560	6	US-09-925-065A-103434	Sequence 103434,
c 180	6	20.0	560	6	US-09-925-065A-156687	Sequence 156687,
c 181	6	20.0	560	6	US-09-925-065A-240219	Sequence 240219,
c 182	6	20.0	561	6	US-09-925-065A-103433	Sequence 103433,
c 183	6	20.0	561	6	US-09-925-065A-399749	Sequence 399749,
184	6	20.0	561	6	US-09-925-065A-611942	Sequence 611942,
c 185	6	20.0	561	6	US-09-925-065A-748713	Sequence 748713,
186	6	20.0	562	6	US-09-925-065A-649469	Sequence 649469,
c 187	6	20.0	562	6	US-09-925-065A-782342	Sequence 782342,
c 188	6	20.0	562	6	US-09-925-065A-843127	Sequence 843127,
189	6	20.0	563	6	US-09-925-065A-449368	Sequence 449368,
c 190	6	20.0	564	6	US-09-925-065A-404422	Sequence 404422,
191	6	20.0	564	6	US-09-925-065A-814414	Sequence 814414,
192	6	20.0	565	6	US-09-925-065A-212333	Sequence 212333,
193	6	20.0	565	6	US-09-925-065A-657373	Sequence 657373,
194	6	20.0	569	6	US-09-925-065A-649886	Sequence 649886,
195	6	20.0	569	6	US-09-925-065A-649887	Sequence 649887,
196	6	20.0	569	6	US-09-925-065A-734209	Sequence 734209,
197	6	20.0	569	6	US-09-925-065A-734210	Sequence 734210,
c 198	6	20.0	571	6	US-09-925-065A-166372	Sequence 166372,
c 199	6	20.0	572	6	US-09-925-065A-397503	Sequence 397503,
c 200	6	20.0	573	6	US-09-925-065A-429737	Sequence 429737,
201	6	20.0	574	6	US-09-925-065A-378726	Sequence 378726,
c 202	6	20.0	574	6	US-09-925-065A-733492	Sequence 733492,
203	6	20.0	575	6	US-09-925-065A-165240	Sequence 165240,
c 204	6	20.0	575	6	US-09-925-065A-492813	Sequence 492813,
c 205	6	20.0	575	6	US-09-925-065A-492814	Sequence 492814,
206	6	20.0	575	6	US-09-925-065A-938868	Sequence 938868,
207	6	20.0	575	6	US-09-925-065A-938869	Sequence 938869,
208	6	20.0	576	6	US-09-925-065A-328566	Sequence 328566,
c 209	6	20.0	576	6	US-09-925-065A-632034	Sequence 632034,
c 210	6	20.0	576	6	US-09-925-065A-632035	Sequence 632035,
c 211	6	20.0	576	6	US-09-925-065A-632036	Sequence 632036,
212	6	20.0	577	6	US-09-925-065A-416541	Sequence 416541,
c 213	6	20.0	577	6	US-09-925-065A-869925	Sequence 869925,
214	6	20.0	577	6	US-09-925-065A-882171	Sequence 882171,
c 215	6	20.0	577	6	US-09-925-065A-901449	Sequence 901449,
c 216	6	20.0	577	6	US-09-925-065A-901450	Sequence 901450,
217	6	20.0	577	6	US-09-925-065A-909431	Sequence 909431,
218	6	20.0	577	6	US-09-925-065A-909432	Sequence 909432,
c 219	6	20.0	577	6	US-09-925-065A-936019	Sequence 936019,
220	6	20.0	578	6	US-09-925-065A-223701	Sequence 223701,
c 221	6	20.0	580	6	US-09-925-065A-277200	Sequence 277200,
c 222	6	20.0	580	6	US-09-925-065A-277201	Sequence 277201,
223	6	20.0	580	6	US-09-925-065A-440891	Sequence 440891,

c 224	6	20.0	580	6	US-09-925-065A-557305	Sequence 557305,
225	6	20.0	580	6	US-09-925-065A-922811	Sequence 922811,
226	6	20.0	581	6	US-09-925-065A-119754	Sequence 119754,
c 227	6	20.0	581	6	US-09-925-065A-190489	Sequence 190489,
c 228	6	20.0	581	6	US-09-925-065A-190490	Sequence 190490,
c 229	6	20.0	581	6	US-09-925-065A-874458	Sequence 874458,
c 230	6	20.0	581	6	US-09-925-065A-874459	Sequence 874459,
c 231	6	20.0	581	6	US-09-925-065A-904300	Sequence 904300,
232	6	20.0	582	6	US-09-925-065A-297555	Sequence 297555,
c 233	6	20.0	582	6	US-09-925-065A-334112	Sequence 334112,
c 234	6	20.0	582	6	US-09-925-065A-334113	Sequence 334113,
c 235	6	20.0	582	6	US-09-925-065A-469456	Sequence 469456,
236	6	20.0	582	6	US-09-925-065A-626318	Sequence 626318,
237	6	20.0	582	6	US-09-925-065A-710163	Sequence 710163,
238	6	20.0	582	6	US-09-925-065A-710164	Sequence 710164,
239	6	20.0	582	6	US-09-925-065A-710165	Sequence 710165,
c 240	6	20.0	583	6	US-09-925-065A-152564	Sequence 152564,
c 241	6	20.0	583	6	US-09-925-065A-152565	Sequence 152565,
c 242	6	20.0	583	6	US-09-925-065A-152566	Sequence 152566,
c 243	6	20.0	583	6	US-09-925-065A-152567	Sequence 152567,
244	6	20.0	583	6	US-09-925-065A-250481	Sequence 250481,
245	6	20.0	583	6	US-09-925-065A-299836	Sequence 299836,
c 246	6	20.0	584	6	US-09-925-065A-941617	Sequence 941617,
c 247	6	20.0	584	6	US-09-925-065A-941618	Sequence 941618,
c 248	6	20.0	585	6	US-09-925-065A-753296	Sequence 753296,
249	6	20.0	585	6	US-09-925-065A-896177	Sequence 896177,
250	6	20.0	586	6	US-09-925-065A-429909	Sequence 429909,
251	6	20.0	586	6	US-09-925-065A-429910	Sequence 429910,
c 252	6	20.0	587	6	US-09-925-065A-652296	Sequence 652296,
c 253	6	20.0	588	6	US-09-925-065A-21277	Sequence 21277, A
c 254	6	20.0	591	6	US-09-925-065A-650784	Sequence 650784,
c 255	6	20.0	591	6	US-09-925-065A-650785	Sequence 650785,
c 256	6	20.0	591	6	US-09-925-065A-713026	Sequence 713026,
c 257	6	20.0	591	6	US-09-925-065A-713027	Sequence 713027,
c 258	6	20.0	591	6	US-09-925-065A-713028	Sequence 713028,
259	6	20.0	592	6	US-09-925-065A-570114	Sequence 570114,
c 260	6	20.0	594	6	US-09-925-065A-549928	Sequence 549928,
c 261	6	20.0	594	6	US-09-925-065A-712739	Sequence 712739,
262	6	20.0	594	6	US-09-925-065A-921288	Sequence 921288,
263	6	20.0	594	6	US-09-925-065A-930365	Sequence 930365,
264	6	20.0	595	6	US-09-925-065A-122755	Sequence 122755,
265	6	20.0	595	6	US-09-925-065A-122756	Sequence 122756,
266	6	20.0	595	6	US-09-925-065A-122757	Sequence 122757,
c 267	6	20.0	595	6	US-09-925-065A-623586	Sequence 623586,
268	6	20.0	595	6	US-09-925-065A-667951	Sequence 667951,
269	6	20.0	596	6	US-09-925-065A-534821	Sequence 534821,
c 270	6	20.0	597	6	US-09-925-065A-275874	Sequence 275874,
271	6	20.0	597	6	US-09-925-065A-357220	Sequence 357220,
c 272	6	20.0	598	8	US-10-750-185-21227	Sequence 21227, A
c 273	6	20.0	598	8	US-10-750-623-21227	Sequence 21227, A
274	6	20.0	600	8	US-10-750-185-249	Sequence 249, App
275	6	20.0	600	8	US-10-750-185-1390	Sequence 1390, Ap
276	6	20.0	600	8	US-10-750-185-2363	Sequence 2363, Ap
277	6	20.0	600	8	US-10-750-623-249	Sequence 249, App
278	6	20.0	600	8	US-10-750-623-1390	Sequence 1390, Ap
279	6	20.0	600	8	US-10-750-623-2363	Sequence 2363, Ap
280	6	20.0	600	12	US-11-136-527-7665	Sequence 7665, Ap
c 281	6	20.0	601	6	US-09-925-065A-431857	Sequence 431857,
282	6	20.0	603	6	US-09-925-065A-81159	Sequence 81159, A
283	6	20.0	603	6	US-09-925-065A-81160	Sequence 81160, A
284	6	20.0	603	6	US-09-925-065A-81161	Sequence 81161, A
285	6	20.0	603	6	US-09-925-065A-588934	Sequence 588934,
c 286	6	20.0	603	6	US-09-925-065A-622145	Sequence 622145,
c 287	6	20.0	603	6	US-09-925-065A-622146	Sequence 622146,
c 288	6	20.0	604	6	US-09-925-065A-146201	Sequence 146201,
c 289	6	20.0	604	6	US-09-925-065A-355307	Sequence 355307,
c 290	6	20.0	604	6	US-09-925-065A-355308	Sequence 355308,
291	6	20.0	604	6	US-09-925-065A-357158	Sequence 357158,
c 292	6	20.0	606	6	US-09-925-065A-48331	Sequence 48331, A
c 293	6	20.0	606	6	US-09-925-065A-258100	Sequence 258100,
c 294	6	20.0	606	6	US-09-925-065A-258101	Sequence 258101,
c 295	6	20.0	606	6	US-09-925-065A-258102	Sequence 258102,
296	6	20.0	606	6	US-09-925-065A-543797	Sequence 543797,
297	6	20.0	606	6	US-09-925-065A-543798	Sequence 543798,
c 298	6	20.0	606	6	US-09-925-065A-575932	Sequence 575932,
c 299	6	20.0	606	6	US-09-925-065A-834694	Sequence 834694,
300	6	20.0	607	6	US-09-925-065A-254618	Sequence 254618,
301	6	20.0	609	6	US-09-925-065A-760518	Sequence 760518,
c 302	6	20.0	609	6	US-09-925-065A-891938	Sequence 891938,
c 303	6	20.0	609	6	US-09-925-065A-891939	Sequence 891939,
c 304	6	20.0	609	6	US-09-925-065A-914766	Sequence 914766,
305	6	20.0	610	6	US-09-925-065A-215370	Sequence 215370,
c 306	6	20.0	610	6	US-09-925-065A-244058	Sequence 244058,
c 307	6	20.0	610	6	US-09-925-065A-609920	Sequence 609920,
c 308	6	20.0	610	6	US-09-925-065A-609921	Sequence 609921,
c 309	6	20.0	610	6	US-09-925-065A-609922	Sequence 609922,
310	6	20.0	610	6	US-09-925-065A-798636	Sequence 798636,
311	6	20.0	610	6	US-09-925-065A-852772	Sequence 852772,
c 312	6	20.0	611	6	US-09-925-065A-102390	Sequence 102390,
c 313	6	20.0	612	6	US-09-925-065A-116514	Sequence 116514,
314	6	20.0	612	6	US-09-925-065A-391944	Sequence 391944,
315	6	20.0	613	6	US-09-925-065A-265418	Sequence 265418,
c 316	6	20.0	613	6	US-09-925-065A-924293	Sequence 924293,
317	6	20.0	615	6	US-09-925-065A-85201	Sequence 85201, A
318	6	20.0	615	6	US-09-925-065A-85202	Sequence 85202, A
319	6	20.0	615	6	US-09-925-065A-85203	Sequence 85203, A
c 320	6	20.0	615	6	US-09-925-065A-334165	Sequence 334165,
c 321	6	20.0	615	6	US-09-925-065A-334167	Sequence 334167,
c 322	6	20.0	615	6	US-09-925-065A-878206	Sequence 878206,
c 323	6	20.0	615	6	US-09-925-065A-878207	Sequence 878207,
c 324	6	20.0	615	6	US-09-925-065A-878208	Sequence 878208,
c 325	6	20.0	615	6	US-09-925-065A-878209	Sequence 878209,
c 326	6	20.0	616	6	US-09-925-065A-279639	Sequence 279639,
327	6	20.0	616	6	US-09-925-065A-384912	Sequence 384912,
c 328	6	20.0	616	6	US-09-925-065A-393932	Sequence 393932,
329	6	20.0	616	6	US-09-925-065A-532579	Sequence 532579,
c 330	6	20.0	616	6	US-09-925-065A-556565	Sequence 556565,
331	6	20.0	617	6	US-09-925-065A-395194	Sequence 395194,
332	6	20.0	617	6	US-09-925-065A-851221	Sequence 851221,
333	6	20.0	619	6	US-09-925-065A-453134	Sequence 453134,
c 334	6	20.0	619	6	US-09-925-065A-642412	Sequence 642412,
c 335	6	20.0	619	6	US-09-925-065A-642413	Sequence 642413,
c 336	6	20.0	619	6	US-09-925-065A-830191	Sequence 830191,
337	6	20.0	620	6	US-09-925-065A-126975	Sequence 126975,
338	6	20.0	620	6	US-09-925-065A-136004	Sequence 136004,
c 339	6	20.0	620	6	US-09-925-065A-399750	Sequence 399750,
c 340	6	20.0	620	6	US-09-925-065A-399751	Sequence 399751,
c 341	6	20.0	621	6	US-09-925-065A-389520	Sequence 389520,
c 342	6	20.0	621	6	US-09-925-065A-389521	Sequence 389521,
c 343	6	20.0	621	6	US-09-925-065A-389522	Sequence 389522,
c 344	6	20.0	621	6	US-09-925-065A-415707	Sequence 415707,
345	6	20.0	622	6	US-09-925-065A-405915	Sequence 405915,
346	6	20.0	622	6	US-09-925-065A-642411	Sequence 642411,
347	6	20.0	622	6	US-09-925-065A-684894	Sequence 684894,
c 348	6	20.0	623	6	US-09-925-065A-277199	Sequence 277199,
349	6	20.0	623	6	US-09-925-065A-343588	Sequence 343588,
350	6	20.0	623	6	US-09-925-065A-449084	Sequence 449084,
351	6	20.0	623	6	US-09-925-065A-639364	Sequence 639364,
352	6	20.0	623	6	US-09-925-065A-658800	Sequence 658800,
353	6	20.0	628	6	US-09-925-065A-524870	Sequence 524870,
354	6	20.0	628	6	US-09-925-065A-524871	Sequence 524871,
355	6	20.0	628	6	US-09-925-065A-741720	Sequence 741720,
c 356	6	20.0	629	6	US-09-925-065A-789500	Sequence 789500,
357	6	20.0	630	6	US-09-925-065A-247810	Sequence 247810,
358	6	20.0	631	6	US-09-925-065A-774513	Sequence 774513,
359	6	20.0	633	6	US-09-925-065A-534342	Sequence 534342,
c 360	6	20.0	633	6	US-09-925-065A-790937	Sequence 790937,
361	6	20.0	634	6	US-09-925-065A-668969	Sequence 668969,
c 362	6	20.0	634	6	US-09-925-065A-899217	Sequence 899217,
c 363	6	20.0	634	6	US-09-925-065A-899218	Sequence 899218,
364	6	20.0	636	6	US-09-925-065A-554580	Sequence 554580,
365	6	20.0	636	6	US-09-925-065A-901667	Sequence 901667,
c 366	6	20.0	637	6	US-09-925-065A-75347	Sequence 75347, A
367	6	20.0	637	6	US-09-925-065A-479888	Sequence 479888,
c 368	6	20.0	637	6	US-09-925-065A-670197	Sequence 670197,
c 369	6	20.0	637	6	US-09-925-065A-777277	Sequence 777277,

	370	6	20.0	640	6	US-09-925-065A-885237 Sequence 885237,
	371	6	20.0	641	6	US-09-925-065A-722902 Sequence 722902,
	372	6	20.0	641	6	US-09-925-065A-722903 Sequence 722903,
c	373	6	20.0	642	6	US-09-925-065A-492701 Sequence 492701,
c	374	6	20.0	642	6	US-09-925-065A-760449 Sequence 760449,
c	375	6	20.0	642	6	US-09-925-065A-829354 Sequence 829354,
	376	6	20.0	643	6	US-09-925-065A-424383 Sequence 424383,
	377	6	20.0	643	6	US-09-925-065A-424384 Sequence 424384,
	378	6	20.0	643	6	US-09-925-065A-424385 Sequence 424385,
c	379	6	20.0	643	6	US-09-925-065A-583886 Sequence 583886,
c	380	6	20.0	643	6	US-09-925-065A-583887 Sequence 583887,
c	381	6	20.0	643	6	US-09-925-065A-583888 Sequence 583888,
c	382	6	20.0	643	6	US-09-925-065A-856425 Sequence 856425,
c	383	6	20.0	644	6	US-09-925-065A-179456 Sequence 179456,
	384	6	20.0	644	6	US-09-925-065A-744282 Sequence 744282,
	385	6	20.0	648	6	US-09-925-065A-815816 Sequence 815816,
c	386	6	20.0	648	6	US-09-925-065A-896418 Sequence 896418,
c	387	6	20.0	648	6	US-09-925-065A-916987 Sequence 916987,
c	388	6	20.0	649	6	US-09-925-065A-1368 Sequence 1368, Ap
	389	6	20.0	649	6	US-09-925-065A-56971 Sequence 56971, A
	390	6	20.0	650	6	US-09-925-065A-954664 Sequence 954664,
	391	6	20.0	652	6	US-09-925-065A-498800 Sequence 498800,
	392	6	20.0	652	6	US-09-925-065A-827548 Sequence 827548,
c	393	6	20.0	656	6	US-09-925-065A-99276 Sequence 99276, A
c	394	6	20.0	658	6	US-09-925-065A-267724 Sequence 267724,
	395	6	20.0	658	6	US-09-925-065A-740040 Sequence 740040,
	396	6	20.0	658	6	US-09-925-065A-740041 Sequence 740041,
	397	6	20.0	658	6	US-09-925-065A-816271 Sequence 816271,
	398	6	20.0	658	6	US-09-925-065A-896349 Sequence 896349,
c	399	6	20.0	659	6	US-09-925-065A-717553 Sequence 717553,
c	400	6	20.0	659	6	US-09-925-065A-717554 Sequence 717554,
c	401	6	20.0	662	6	US-09-925-065A-672274 Sequence 672274,
c	402	6	20.0	662	6	US-09-925-065A-672275 Sequence 672275,
	403	6	20.0	662	6	US-09-925-065A-879284 Sequence 879284,
	404	6	20.0	665	6	US-09-925-065A-88995 Sequence 88995, A
c	405	6	20.0	669	6	US-09-925-065A-687871 Sequence 687871,
c	406	6	20.0	669	6	US-09-925-065A-687872 Sequence 687872,
c	407	6	20.0	671	6	US-09-925-065A-885097 Sequence 885097,
c	408	6	20.0	674	6	US-09-925-065A-539560 Sequence 539560,
c	409	6	20.0	674	6	US-09-925-065A-539561 Sequence 539561,
c	410	6	20.0	676	12	US-11-136-527-3569 Sequence 3569, Ap
c	411	6	20.0	677	6	US-09-925-065A-199686 Sequence 199686,
c	412	6	20.0	677	6	US-09-925-065A-199687 Sequence 199687,
c	413	6	20.0	689	6	US-09-925-065A-265048 Sequence 265048,
c	414	6	20.0	693	8	US-10-467-657-6995 Sequence 6995, Ap
	415	6	20.0	693	8	US-10-467-657-7947 Sequence 7947, Ap
	416	6	20.0	709	8	US-10-750-185-63486 Sequence 63486, A
	417	6	20.0	709	8	US-10-750-623-63486 Sequence 63486, A
	418	6	20.0	716	6	US-09-925-065A-753713 Sequence 753713,
c	419	6	20.0	727	6	US-09-925-065A-944125 Sequence 944125,
c	420	6	20.0	727	6	US-09-925-065A-944126 Sequence 944126,
c	421	6	20.0	727	6	US-09-925-065A-944127 Sequence 944127,
c	422	6	20.0	734	6	US-09-925-065A-422894 Sequence 422894,
c	423	6	20.0	735	6	US-09-925-065A-11310 Sequence 11310, A
c	424	6	20.0	735	6	US-09-925-065A-11311 Sequence 11311, A
c	425	6	20.0	749	8	US-10-750-185-59887 Sequence 59887, A
c	426	6	20.0	749	8	US-10-750-623-59887 Sequence 59887, A
	427	6	20.0	753	12	US-11-098-686-9961 Sequence 9961, Ap
	428	6	20.0	783	6	US-09-925-065A-9117 Sequence 9117, Ap
	429	6	20.0	787	6	US-09-925-065A-930523 Sequence 930523,
c	430	6	20.0	794	6	US-09-925-065A-927510 Sequence 927510,
	431	6	20.0	796	6	US-09-925-065A-78429 Sequence 78429, A
	432	6	20.0	796	6	US-09-925-065A-78430 Sequence 78430, A
	433	6	20.0	796	6	US-09-925-065A-78431 Sequence 78431, A
	434	6	20.0	798	6	US-09-925-065A-85197 Sequence 85197, A
c	435	6	20.0	799	6	US-09-925-065A-44054 Sequence 44054, A
c	436	6	20.0	799	6	US-09-925-065A-44055 Sequence 44055, A
	437	6	20.0	802	6	US-09-925-065A-929696 Sequence 929696,
	438	6	20.0	802	6	US-09-925-065A-950345 Sequence 950345,
	439	6	20.0	820	8	US-10-750-185-44705 Sequence 44705, A
	440	6	20.0	820	8	US-10-750-623-44705 Sequence 44705, A
	441	6	20.0	821	6	US-09-925-065A-26564 Sequence 26564, A
c	442	6	20.0	844	6	US-09-925-065A-7777 Sequence 7777, Ap
c	443	6	20.0	851	6	US-09-925-065A-722202 Sequence 722202,
	444	6	20.0	862	8	US-10-750-185-63117 Sequence 63117, A
	445	6	20.0	862	8	US-10-750-623-63117 Sequence 63117, A
c	446	6	20.0	864	6	US-09-925-065A-85524 Sequence 85524, A
c	447	6	20.0	891	12	US-11-055-822-1139 Sequence 1139, Ap
	448	6	20.0	899	8	US-10-750-185-30941 Sequence 30941, A
	449	6	20.0	899	8	US-10-750-623-30941 Sequence 30941, A
	450	6	20.0	916	8	US-10-750-185-28072 Sequence 28072, A
	451	6	20.0	916	8	US-10-750-623-28072 Sequence 28072, A
c	452	6	20.0	951	8	US-10-750-185-52680 Sequence 52680, A
c	453	6	20.0	951	8	US-10-750-623-52680 Sequence 52680, A
c	454	6	20.0	971	6	US-09-925-065A-15001 Sequence 15001, A
	455	6	20.0	978	6	US-09-925-065A-70772 Sequence 70772, A
	456	6	20.0	978	6	US-09-925-065A-70773 Sequence 70773, A
	457	6	20.0	978	6	US-09-925-065A-70774 Sequence 70774, A
	458	6	20.0	978	6	US-09-925-065A-70775 Sequence 70775, A
c	459	6	20.0	983	6	US-09-925-065A-551799 Sequence 551799,
	460	6	20.0	993	8	US-10-750-185-42801 Sequence 42801, A
	461	6	20.0	993	8	US-10-750-623-42801 Sequence 42801, A
c	462	6	20.0	1012	8	US-10-750-185-48092 Sequence 48092, A
c	463	6	20.0	1012	8	US-10-750-623-48092 Sequence 48092, A
c	464	6	20.0	1022	12	US-11-136-527-3489 Sequence 3489, Ap
c	465	6	20.0	1035	8	US-10-750-185-63665 Sequence 63665, A
c	466	6	20.0	1035	8	US-10-750-623-63665 Sequence 63665, A
	467	6	20.0	1042	8	US-10-750-185-29001 Sequence 29001, A
	468	6	20.0	1042	8	US-10-750-623-29001 Sequence 29001, A
	469	6	20.0	1047	12	US-11-074-176-83 Sequence 83, Appl
	470	6	20.0	1074	8	US-10-750-185-48393 Sequence 48393, A
	471	6	20.0	1074	8	US-10-750-623-48393 Sequence 48393, A
c	472	6	20.0	1095	8	US-10-750-185-26931 Sequence 26931, A
c	473	6	20.0	1095	8	US-10-750-623-26931 Sequence 26931, A
	474	6	20.0	1106	6	US-09-925-065A-89940 Sequence 89940, A
c	475	6	20.0	1115	8	US-10-750-185-36488 Sequence 36488, A
c	476	6	20.0	1115	8	US-10-750-623-36488 Sequence 36488, A
c	477	6	20.0	1118	8	US-10-750-185-47591 Sequence 47591, A
c	478	6	20.0	1118	8	US-10-750-623-47591 Sequence 47591, A
	479	6	20.0	1127	8	US-10-750-185-54535 Sequence 54535, A
	480	6	20.0	1127	8	US-10-750-623-54535 Sequence 54535, A
c	481	6	20.0	1129	6	US-09-925-065A-685347 Sequence 685347,
c	482	6	20.0	1129	6	US-09-925-065A-685348 Sequence 685348,
c	483	6	20.0	1131	8	US-10-750-185-43994 Sequence 43994, A
c	484	6	20.0	1131	8	US-10-750-623-43994 Sequence 43994, A
	485	6	20.0	1135	8	US-10-750-185-63430 Sequence 63430, A
	486	6	20.0	1135	8	US-10-750-623-63430 Sequence 63430, A
	487	6	20.0	1136	6	US-09-925-065A-295293 Sequence 295293,
	488	6	20.0	1176	8	US-10-750-185-59409 Sequence 59409, A
	489	6	20.0	1176	8	US-10-750-623-59409 Sequence 59409, A
	490	6	20.0	1198	6	US-09-925-065A-703565 Sequence 703565,
c	491	6	20.0	1203	6	US-09-925-065A-15797 Sequence 15797, A
	492	6	20.0	1203	8	US-10-750-185-35846 Sequence 35846, A
	493	6	20.0	1203	8	US-10-750-623-35846 Sequence 35846, A
c	494	6	20.0	1255	6	US-09-925-065A-71277 Sequence 71277, A
	495	6	20.0	1284	6	US-09-925-065A-68313 Sequence 68313, A
	496	6	20.0	1300	6	US-09-925-065A-2864 Sequence 2864, Ap
	497	6	20.0	1300	6	US-09-925-065A-2865 Sequence 2865, Ap
	498	6	20.0	1305	6	US-09-925-065A-2215 Sequence 2215, Ap
	499	6	20.0	1315	8	US-10-750-185-62090 Sequence 62090, A
	500	6	20.0	1315	8	US-10-750-623-62090 Sequence 62090, A
	501	6	20.0	1341	8	US-10-750-185-25260 Sequence 25260, A
	502	6	20.0	1341	8	US-10-750-623-25260 Sequence 25260, A
c	503	6	20.0	1347	6	US-09-925-065A-25430 Sequence 25430, A
	504	6	20.0	1368	6	US-09-925-065A-715512 Sequence 715512,
c	505	6	20.0	1371	6	US-09-925-065A-711007 Sequence 711007,
c	506	6	20.0	1371	6	US-09-925-065A-711008 Sequence 711008,
c	507	6	20.0	1407	8	US-10-750-185-62126 Sequence 62126, A
c	508	6	20.0	1407	8	US-10-750-623-62126 Sequence 62126, A
	509	6	20.0	1415	8	US-10-750-185-45779 Sequence 45779, A
	510	6	20.0	1415	8	US-10-750-623-45779 Sequence 45779, A
	511	6	20.0	1417	8	US-10-750-185-32389 Sequence 32389, A
	512	6	20.0	1417	8	US-10-750-623-32389 Sequence 32389, A
	513	6	20.0	1445	8	US-10-750-185-30048 Sequence 30048, A
	514	6	20.0	1445	8	US-10-750-623-30048 Sequence 30048, A
c	515	6	20.0	1551	7	US-10-506-448A-1 Sequence 1, Appli

c 516	6	20.0	1558	8	US-10-750-185-30162	Sequence 30162, A
c 517	6	20.0	1558	8	US-10-750-623-30162	Sequence 30162, A
c 518	6	20.0	1587	8	US-10-750-185-51521	Sequence 51521, A
c 519	6	20.0	1587	8	US-10-750-623-51521	Sequence 51521, A
c 520	6	20.0	1588	8	US-10-750-185-43785	Sequence 43785, A
c 521	6	20.0	1588	8	US-10-750-623-43785	Sequence 43785, A
522	6	20.0	1603	6	US-09-925-065A-12675	Sequence 12675, A
c 523	6	20.0	1603	6	US-09-925-065A-37093	Sequence 37093, A
524	6	20.0	1615	8	US-10-750-185-37834	Sequence 37834, A
525	6	20.0	1615	8	US-10-750-623-37834	Sequence 37834, A
526	6	20.0	1617	8	US-10-467-657-3869	Sequence 3869, Ap
c 527	6	20.0	1643	8	US-10-453-372-589	Sequence 589, App
528	6	20.0	1645	6	US-09-925-065A-719335	Sequence 719335,
c 529	6	20.0	1648	8	US-10-453-372-573	Sequence 573, App
c 530	6	20.0	1648	8	US-10-453-372-587	Sequence 587, App
531	6	20.0	1650	6	US-09-925-065A-549705	Sequence 549705,
532	6	20.0	1661	6	US-09-925-065A-57231	Sequence 57231, A
c 533	6	20.0	1668	8	US-10-453-372-581	Sequence 581, App
c 534	6	20.0	1668	8	US-10-453-372-583	Sequence 583, App
c 535	6	20.0	1685	8	US-10-750-185-55827	Sequence 55827, A
c 536	6	20.0	1685	8	US-10-750-623-55827	Sequence 55827, A
537	6	20.0	1710	8	US-10-750-185-25646	Sequence 25646, A
538	6	20.0	1710	8	US-10-750-623-25646	Sequence 25646, A
c 539	6	20.0	1712	6	US-09-925-065A-45965	Sequence 45965, A
c 540	6	20.0	1722	8	US-10-453-372-565	Sequence 565, App
541	6	20.0	1740	8	US-10-750-185-46486	Sequence 46486, A
542	6	20.0	1740	8	US-10-750-623-46486	Sequence 46486, A
c 543	6	20.0	1741	8	US-10-750-185-47781	Sequence 47781, A
c 544	6	20.0	1741	8	US-10-750-623-47781	Sequence 47781, A
c 545	6	20.0	1758	8	US-10-453-372-595	Sequence 595, App
c 546	6	20.0	1762	8	US-10-453-372-597	Sequence 597, App
c 547	6	20.0	1780	12	US-11-136-527-3695	Sequence 3695, Ap
c 548	6	20.0	1792	12	US-11-127-832-16	Sequence 16, Appl
549	6	20.0	1830	8	US-10-750-185-56734	Sequence 56734, A
550	6	20.0	1830	8	US-10-750-623-56734	Sequence 56734, A
c 551	6	20.0	1831	6	US-09-925-065A-41754	Sequence 41754, A
c 552	6	20.0	1831	6	US-09-925-065A-41755	Sequence 41755, A
c 553	6	20.0	1831	6	US-09-925-065A-41756	Sequence 41756, A
c 554	6	20.0	1833	8	US-10-750-185-56650	Sequence 56650, A
c 555	6	20.0	1833	8	US-10-750-623-56650	Sequence 56650, A
556	6	20.0	1847	6	US-09-925-065A-723850	Sequence 723850,
557	6	20.0	1861	8	US-10-750-185-39687	Sequence 39687, A
558	6	20.0	1861	8	US-10-750-623-39687	Sequence 39687, A
c 559	6	20.0	1872	8	US-10-750-185-55267	Sequence 55267, A
c 560	6	20.0	1872	8	US-10-750-623-55267	Sequence 55267, A
c 561	6	20.0	1880	8	US-10-750-185-53199	Sequence 53199, A
c 562	6	20.0	1880	8	US-10-750-623-53199	Sequence 53199, A
c 563	6	20.0	1891	12	US-11-196-400-4	Sequence 4, Appli
c 564	6	20.0	1904	8	US-10-750-185-39758	Sequence 39758, A
c 565	6	20.0	1904	8	US-10-750-623-39758	Sequence 39758, A
c 566	6	20.0	1917	8	US-10-750-185-26353	Sequence 26353, A
c 567	6	20.0	1917	8	US-10-750-623-26353	Sequence 26353, A
c 568	6	20.0	1923	12	US-11-136-527-3435	Sequence 3435, Ap
c 569	6	20.0	1939	6	US-09-925-065A-551922	Sequence 551922,
c 570	6	20.0	1941	12	US-11-136-527-2952	Sequence 2952, Ap
571	6	20.0	1962	8	US-10-750-185-55778	Sequence 55778, A
572	6	20.0	1962	8	US-10-750-623-55778	Sequence 55778, A
573	6	20.0	1966	8	US-10-750-185-60037	Sequence 60037, A
574	6	20.0	1966	8	US-10-750-623-60037	Sequence 60037, A
c 575	6	20.0	1971	12	US-11-124-291-1	Sequence 1, Appli
576	6	20.0	2001	12	US-11-043-752-3343	Sequence 3343, Ap
577	6	20.0	2002	6	US-09-925-065A-95214	Sequence 95214, A
c 578	6	20.0	2004	9	US-11-183-205-23	Sequence 23, Appl
579	6	20.0	2054	8	US-10-750-185-24673	Sequence 24673, A
580	6	20.0	2054	8	US-10-750-623-24673	Sequence 24673, A
c 581	6	20.0	2058	8	US-10-453-372-567	Sequence 567, App
c 582	6	20.0	2161	8	US-10-510-386-211	Sequence 211, App
c 583	6	20.0	2242	9	US-11-072-512-1897	Sequence 1897, Ap
584	6	20.0	2246	8	US-10-750-185-45870	Sequence 45870, A
585	6	20.0	2246	8	US-10-750-623-45870	Sequence 45870, A
586	6	20.0	2275	6	US-09-925-065A-551671	Sequence 551671,
587	6	20.0	2283	8	US-10-750-185-63183	Sequence 63183, A
588	6	20.0	2283	8	US-10-750-623-63183	Sequence 63183, A
589	6	20.0	2296	8	US-10-750-185-62004	Sequence 62004, A
590	6	20.0	2296	8	US-10-750-623-62004	Sequence 62004, A
591	6	20.0	2334	8	US-10-467-657-1685	Sequence 1685, Ap
592	6	20.0	2337	9	US-11-072-512-1530	Sequence 1530, Ap
c 593	6	20.0	2397	8	US-10-453-372-569	Sequence 569, App
594	6	20.0	2429	9	US-11-072-512-1792	Sequence 1792, Ap
c 595	6	20.0	2433	8	US-10-453-372-579	Sequence 579, App
596	6	20.0	2439	8	US-10-750-185-43366	Sequence 43366, A
597	6	20.0	2439	8	US-10-750-623-43366	Sequence 43366, A
c 598	6	20.0	2481	8	US-10-453-372-599	Sequence 599, App
c 599	6	20.0	2526	7	US-10-877-346-3	Sequence 3, Appli
c 600	6	20.0	2531	7	US-10-877-346-4	Sequence 4, Appli
c 601	6	20.0	2531	8	US-10-453-372-593	Sequence 593, App
c 602	6	20.0	2539	8	US-10-453-372-585	Sequence 585, App
c 603	6	20.0	2548	8	US-10-453-372-601	Sequence 601, App
c 604	6	20.0	2555	7	US-10-989-767A-656	Sequence 656, App
605	6	20.0	2587	8	US-10-750-185-32185	Sequence 32185, A
606	6	20.0	2587	8	US-10-750-623-32185	Sequence 32185, A
c 607	6	20.0	2603	6	US-09-925-065A-718499	Sequence 718499,
c 608	6	20.0	2603	6	US-09-925-065A-718500	Sequence 718500,
609	6	20.0	2606	9	US-11-072-512-17	Sequence 17, Appl
c 610	6	20.0	2615	6	US-09-925-065A-80174	Sequence 80174, A
c 611	6	20.0	2615	6	US-09-925-065A-80175	Sequence 80175, A
612	6	20.0	2662	12	US-11-226-701-3	Sequence 3, Appli
c 613	6	20.0	2711	9	US-11-072-512-15	Sequence 15, Appl
c 614	6	20.0	2735	6	US-09-925-065A-714787	Sequence 714787,
615	6	20.0	2736	8	US-10-858-730-38	Sequence 38, Appl
c 616	6	20.0	2736	12	US-11-120-308-123	Sequence 123, App
c 617	6	20.0	2838	7	US-10-877-346-1	Sequence 1, Appli
c 618	6	20.0	2838	8	US-10-453-372-591	Sequence 591, App
619	6	20.0	2840	6	US-09-925-065A-700073	Sequence 700073,
c 620	6	20.0	2977	8	US-10-750-185-55153	Sequence 55153, A
c 621	6	20.0	2977	8	US-10-750-623-55153	Sequence 55153, A
622	6	20.0	3081	8	US-10-750-185-39843	Sequence 39843, A
623	6	20.0	3081	8	US-10-750-623-39843	Sequence 39843, A
624	6	20.0	3109	8	US-10-750-185-54891	Sequence 54891, A
625	6	20.0	3109	8	US-10-750-623-54891	Sequence 54891, A
626	6	20.0	3112	8	US-10-750-185-60162	Sequence 60162, A
627	6	20.0	3112	8	US-10-750-623-60162	Sequence 60162, A
628	6	20.0	3114	12	US-11-052-554A-633	Sequence 633, App
629	6	20.0	3119	12	US-11-124-368A-98	Sequence 98, Appl
630	6	20.0	3173	12	US-11-124-368A-95	Sequence 95, Appl
c 631	6	20.0	3436	8	US-10-793-626-3556	Sequence 3556, Ap
c 632	6	20.0	3452	7	US-10-943-015-3	Sequence 3, Appli
c 633	6	20.0	3563	6	US-09-925-065A-680878	Sequence 680878,
634	6	20.0	3567	12	US-11-074-176-133	Sequence 133, App
635	6	20.0	3712	8	US-10-750-185-33047	Sequence 33047, A
636	6	20.0	3712	8	US-10-750-623-33047	Sequence 33047, A
637	6	20.0	3870	8	US-10-947-249-58	Sequence 58, Appl
638	6	20.0	4863	12	US-11-000-688-263	Sequence 263, App
639	6	20.0	4871	8	US-10-995-561-506	Sequence 506, App
640	6	20.0	5190	12	US-11-091-883-31	Sequence 31, Appl
641	6	20.0	5190	12	US-11-091-883-177	Sequence 177, App
c 642	6	20.0	5264	7	US-10-766-317-7	Sequence 7, Appli
c 643	6	20.0	5361	12	US-11-196-400-2	Sequence 2, Appli
c 644	6	20.0	5433	7	US-10-766-317-1	Sequence 1, Appli
c 645	6	20.0	5433	12	US-11-000-688-404	Sequence 404, App
c 646	6	20.0	5575	12	US-11-136-527-3245	Sequence 3245, Ap
c 647	6	20.0	5601	7	US-10-766-317-5	Sequence 5, Appli
c 648	6	20.0	6152	12	US-11-196-400-1	Sequence 1, Appli
649	6	20.0	9474	12	US-11-155-232-1	Sequence 1, Appli
650	6	20.0	9645	12	US-11-186-284-48	Sequence 48, Appl
651	6	20.0	9646	12	US-11-080-991-53	Sequence 53, Appl
c 652	6	20.0	10511	7	US-10-766-317-3	Sequence 3, Appli
653	6	20.0	21442	8	US-10-995-561-13469	Sequence 13469, A
654	6	20.0	26323	12	US-11-005-030-1	Sequence 1, Appli
655	6	20.0	38492	12	US-11-124-368A-2916	Sequence 2916, Ap
656	6	20.0	47622	8	US-10-995-561-13431	Sequence 13431, A
657	6	20.0	53328	8	US-10-995-561-13243	Sequence 13243, A
c 658	6	20.0	53331	8	US-10-995-561-13476	Sequence 13476, A
659	6	20.0	56448	8	US-10-995-561-13369	Sequence 13369, A
660	6	20.0	57489	8	US-10-927-466-100	Sequence 100, App
661	6	20.0	67088	8	US-10-995-561-13365	Sequence 13365, A

	662	6	20.0	73072	12	US-11-124-368A-2919	Sequence 2919, Ap
c	663	6	20.0	77246	12	US-11-124-368A-2907	Sequence 2907, Ap
c	664	6	20.0	83712	8	US-10-995-561-13366	Sequence 13366, A
	665	6	20.0	91561	12	US-11-124-368A-2896	Sequence 2896, Ap
	666	6	20.0	96109	12	US-11-124-368A-2895	Sequence 2895, Ap
	667	6	20.0	100000	12	US-11-124-368A-2901	Sequence 2901, Ap
c	668	6	20.0	100000	12	US-11-124-368A-2901	Sequence 2901, Ap
c	669	6	20.0	100000	12	US-11-124-367A-4999	Sequence 4999, Ap
c	670	6	20.0	135019	8	US-10-849-438-11	Sequence 11, Appl
	671	6	20.0	147700	8	US-10-857-780-3	Sequence 3, Appli
	672	6	20.0	148220	12	US-11-121-086-90	Sequence 90, Appl
	673	6	20.0	149382	8	US-10-995-561-13272	Sequence 13272, A
c	674	6	20.0	149382	8	US-10-995-561-13272	Sequence 13272, A
c	675	6	20.0	159660	12	US-11-112-908-43	Sequence 43, Appl
c	676	6	20.0	162173	12	US-11-121-086-72	Sequence 72, Appl
	677	6	20.0	170995	12	US-11-121-086-35	Sequence 35, Appl
c	678	6	20.0	170995	12	US-11-121-086-35	Sequence 35, Appl
c	679	6	20.0	172147	12	US-11-112-908-22	Sequence 22, Appl
c	680	6	20.0	172649	12	US-11-121-086-36	Sequence 36, Appl
c	681	6	20.0	179666	12	US-11-121-086-67	Sequence 67, Appl
	682	6	20.0	180574	12	US-11-121-086-70	Sequence 70, Appl
c	683	6	20.0	180654	12	US-11-121-086-58	Sequence 58, Appl
c	684	6	20.0	182190	12	US-11-121-086-102	Sequence 102, App
	685	6	20.0	185393	12	US-11-121-086-101	Sequence 101, App
c	686	6	20.0	186442	12	US-11-121-086-104	Sequence 104, App
c	687	6	20.0	187786	8	US-10-995-561-13474	Sequence 13474, A
c	688	6	20.0	187986	8	US-10-995-561-13252	Sequence 13252, A
	689	6	20.0	188056	12	US-11-120-925-1	Sequence 1, Appli
c	690	6	20.0	188682	12	US-11-112-908-23	Sequence 23, Appl
	691	6	20.0	201990	8	US-10-995-561-13303	Sequence 13303, A
	692	6	20.0	319608	12	US-11-145-703-1	Sequence 1, Appli
c	693	6	20.0	321019	8	US-10-995-561-13204	Sequence 13204, A
	694	6	20.0	380749	8	US-10-995-561-13216	Sequence 13216, A
c	695	6	20.0	380749	8	US-10-995-561-13216	Sequence 13216, A
	696	6	20.0	398287	8	US-10-995-561-13396	Sequence 13396, A
c	697	6	20.0	1080000	8	US-10-928-446A-1	Sequence 1, Appli
c	698	6	20.0	1080000	8	US-10-928-446A-181	Sequence 181, App
c	699	6	20.0	1080000	8	US-10-928-446A-183	Sequence 183, App
c	700	6	20.0	1080000	8	US-10-928-446A-185	Sequence 185, App
c	701	6	20.0	1080000	8	US-10-928-446A-187	Sequence 187, App
c	702	6	20.0	1080000	8	US-10-928-446A-189	Sequence 189, App
c	703	6	20.0	1080000	8	US-10-928-446A-191	Sequence 191, App
c	704	6	20.0	1080000	8	US-10-928-446A-193	Sequence 193, App
c	705	6	20.0	1080000	8	US-10-928-446A-195	Sequence 195, App
c	706	6	20.0	1080000	8	US-10-928-446A-197	Sequence 197, App
c	707	6	20.0	1080000	8	US-10-928-446A-199	Sequence 199, App
c	708	6	20.0	1080000	8	US-10-928-446A-201	Sequence 201, App
	709	6	20.0	1457619	12	US-11-098-686-8739	Sequence 8739, Ap
	710	6	20.0	1691140	12	US-11-091-018-1	Sequence 1, Appli
c	711	6	20.0	1691140	12	US-11-091-018-1	Sequence 1, Appli
	712	5	16.7	18	8	US-10-310-914A-218344	Sequence 218344,
	713	5	16.7	18	8	US-10-310-914A-525416	Sequence 525416,
	714	5	16.7	18	8	US-10-310-914A-638530	Sequence 638530,
	715	5	16.7	18	8	US-10-310-914A-649768	Sequence 649768,
	716	5	16.7	18	8	US-10-310-914A-960433	Sequence 960433,
c	717	5	16.7	18	8	US-10-310-914A-987815	Sequence 987815,
	718	5	16.7	18	8	US-10-310-914A-1105051	Sequence 1105051,
	719	5	16.7	19	8	US-10-310-914A-168111	Sequence 168111,
	720	5	16.7	19	8	US-10-310-914A-243954	Sequence 243954,
	721	5	16.7	19	8	US-10-310-914A-473366	Sequence 473366,
c	722	5	16.7	19	8	US-10-310-914A-527865	Sequence 527865,
	723	5	16.7	19	8	US-10-310-914A-638556	Sequence 638556,
	724	5	16.7	19	8	US-10-310-914A-649769	Sequence 649769,
	725	5	16.7	19	8	US-10-310-914A-675293	Sequence 675293,
	726	5	16.7	19	8	US-10-310-914A-874659	Sequence 874659,
c	727	5	16.7	19	8	US-10-310-914A-1029708	Sequence 1029708,
	728	5	16.7	19	8	US-10-310-914A-1037731	Sequence 1037731,
	729	5	16.7	19	8	US-10-310-914A-1251832	Sequence 1251832,
c	730	5	16.7	19	10	US-11-101-244-2915	Sequence 2915, Ap
c	731	5	16.7	19	10	US-11-101-244-30271	Sequence 30271, A
c	732	5	16.7	19	10	US-11-101-244-30360	Sequence 30360, A
c	733	5	16.7	19	10	US-11-101-244-30450	Sequence 30450, A
	734	5	16.7	19	10	US-11-101-244-51390	Sequence 51390, A
c	735	5	16.7	19	10	US-11-101-244-52336	Sequence 52336, A
	736	5	16.7	19	10	US-11-101-244-72502	Sequence 72502, A
	737	5	16.7	19	10	US-11-101-244-72601	Sequence 72601, A
	738	5	16.7	19	10	US-11-101-244-72701	Sequence 72701, A
	739	5	16.7	19	10	US-11-101-244-72801	Sequence 72801, A
	740	5	16.7	19	10	US-11-101-244-81811	Sequence 81811, A
c	741	5	16.7	19	10	US-11-101-244-97750	Sequence 97750, A
c	742	5	16.7	19	10	US-11-101-244-98579	Sequence 98579, A
c	743	5	16.7	19	10	US-11-101-244-100196	Sequence 100196,
c	744	5	16.7	19	10	US-11-101-244-144844	Sequence 144844,
c	745	5	16.7	19	10	US-11-101-244-158846	Sequence 158846,
	746	5	16.7	19	10	US-11-101-244-193051	Sequence 193051,
	747	5	16.7	19	10	US-11-101-244-237720	Sequence 237720,
c	748	5	16.7	19	10	US-11-101-244-265100	Sequence 265100,
c	749	5	16.7	19	10	US-11-101-244-296248	Sequence 296248,
c	750	5	16.7	19	10	US-11-101-244-312178	Sequence 312178,
c	751	5	16.7	19	10	US-11-101-244-379945	Sequence 379945,
c	752	5	16.7	19	10	US-11-101-244-382351	Sequence 382351,
c	753	5	16.7	19	10	US-11-101-244-382363	Sequence 382363,
c	754	5	16.7	19	10	US-11-101-244-386449	Sequence 386449,
c	755	5	16.7	19	10	US-11-101-244-386479	Sequence 386479,
c	756	5	16.7	19	10	US-11-101-244-389708	Sequence 389708,
c	757	5	16.7	19	10	US-11-101-244-438047	Sequence 438047,
c	758	5	16.7	19	10	US-11-101-244-438100	Sequence 438100,
c	759	5	16.7	19	10	US-11-101-244-441552	Sequence 441552,
c	760	5	16.7	19	10	US-11-101-244-454495	Sequence 454495,
	761	5	16.7	19	10	US-11-101-244-476358	Sequence 476358,
	762	5	16.7	19	10	US-11-101-244-507702	Sequence 507702,
	763	5	16.7	19	10	US-11-101-244-546666	Sequence 546666,
	764	5	16.7	19	10	US-11-101-244-578854	Sequence 578854,
	765	5	16.7	19	10	US-11-101-244-578858	Sequence 578858,
	766	5	16.7	19	10	US-11-101-244-578870	Sequence 578870,
c	767	5	16.7	19	10	US-11-101-244-587313	Sequence 587313,
	768	5	16.7	19	10	US-11-101-244-608876	Sequence 608876,
c	769	5	16.7	19	10	US-11-101-244-622216	Sequence 622216,
c	770	5	16.7	19	10	US-11-101-244-623676	Sequence 623676,
c	771	5	16.7	19	10	US-11-101-244-643102	Sequence 643102,
	772	5	16.7	19	10	US-11-101-244-664991	Sequence 664991,
	773	5	16.7	19	10	US-11-101-244-668553	Sequence 668553,
	774	5	16.7	19	10	US-11-101-244-668625	Sequence 668625,
c	775	5	16.7	19	10	US-11-101-244-728586	Sequence 728586,
c	776	5	16.7	19	10	US-11-101-244-728671	Sequence 728671,
c	777	5	16.7	19	10	US-11-101-244-752005	Sequence 752005,
c	778	5	16.7	19	10	US-11-101-244-752057	Sequence 752057,
	779	5	16.7	19	10	US-11-101-244-754074	Sequence 754074,
	780	5	16.7	19	10	US-11-101-244-754169	Sequence 754169,
	781	5	16.7	19	10	US-11-101-244-754238	Sequence 754238,
	782	5	16.7	19	10	US-11-101-244-764247	Sequence 764247,
c	783	5	16.7	19	10	US-11-101-244-775343	Sequence 775343,
c	784	5	16.7	19	10	US-11-101-244-775368	Sequence 775368,
c	785	5	16.7	19	10	US-11-101-244-775417	Sequence 775417,
c	786	5	16.7	19	10	US-11-101-244-775443	Sequence 775443,
c	787	5	16.7	19	10	US-11-101-244-775467	Sequence 775467,
c	788	5	16.7	19	10	US-11-101-244-775508	Sequence 775508,
	789	5	16.7	19	10	US-11-101-244-776623	Sequence 776623,
	790	5	16.7	19	10	US-11-101-244-776630	Sequence 776630,
	791	5	16.7	19	10	US-11-101-244-776721	Sequence 776721,
	792	5	16.7	19	10	US-11-101-244-776729	Sequence 776729,
	793	5	16.7	19	10	US-11-101-244-777143	Sequence 777143,
c	794	5	16.7	19	10	US-11-101-244-799478	Sequence 799478,
c	795	5	16.7	19	10	US-11-101-244-799482	Sequence 799482,
c	796	5	16.7	19	10	US-11-101-244-811124	Sequence 811124,
	797	5	16.7	19	10	US-11-101-244-819753	Sequence 819753,
	798	5	16.7	19	10	US-11-101-244-827659	Sequence 827659,
	799	5	16.7	19	10	US-11-101-244-827756	Sequence 827756,
	800	5	16.7	19	10	US-11-101-244-828230	Sequence 828230,
	801	5	16.7	19	10	US-11-101-244-843600	Sequence 843600,
	802	5	16.7	19	10	US-11-101-244-843613	Sequence 843613,
c	803	5	16.7	19	10	US-11-101-244-845035	Sequence 845035,
	804	5	16.7	19	10	US-11-101-244-858658	Sequence 858658,
	805	5	16.7	19	10	US-11-101-244-868720	Sequence 868720,
	806	5	16.7	19	10	US-11-101-244-875889	Sequence 875889,
	807	5	16.7	19	10	US-11-101-244-877893	Sequence 877893,

808	5	16.7	19	10	US-11-101-244-877916	Sequence 877916,
809	5	16.7	19	10	US-11-101-244-935451	Sequence 935451,
810	5	16.7	19	10	US-11-101-244-939425	Sequence 939425,
c 811	5	16.7	19	10	US-11-101-244-961652	Sequence 961652,
c 812	5	16.7	19	10	US-11-101-244-961728	Sequence 961728,
c 813	5	16.7	19	10	US-11-101-244-966484	Sequence 966484,
c 814	5	16.7	19	10	US-11-101-244-966485	Sequence 966485,
c 815	5	16.7	19	10	US-11-101-244-966503	Sequence 966503,
c 816	5	16.7	19	10	US-11-101-244-976206	Sequence 976206,
c 817	5	16.7	19	10	US-11-101-244-987622	Sequence 987622,
818	5	16.7	19	10	US-11-101-244-990901	Sequence 990901,
819	5	16.7	19	10	US-11-101-244-1009479	Sequence 1009479,
c 820	5	16.7	19	10	US-11-101-244-1014086	Sequence 1014086,
c 821	5	16.7	19	10	US-11-101-244-1044549	Sequence 1044549,
c 822	5	16.7	19	10	US-11-101-244-1044588	Sequence 1044588,
c 823	5	16.7	19	10	US-11-101-244-1052279	Sequence 1052279,
824	5	16.7	19	10	US-11-101-244-1105065	Sequence 1105065,
825	5	16.7	19	10	US-11-101-244-1105087	Sequence 1105087,
826	5	16.7	19	10	US-11-101-244-1110679	Sequence 1110679,
827	5	16.7	19	10	US-11-101-244-1110688	Sequence 1110688,
828	5	16.7	19	10	US-11-101-244-1110746	Sequence 1110746,
829	5	16.7	19	10	US-11-101-244-1110752	Sequence 1110752,
830	5	16.7	19	10	US-11-101-244-1115542	Sequence 1115542,
c 831	5	16.7	19	10	US-11-101-244-1136407	Sequence 1136407,
832	5	16.7	19	10	US-11-101-244-1152790	Sequence 1152790,
c 833	5	16.7	19	10	US-11-101-244-1163039	Sequence 1163039,
c 834	5	16.7	19	10	US-11-101-244-1216201	Sequence 1216201,
835	5	16.7	19	10	US-11-101-244-1240181	Sequence 1240181,
836	5	16.7	19	10	US-11-101-244-1252461	Sequence 1252461,
837	5	16.7	19	10	US-11-101-244-1254312	Sequence 1254312,
838	5	16.7	19	10	US-11-101-244-1272214	Sequence 1272214,
839	5	16.7	19	10	US-11-101-244-1272235	Sequence 1272235,
840	5	16.7	19	10	US-11-101-244-1283701	Sequence 1283701,
c 841	5	16.7	19	10	US-11-101-244-1297518	Sequence 1297518,
c 842	5	16.7	19	10	US-11-101-244-1333999	Sequence 1333999,
843	5	16.7	19	10	US-11-101-244-1361067	Sequence 1361067,
844	5	16.7	19	10	US-11-101-244-1361165	Sequence 1361165,
c 845	5	16.7	19	10	US-11-101-244-1361257	Sequence 1361257,
c 846	5	16.7	19	10	US-11-101-244-1361354	Sequence 1361354,
847	5	16.7	19	10	US-11-101-244-1364796	Sequence 1364796,
848	5	16.7	19	10	US-11-101-244-1364875	Sequence 1364875,
849	5	16.7	19	10	US-11-101-244-1364911	Sequence 1364911,
850	5	16.7	19	10	US-11-101-244-1374232	Sequence 1374232,
851	5	16.7	19	10	US-11-101-244-1374295	Sequence 1374295,
c 852	5	16.7	19	10	US-11-101-244-1421081	Sequence 1421081,
c 853	5	16.7	19	10	US-11-101-244-1438626	Sequence 1438626,
c 854	5	16.7	19	10	US-11-101-244-1453542	Sequence 1453542,
c 855	5	16.7	19	10	US-11-101-244-1493212	Sequence 1493212,
c 856	5	16.7	19	10	US-11-101-244-1493288	Sequence 1493288,
c 857	5	16.7	19	10	US-11-101-244-1497502	Sequence 1497502,
c 858	5	16.7	19	10	US-11-101-244-1558254	Sequence 1558254,
c 859	5	16.7	19	10	US-11-101-244-1576582	Sequence 1576582,
c 860	5	16.7	19	11	US-11-083-784-2915	Sequence 2915, Ap
c 861	5	16.7	19	11	US-11-083-784-30271	Sequence 30271, A
c 862	5	16.7	19	11	US-11-083-784-30360	Sequence 30360, A
c 863	5	16.7	19	11	US-11-083-784-30450	Sequence 30450, A
864	5	16.7	19	11	US-11-083-784-51390	Sequence 51390, A
c 865	5	16.7	19	11	US-11-083-784-52336	Sequence 52336, A
866	5	16.7	19	11	US-11-083-784-72502	Sequence 72502, A
867	5	16.7	19	11	US-11-083-784-72601	Sequence 72601, A
868	5	16.7	19	11	US-11-083-784-72701	Sequence 72701, A
869	5	16.7	19	11	US-11-083-784-72801	Sequence 72801, A
870	5	16.7	19	11	US-11-083-784-81811	Sequence 81811, A
c 871	5	16.7	19	11	US-11-083-784-97750	Sequence 97750, A
c 872	5	16.7	19	11	US-11-083-784-98579	Sequence 98579, A
c 873	5	16.7	19	11	US-11-083-784-100196	Sequence 100196,
c 874	5	16.7	19	11	US-11-083-784-144844	Sequence 144844,
c 875	5	16.7	19	11	US-11-083-784-158846	Sequence 158846,
876	5	16.7	19	11	US-11-083-784-193051	Sequence 193051,
877	5	16.7	19	11	US-11-083-784-237720	Sequence 237720,
c 878	5	16.7	19	11	US-11-083-784-265100	Sequence 265100,
c 879	5	16.7	19	11	US-11-083-784-296248	Sequence 296248,
c 880	5	16.7	19	11	US-11-083-784-312178	Sequence 312178,
c 881	5	16.7	19	11	US-11-083-784-379945	Sequence 379945,
c 882	5	16.7	19	11	US-11-083-784-382351	Sequence 382351,
c 883	5	16.7	19	11	US-11-083-784-382363	Sequence 382363,
c 884	5	16.7	19	11	US-11-083-784-386449	Sequence 386449,
c 885	5	16.7	19	11	US-11-083-784-386479	Sequence 386479,
c 886	5	16.7	19	11	US-11-083-784-389708	Sequence 389708,
c 887	5	16.7	19	11	US-11-083-784-438047	Sequence 438047,
c 888	5	16.7	19	11	US-11-083-784-438100	Sequence 438100,
c 889	5	16.7	19	11	US-11-083-784-441552	Sequence 441552,
c 890	5	16.7	19	11	US-11-083-784-454495	Sequence 454495,
891	5	16.7	19	11	US-11-083-784-476358	Sequence 476358,
892	5	16.7	19	11	US-11-083-784-507702	Sequence 507702,
893	5	16.7	19	11	US-11-083-784-546666	Sequence 546666,
894	5	16.7	19	11	US-11-083-784-578854	Sequence 578854,
895	5	16.7	19	11	US-11-083-784-578858	Sequence 578858,
896	5	16.7	19	11	US-11-083-784-578870	Sequence 578870,
c 897	5	16.7	19	11	US-11-083-784-587313	Sequence 587313,
898	5	16.7	19	11	US-11-083-784-608876	Sequence 608876,
c 899	5	16.7	19	11	US-11-083-784-622216	Sequence 622216,
c 900	5	16.7	19	11	US-11-083-784-623676	Sequence 623676,
c 901	5	16.7	19	11	US-11-083-784-643102	Sequence 643102,
902	5	16.7	19	11	US-11-083-784-664991	Sequence 664991,
903	5	16.7	19	11	US-11-083-784-668553	Sequence 668553,
904	5	16.7	19	11	US-11-083-784-668625	Sequence 668625,
c 905	5	16.7	19	11	US-11-083-784-728586	Sequence 728586,
c 906	5	16.7	19	11	US-11-083-784-728671	Sequence 728671,
c 907	5	16.7	19	11	US-11-083-784-752005	Sequence 752005,
c 908	5	16.7	19	11	US-11-083-784-752057	Sequence 752057,
909	5	16.7	19	11	US-11-083-784-754074	Sequence 754074,
910	5	16.7	19	11	US-11-083-784-754169	Sequence 754169,
911	5	16.7	19	11	US-11-083-784-754238	Sequence 754238,
912	5	16.7	19	11	US-11-083-784-764247	Sequence 764247,
c 913	5	16.7	19	11	US-11-083-784-775343	Sequence 775343,
c 914	5	16.7	19	11	US-11-083-784-775368	Sequence 775368,
c 915	5	16.7	19	11	US-11-083-784-775417	Sequence 775417,
c 916	5	16.7	19	11	US-11-083-784-775443	Sequence 775443,
c 917	5	16.7	19	11	US-11-083-784-775467	Sequence 775467,
c 918	5	16.7	19	11	US-11-083-784-775508	Sequence 775508,
919	5	16.7	19	11	US-11-083-784-776623	Sequence 776623,
920	5	16.7	19	11	US-11-083-784-776630	Sequence 776630,
921	5	16.7	19	11	US-11-083-784-776721	Sequence 776721,
922	5	16.7	19	11	US-11-083-784-776729	Sequence 776729,
923	5	16.7	19	11	US-11-083-784-777143	Sequence 777143,
c 924	5	16.7	19	11	US-11-083-784-799478	Sequence 799478,
c 925	5	16.7	19	11	US-11-083-784-799482	Sequence 799482,
c 926	5	16.7	19	11	US-11-083-784-811124	Sequence 811124,
927	5	16.7	19	11	US-11-083-784-819753	Sequence 819753,
928	5	16.7	19	11	US-11-083-784-827659	Sequence 827659,
929	5	16.7	19	11	US-11-083-784-827756	Sequence 827756,
930	5	16.7	19	11	US-11-083-784-828230	Sequence 828230,
931	5	16.7	19	11	US-11-083-784-843600	Sequence 843600,
932	5	16.7	19	11	US-11-083-784-843613	Sequence 843613,
c 933	5	16.7	19	11	US-11-083-784-845035	Sequence 845035,
934	5	16.7	19	11	US-11-083-784-858658	Sequence 858658,
935	5	16.7	19	11	US-11-083-784-868720	Sequence 868720,
936	5	16.7	19	11	US-11-083-784-875889	Sequence 875889,
937	5	16.7	19	11	US-11-083-784-877893	Sequence 877893,
938	5	16.7	19	11	US-11-083-784-877916	Sequence 877916,
939	5	16.7	19	11	US-11-083-784-935451	Sequence 935451,
940	5	16.7	19	11	US-11-083-784-939425	Sequence 939425,
c 941	5	16.7	19	11	US-11-083-784-961652	Sequence 961652,
c 942	5	16.7	19	11	US-11-083-784-961728	Sequence 961728,
c 943	5	16.7	19	11	US-11-083-784-966484	Sequence 966484,
c 944	5	16.7	19	11	US-11-083-784-966485	Sequence 966485,
c 945	5	16.7	19	11	US-11-083-784-966503	Sequence 966503,
c 946	5	16.7	19	11	US-11-083-784-976206	Sequence 976206,
c 947	5	16.7	19	11	US-11-083-784-987622	Sequence 987622,
948	5	16.7	19	11	US-11-083-784-990901	Sequence 990901,
949	5	16.7	19	11	US-11-083-784-1009479	Sequence 1009479,
c 950	5	16.7	19	11	US-11-083-784-1014086	Sequence 1014086,
c 951	5	16.7	19	11	US-11-083-784-1044549	Sequence 1044549,
c 952	5	16.7	19	11	US-11-083-784-1044588	Sequence 1044588,
c 953	5	16.7	19	11	US-11-083-784-1052279	Sequence 1052279,

954	5	16.7	19	11	US-11-083-784-1105065	Sequence 1105065,
955	5	16.7	19	11	US-11-083-784-1105087	Sequence 1105087,
956	5	16.7	19	11	US-11-083-784-1110679	Sequence 1110679,
957	5	16.7	19	11	US-11-083-784-1110688	Sequence 1110688,
958	5	16.7	19	11	US-11-083-784-1110746	Sequence 1110746,
959	5	16.7	19	11	US-11-083-784-1110752	Sequence 1110752,
960	5	16.7	19	11	US-11-083-784-1115542	Sequence 1115542,
c 961	5	16.7	19	11	US-11-083-784-1136407	Sequence 1136407,
962	5	16.7	19	11	US-11-083-784-1152790	Sequence 1152790,
c 963	5	16.7	19	11	US-11-083-784-1163039	Sequence 1163039,
c 964	5	16.7	19	11	US-11-083-784-1216201	Sequence 1216201,
965	5	16.7	19	11	US-11-083-784-1240181	Sequence 1240181,
966	5	16.7	19	11	US-11-083-784-1252461	Sequence 1252461,
967	5	16.7	19	11	US-11-083-784-1254312	Sequence 1254312,
968	5	16.7	19	11	US-11-083-784-1272214	Sequence 1272214,
969	5	16.7	19	11	US-11-083-784-1272235	Sequence 1272235,
970	5	16.7	19	11	US-11-083-784-1283701	Sequence 1283701,
c 971	5	16.7	19	11	US-11-083-784-1297518	Sequence 1297518,
c 972	5	16.7	19	11	US-11-083-784-1333999	Sequence 1333999,
973	5	16.7	19	11	US-11-083-784-1361067	Sequence 1361067,
974	5	16.7	19	11	US-11-083-784-1361165	Sequence 1361165,
c 975	5	16.7	19	11	US-11-083-784-1361257	Sequence 1361257,
c 976	5	16.7	19	11	US-11-083-784-1361354	Sequence 1361354,
977	5	16.7	19	11	US-11-083-784-1364796	Sequence 1364796,
978	5	16.7	19	11	US-11-083-784-1364875	Sequence 1364875,
979	5	16.7	19	11	US-11-083-784-1364911	Sequence 1364911,
980	5	16.7	19	11	US-11-083-784-1374232	Sequence 1374232,
981	5	16.7	19	11	US-11-083-784-1374295	Sequence 1374295,
c 982	5	16.7	19	11	US-11-083-784-1421081	Sequence 1421081,
c 983	5	16.7	19	11	US-11-083-784-1438626	Sequence 1438626,
c 984	5	16.7	19	11	US-11-083-784-1453542	Sequence 1453542,
c 985	5	16.7	19	11	US-11-083-784-1493212	Sequence 1493212,
c 986	5	16.7	19	11	US-11-083-784-1493288	Sequence 1493288,
c 987	5	16.7	19	11	US-11-083-784-1497502	Sequence 1497502,
c 988	5	16.7	19	11	US-11-083-784-1558254	Sequence 1558254,
c 989	5	16.7	19	11	US-11-083-784-1576582	Sequence 1576582,
990	5	16.7	20	8	US-10-310-914A-206782	Sequence 206782,
991	5	16.7	20	8	US-10-310-914A-260553	Sequence 260553,
c 992	5	16.7	20	8	US-10-310-914A-314018	Sequence 314018,
993	5	16.7	20	8	US-10-310-914A-535062	Sequence 535062,
994	5	16.7	20	8	US-10-310-914A-596611	Sequence 596611,
995	5	16.7	20	8	US-10-310-914A-675294	Sequence 675294,
c 996	5	16.7	20	8	US-10-310-914A-686035	Sequence 686035,
997	5	16.7	20	8	US-10-310-914A-747660	Sequence 747660,
c 998	5	16.7	20	8	US-10-310-914A-769818	Sequence 769818,
999	5	16.7	20	8	US-10-310-914A-989462	Sequence 989462,
c1000	5	16.7	20	8	US-10-310-914A-1029698	Sequence 1029698,

ALIGNMENTS

```
RESULT 1
US-09-925-065A-47024
; Sequence 47024, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47024
;   LENGTH: 416
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-47024

Alignment Scores:
Pred. No.:                5.15          Length:          416
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              26.7%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-47024 (1-416)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        303 ACAGTGTCATTTAATTTGGGAGAG 326

RESULT 2
US-09-925-065A-787599
; Sequence 787599, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 787599
;   LENGTH: 622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-787599

Alignment Scores:
Pred. No.:                7.57          Length:          622
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              26.7%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-787599 (1-622)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db         17 ACAGTGTCATTTAATTTGGGAGAG 40

RESULT 3
US-09-925-065A-694362/c
; Sequence 694362, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
```

```
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 694362
;   LENGTH: 2443
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352,
;   LOCATION: 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362,
;   LOCATION: 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372,
;   LOCATION: 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391,
;   LOCATION: 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401,
;   LOCATION: 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411,
;   LOCATION: 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430,
;   LOCATION: 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440,
;   LOCATION: 2441, 2442
;   OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-694362

Alignment Scores:
Pred. No.:                28.2          Length:          2443
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              26.7%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-694362 (1-2443)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db       2040 ACAGTGTCATTTAATTTGGGAGAG 2017

RESULT 4
US-10-995-561-13271/c
; Sequence 13271, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13271
;   LENGTH: 12648
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13271

Alignment Scores:
Pred. No.:                136           Length:          12648
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              26.7%         Indels:          0
DB:                       8             Gaps:            0

US-10-758-902-1 (1-30) x US-10-995-561-13271 (1-12648)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db      12509 ACAGTGTCATTTAATTTGGGAGAG 12486

RESULT 5
US-11-124-367A-5063/c
; Sequence 5063, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  Hongjin Huang
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Fibrosis Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001519.ORD
;  CURRENT APPLICATION NUMBER: US/11/124,367A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,846
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/582,609
;  PRIOR FILING DATE: 2004-06-25
;  PRIOR APPLICATION NUMBER: US 60/599,554
;  PRIOR FILING DATE: 2004-08-09
;  NUMBER OF SEQ ID NOS: 34460
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5063
;   LENGTH: 31130
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-124-367A-5063

Alignment Scores:
Pred. No.:                324           Length:          31130
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              26.7%         Indels:          0
DB:                       12            Gaps:            0

US-10-758-902-1 (1-30) x US-11-124-367A-5063 (1-31130)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db      30946 ACAGTGTCATTTAATTTGGGAGAG 30923

RESULT 6
US-10-995-561-13334
; Sequence 13334, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13334
;   LENGTH: 31657
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

US-10-995-561-13334

Alignment Scores:

Pred. No.:	329	Length:	31657
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-10-995-561-13334 (1-31657)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        190 ACAGTGTCATTTAATTTGGGAGAG 213
```

RESULT 7
US-10-995-561-13487
; Sequence 13487, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13487
; LENGTH: 41309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13487

Alignment Scores:

Pred. No.:	425	Length:	41309
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-10-995-561-13487 (1-41309)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db      34625 ACAGTGTCATTTAATTTGGGAGAG 34648
```

RESULT 8
US-10-802-796-98
; Sequence 98, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 98
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-98

Alignment Scores:

Pred. No.:	82.4	Length:	439
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-10-802-796-98 (1-439)

```
Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db        364 CAGGATCTCAGAAACGAGCTG 384
```

RESULT 9
US-09-925-065A-455365
; Sequence 455365, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 455365
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-455365

Alignment Scores:

Pred. No.:	97.7	Length:	524
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.3%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x US-09-925-065A-455365 (1-524)

```
Qy          2 AsnThrValSerPheAsnLeu 8
              |||||||||||||||||||||
Db        247 AACACTGTTTCCTTCAATCTA 267
```

RESULT 10
US-09-925-065A-810826
; Sequence 810826, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135

```
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 810826
;   LENGTH: 548
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-810826

Alignment Scores:
Pred. No.:                102             Length:         548
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              23.3%           Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-810826 (1-548)

Qy          1 TyrAsnThrValSerPheAsn 7
              ||||||||||||||||||||
Db        358 TATAACACCGTATCATTTAAT 378

RESULT 11
US-09-925-065A-123248
; Sequence 123248, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 123248
;   LENGTH: 551
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-123248

Alignment Scores:
Pred. No.:                103             Length:         551
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              23.3%           Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-123248 (1-551)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        344 AACACCGTCTCATTTAATCTT 364

RESULT 12
US-09-925-065A-760512/c
; Sequence 760512, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 760512
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-760512

Alignment Scores:
Pred. No.:                104             Length:         561
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              23.3%           Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-760512 (1-561)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        283 AATACGGTCTCTTTTAATTTG 263

RESULT 13
US-09-925-065A-761519
; Sequence 761519, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 761519
;   LENGTH: 565
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
US-09-925-065A-761519

Alignment Scores:
Pred. No.:              105          Length:        565
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     6            Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-761519 (1-565)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        279 AATACGGTCTCTTTTAATTTG 299

RESULT 14
US-09-925-065A-771199
; Sequence 771199, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 771199
;   LENGTH: 566
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-771199

Alignment Scores:
Pred. No.:              105          Length:        566
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     6            Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-771199 (1-566)

Qy          1 TyrAsnThrValSerPheAsn 7
              ||||||||||||||||||||
Db        190 TATAACACTGTTAGTTTTAAT 210

RESULT 15
US-09-925-065A-762385
; Sequence 762385, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 762385
;   LENGTH: 571
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-762385

Alignment Scores:
Pred. No.:              106          Length:        571
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     6            Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-762385 (1-571)

Qy          2 AsnThrValSerPheAsnLeu 8
              ||||||||||||||||||||
Db        279 AATACGGTCTCTTTTAATTTG 299

RESULT 16
US-09-925-065A-305608
; Sequence 305608, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305608
;   LENGTH: 617
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-305608

Alignment Scores:
Pred. No.:              114          Length:        617
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            23.3%        Indels:        0
DB:                     6            Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-305608 (1-617)

Qy         18 IleGlnAspLeuArgAsnGlu 24
              ||||||||||||||||||||
Db        493 ATTCAAGATCTCAGAAATGAA 513
```

```
RESULT 17
US-09-925-065A-305609
; Sequence 305609, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305609
;   LENGTH: 617
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-305609

Alignment Scores:
Pred. No.:              114          Length:         617
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            23.3%        Indels:         0
DB:                     6            Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-305609 (1-617)

Qy          18 IleGlnAspLeuArgAsnGlu 24
               |||||||||||||||||||||
Db         493 ATTCAAGATCTCAGAAATGAA 513

RESULT 18
US-11-000-688-1223/c
; Sequence 1223, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
;  APPLICANT: BERTUCCI, Francois
;  APPLICANT:  HOULGATTE, Remi
;  APPLICANT:  BIRNBAUM, Daniel
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
;  FILE REFERENCE: 1423-R-03
;  CURRENT APPLICATION NUMBER: US/11/000,688
;  CURRENT FILING DATE:  2004-12-01
;  PRIOR APPLICATION NUMBER: US 60/525,987
;  PRIOR FILING DATE: 2003-12-01
;  NUMBER OF SEQ ID NOS: 1596
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1223
;   LENGTH: 1432
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial sequences:primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1432)
;   OTHER INFORMATION: creatine kinase, brain(CKB) gene.
US-11-000-688-1223

Alignment Scores:
Pred. No.:              256          Length:         1432
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            23.3%        Indels:         0
DB:                     12           Gaps:           0

US-10-758-902-1 (1-30) x US-11-000-688-1223 (1-1432)

Qy           5 SerPheAsnLeuGlyGluAla 11
               |||||||||||||||||||
Db         867 AGTTTCAATCTGGGTGAGGCC 847

RESULT 19
US-09-925-065A-89593
; Sequence 89593, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89593
;   LENGTH: 2645
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-89593

Alignment Scores:
Pred. No.:              462          Length:         2645
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            23.3%        Indels:         0
DB:                     6            Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-89593 (1-2645)

Qy           2 AsnThrValSerPheAsnLeu 8
               |||||||||||||||||||
Db         872 AACACCGTCTCATTTAATCTT 892

RESULT 20
US-11-124-367A-5018/c
; Sequence 5018, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  Hongjin Huang
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Fibrosis Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001519.ORD
;  CURRENT APPLICATION NUMBER: US/11/124,367A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,846
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/582,609
;  PRIOR FILING DATE: 2004-06-25
;  PRIOR APPLICATION NUMBER: US 60/599,554
;  PRIOR FILING DATE: 2004-08-09
```

```
;  NUMBER OF SEQ ID NOS: 34460
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5018
;   LENGTH: 21044
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-124-367A-5018

Alignment Scores:
Pred. No.:              3.38e+03        Length:         21044
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.3%           Indels:         0
DB:                     12              Gaps:           0

US-10-758-902-1 (1-30) x US-11-124-367A-5018 (1-21044)

Qy         18 IleGlnAspLeuArgAsnGlu 24
              |||||||||||||||||||||
Db       3315 ATACAAGACTTGAGAAATGAA 3295

RESULT 21
US-11-101-244-98592/c
; Sequence 98592, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 98592
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-98592

Alignment Scores:
Pred. No.:              61.5            Length:         19
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            20.0%           Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-1 (1-30) x US-11-101-244-98592 (1-19)

Qy          6 PheAsnLeuGlyGluAla 11
              ||||||||||||||||||
Db         18 TTCAATCTGGGTGAGGCC 1

RESULT 22
US-11-083-784-98592/c
; Sequence 98592, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 98592
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-98592

Alignment Scores:
Pred. No.:              61.5            Length:         19
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            20.0%           Indels:         0
DB:                     11              Gaps:           0

US-10-758-902-1 (1-30) x US-11-083-784-98592 (1-19)

Qy          6 PheAsnLeuGlyGluAla 11
              ||||||||||||||||||
Db         18 TTCAATCTGGGTGAGGCC 1

RESULT 23
US-10-310-914A-1135670
; Sequence 1135670, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1135670
;   LENGTH: 22
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-1135670

Alignment Scores:
Pred. No.:              70.8            Length:         22
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            20.0%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-10-310-914A-1135670 (1-22)

Qy         21 LeuArgAsnGluLeuAla 26
              ||||||||||||||||||
Db          2 CUCAGGAAUGAGCUGGCA 19

RESULT 24
US-10-310-914A-723268
; Sequence 723268, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
```

```
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 723268
;   LENGTH: 24
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-723268

Alignment Scores:
Pred. No.:                77              Length:         24
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              20.0%           Indels:         0
DB:                       8               Gaps:           0

US-10-758-902-1 (1-30) x US-10-310-914A-723268 (1-24)

Qy          6 PheAsnLeuGlyGluAla 11
              ||||||||||||||||||
Db          6 UUUAACCUCGGGGAAGCC 23

RESULT 25
US-10-310-914A-424632/c
; Sequence 424632, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 424632
;   LENGTH: 25
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-424632

Alignment Scores:
Pred. No.:                80.1            Length:         25
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              20.0%           Indels:         0
DB:                       8               Gaps:           0

US-10-758-902-1 (1-30) x US-10-310-914A-424632 (1-25)

Qy          5 SerPheAsnLeuGlyGlu 10
              ||||||||||||||||||
Db         24 TCATTTAATTTGGGAGAG 7

RESULT 26
US-11-121-849-28958
; Sequence 28958, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 28958
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-28958

Alignment Scores:
Pred. No.:                80.1            Length:         25
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              20.0%           Indels:         0
DB:                       12              Gaps:           0

US-10-758-902-1 (1-30) x US-11-121-849-28958 (1-25)

Qy         16 ThrPheIleGlnAspLeu 21
              |||||||||||||||||||
Db          6 ACTTTCATCCAAGACCTG 23

RESULT 27
US-11-121-849-43082
; Sequence 43082, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43082
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-43082

Alignment Scores:
Pred. No.:                80.1            Length:         25
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              20.0%           Indels:         0
DB:                       12              Gaps:           0

US-10-758-902-1 (1-30) x US-11-121-849-43082 (1-25)

Qy          4 ValSerPheAsnLeuGly 9
              |||||||||||||||||||
Db          7 GTCAGTTTCAACTTGGGG 24

RESULT 28
US-11-121-849-43083
; Sequence 43083, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
```

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43083
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-43083

Alignment Scores:

Pred. No.:	80.1	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	20.0%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-1 (1-30) x US-11-121-849-43083 (1-25)

```
Qy          4 ValSerPheAsnLeuGly 9
              |||||||||||||||||||
Db          3 GTCAGTTTCAACTTGGGG 20
```

RESULT 29
US-11-121-849-43733
; Sequence 43733, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43733
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-43733

Alignment Scores:

Pred. No.:	80.1	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	20.0%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-1 (1-30) x US-11-121-849-43733 (1-25)

```
Qy         18 IleGlnAspLeuArgAsn 23
              |||||||||||||||||||
Db          1 ATACAGGATCTCAGAAAT 18
```

RESULT 30
US-11-121-849-153896
; Sequence 153896, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 153896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-153896

Alignment Scores:

Pred. No.:	80.1	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	20.0%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-1 (1-30) x US-11-121-849-153896 (1-25)

```
Qy         25 LeuAlaLysGlyThrPro 30
              ||||||||||||||||||
Db          7 CTGGCAAAGGGTACCCCT 24
```

RESULT 31
US-11-121-849-287209
; Sequence 287209, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 287209
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-287209

Alignment Scores:

Pred. No.:	80.1	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	20.0%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-1 (1-30) x US-11-121-849-287209 (1-25)

```
Qy          4 ValSerPheAsnLeuGly 9
              |||||||||||||||||||
Db          1 GTAAGTTTTAATCTTGGA 18
```

RESULT 32
US-11-121-849-306644
; Sequence 306644, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 306644
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-306644

```
Alignment Scores:
Pred. No.:              80.1          Length:        25
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            20.0%         Indels:        0
DB:                     12            Gaps:          0

US-10-758-902-1 (1-30) x US-11-121-849-306644 (1-25)

Qy          4 ValSerPheAsnLeuGly 9
              |||||||||||||||||
Db          6 GTCAGTTTCAACTTGGGG 23

RESULT 33
US-11-121-849-306829
; Sequence 306829, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 306829
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-306829

Alignment Scores:
Pred. No.:              80.1          Length:        25
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            20.0%         Indels:        0
DB:                     12            Gaps:          0

US-10-758-902-1 (1-30) x US-11-121-849-306829 (1-25)

Qy          4 ValSerPheAsnLeuGly 9
              |||||||||||||||||
Db          6 GTCAGTTTCAACTTGGGG 23

RESULT 34
US-11-121-849-438584
; Sequence 438584, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 438584
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-438584

Alignment Scores:
Pred. No.:              80.1          Length:        25
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            20.0%         Indels:        0
DB:                     12            Gaps:          0

US-10-758-902-1 (1-30) x US-11-121-849-438584 (1-25)

Qy         16 ThrPheIleGlnAspLeu 21
              |||||||||||||||||||
Db          1 ACTTTCATTCAGGATTTG 18

RESULT 35
US-11-121-849-492968/c
; Sequence 492968, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 492968
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-492968

Alignment Scores:
Pred. No.:              80.1          Length:        25
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            20.0%         Indels:        0
DB:                     12            Gaps:          0

US-10-758-902-1 (1-30) x US-11-121-849-492968 (1-25)

Qy         20 AspLeuArgAsnGluLeu 25
              |||||||||||||||||||
Db         20 GACTTAAGAAATGAGCTC 3

RESULT 36
US-11-121-849-671499
; Sequence 671499, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 671499
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-671499

Alignment Scores:
Pred. No.:              80.1          Length:        25
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
```

```
Query Match:            20.0%          Indels:        0
DB:                     12             Gaps:          0

US-10-758-902-1 (1-30) x US-11-121-849-671499 (1-25)

Qy         13 GluTyrProThrPheIle 18
              ||||||||||||||||||
Db          8 GAATACCCAACCTTTATA 25

RESULT 37
US-11-121-849-671500
; Sequence 671500, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 671500
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-671500

Alignment Scores:
Pred. No.:              80.1           Length:        25
Score:                  6.00           Matches:       6
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            20.0%          Indels:        0
DB:                     12             Gaps:          0

US-10-758-902-1 (1-30) x US-11-121-849-671500 (1-25)

Qy         13 GluTyrProThrPheIle 18
              ||||||||||||||||||
Db          6 GAATACCCAACCTTTATA 23

RESULT 38
US-11-121-849-671501
; Sequence 671501, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 671501
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-671501

Alignment Scores:
Pred. No.:              80.1           Length:        25
Score:                  6.00           Matches:       6
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            20.0%          Indels:        0
DB:                     12             Gaps:          0

US-10-758-902-1 (1-30) x US-11-121-849-671501 (1-25)

Qy         13 GluTyrProThrPheIle 18
              ||||||||||||||||||
Db          5 GAATACCCAACCTTTATA 22

RESULT 39
US-11-121-849-671502
; Sequence 671502, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 671502
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-671502

Alignment Scores:
Pred. No.:              80.1           Length:        25
Score:                  6.00           Matches:       6
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            20.0%          Indels:        0
DB:                     12             Gaps:          0

US-10-758-902-1 (1-30) x US-11-121-849-671502 (1-25)

Qy         13 GluTyrProThrPheIle 18
              ||||||||||||||||||
Db          3 GAATACCCAACCTTTATA 20

RESULT 40
US-10-310-914A-1229715/c
; Sequence 1229715, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1229715
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-1229715

Alignment Scores:
Pred. No.:              83.1           Length:        26
Score:                  6.00           Matches:       6
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            20.0%          Indels:        0
DB:                     8              Gaps:          0

US-10-758-902-1 (1-30) x US-10-310-914A-1229715 (1-26)

Qy          4 ValSerPheAsnLeuGly 9
              ||||||||||||||||||
```

Db 23 GTTTCCTTCAACCTTGGT 6

Search completed: February 20, 2006, 03:14:51
Job time : 134.251 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:56:48 ; Search time 1034.92 Seconds
(without alignments)
1356.257 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 30
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 1

Total number of hits satisfying chosen parameters: 82154958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160835_4063/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=oligo.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US10758902_@CGN_1_1_10172_@runat_17022006_160835_4063 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	9	30.0	720	5	BX849231	BX849231 BX849231
c	2	9	30.0	909	5	BU911748	BU911748 AGENCOURT
	3	8	26.7	225	1	AA328059	AA328059 EST31482
c	4	8	26.7	246	2	BF352328	BF352328 RC6-HT059
	5	8	26.7	264	1	AW887063	AW887063 RC1-OT008
	6	8	26.7	415	5	BY550514	BY550514 BY550514
	7	8	26.7	420	8	DN507933	DN507933 HL0200030
c	8	8	26.7	445	2	BF451736	BF451736 uz78f04.y
	9	8	26.7	452	2	BF807534	BF807534 RC2-CI009
	10	8	26.7	454	1	AJ653060	AJ653060 AJ653060
	11	8	26.7	501	1	AW748411	AW748411 RC4-BT025
c	12	8	26.7	506	9	CC383551	CC383551 PUHHN58TD
	13	8	26.7	517	2	BG037734	BG037734 dc67d08.y
c	14	8	26.7	520	1	AI035950	AI035950 ub50a10.r
c	15	8	26.7	567	10	CZ658046	CZ658046 OM_Ba020
	16	8	26.7	582	7	CN775134	CN775134 tae69h10.
	17	8	26.7	585	2	BE131785	BE131785 db38b02.y
	18	8	26.7	601	7	CN773487	CN773487 tae61d03.
	19	8	26.7	603	5	BX668613	BX668613 BX668613
	20	8	26.7	612	2	BG924897	BG924897 HNC38-1-E
c	21	8	26.7	617	6	CD354962	CD354962 UI-M-GM0-
	22	8	26.7	623	10	CZ874300	CZ874300 OC_Ba027
c	23	8	26.7	626	7	CN770424	CN770424 tae69h10.
c	24	8	26.7	628	7	CN768873	CN768873 taf20d12.
	25	8	26.7	630	8	DN373796	DN373796 LIB38527_
c	26	8	26.7	642	6	CB844714	CB844714 M2PN-0266
	27	8	26.7	646	3	BJ109333	BJ109333 BJ109333
	28	8	26.7	654	10	CW374967	CW374967 fsbb001f0
	29	8	26.7	676	6	CD469335	CD469335 LeukoS2_3
c	30	8	26.7	690	7	CN773154	CN773154 tae61d03.
c	31	8	26.7	694	6	CB469308	CB469308 sn05_H01.
	32	8	26.7	704	5	BY764463	BY764463 BY764463
c	33	8	26.7	716	10	CW084955	CW084955 104_428_1
	34	8	26.7	736	3	BP677084	BP677084 BP677084
	35	8	26.7	740	1	AJ820130	AJ820130 AJ820130
	36	8	26.7	746	10	CW373064	CW373064 fsbb001f0
	37	8	26.7	758	2	BI089654	BI089654 602854348
	38	8	26.7	771	8	DR103654	DR103654 JHU040H05
c	39	8	26.7	773	7	CO430592	CO430592 UI-M-HX0-
	40	8	26.7	789	7	CO386739	CO386739 AGENCOURT
	41	8	26.7	797	3	BP682823	BP682823 BP682823
	42	8	26.7	802	10	CW375126	CW375126 fsbb001f0
c	43	8	26.7	804	10	CW375127	CW375127 fsbb001f0
	44	8	26.7	805	7	CJ012468	CJ012468 CJ012468
	45	8	26.7	845	6	CD328246	CD328246 AGENCOURT
c	46	8	26.7	873	3	BI736716	BI736716 603360410
	47	8	26.7	914	11	CR211685	CR211685 Forward s
	48	8	26.7	920	5	BX845875	BX845875 BX845875
	49	8	26.7	926	10	CZ930980	CZ930980 248803 To
	50	8	26.7	1007	10	CZ393728	CZ393728 ZMMBF0172
	51	8	26.7	1040	4	HSM802933	AL583911 Homo sapi
c	52	8	26.7	2292	4	AK033904	AK033904 Mus muscu
	53	8	26.7	3765	4	CR627456	CR627456 Homo sapi
	54	7	23.3	57	5	BX686788	BX686788 BX686788
c	55	7	23.3	64	7	CV304460	CV304460 th06d06.g
	56	7	23.3	84	3	BJ057969	BJ057969 BJ057969
	57	7	23.3	133	5	BQ799305	BQ799305 EST 1474
c	58	7	23.3	161	1	AA327033	AA327033 EST30299
	59	7	23.3	174	9	AZ750404	AZ750404 RPCI-24-7
	60	7	23.3	175	1	AV352845	AV352845 AV352845
c	61	7	23.3	200	10	CL272337	CL272337 Ggal_79b_
c	62	7	23.3	213	1	AW890343	AW890343 MR0-NT003
	63	7	23.3	215	6	CD130978	CD130978 MG1-0009P
	64	7	23.3	221	5	BW545127	BW545127 BW545127
	65	7	23.3	223	2	BB450399	BB450399 BB450399
	66	7	23.3	225	11	CPA561540	AJ561540 Cryptospo
c	67	7	23.3	230	1	AA363875	AA363875 EST74349
c	68	7	23.3	259	8	D52539	D52539 HUM081A11B
c	69	7	23.3	261	2	BF918627	BF918627 CM0-NT013
	70	7	23.3	261	2	BI142985	BI142985 rk69b07.y
c	71	7	23.3	264	3	BM688583	BM688583 UI-E-CR0-
	72	7	23.3	266	2	BG932756	BG932756 h91-9 h91
c	73	7	23.3	268	1	AA364980	AA364980 EST75647
	74	7	23.3	268	7	CK576956	CK576956 IST_WI5_1
	75	7	23.3	276	1	AW359025	AW359025 44708 MAR
c	76	7	23.3	277	6	CD141149	CD141149 MG1-0069T
c	77	7	23.3	279	1	AA365761	AA365761 EST76875
c	78	7	23.3	280	6	CD138207	CD138207 MG1-0051T
c	79	7	23.3	282	9	AZ589303	AZ589303 1M0398M07
c	80	7	23.3	285	1	AA364927	AA364927 EST75606

c	81	7	23.3	293	10	CW051314 CW051314 104_291_1
	82	7	23.3	298	8	DN909439 DN909439 Cuc1_3_F1
c	83	7	23.3	300	1	AV184036 AV184036 AV184036
c	84	7	23.3	300	5	C54240 C54240 C54240 Yuji
c	85	7	23.3	300	5	C55282 C55282 C55282 Yuji
c	86	7	23.3	300	5	C55303 C55303 C55303 Yuji
	87	7	23.3	302	1	AJ540020 AJ540020 AJ540020
	88	7	23.3	302	1	AJ540035 AJ540035 AJ540035
c	89	7	23.3	304	7	CF974201 CF974201 PSU_nep1\
c	90	7	23.3	308	1	AA338631 AA338631 EST43673
	91	7	23.3	313	1	AW346045 AW346045 27060 MAR
	92	7	23.3	319	2	BG345544 BG345544 dd88e02.y
	93	7	23.3	323	2	BF958289 BF958289 CM2-NN024
c	94	7	23.3	333	1	AA364332 AA364332 EST74886
	95	7	23.3	333	6	CD181452 CD181452 MS1-0030T
c	96	7	23.3	342	1	AA325293 AA325293 EST28508
c	97	7	23.3	345	6	CD186668 CD186668 MS1-0055G
c	98	7	23.3	345	6	CD308720 CD308720 StrPu691.
c	99	7	23.3	346	3	BM797613 BM797613 K-EST0080
c	100	7	23.3	347	1	AA338423 AA338423 EST43346
c	101	7	23.3	353	6	CD121604 CD121604 ME1-0068P
c	102	7	23.3	354	1	AJ689383 AJ689383 AJ689383
c	103	7	23.3	355	1	AW860296 AW860296 RC0-CT038
c	104	7	23.3	356	6	CA370660 CA370660 650898 NC
	105	7	23.3	356	8	DR029125 DR029125 bda010071
	106	7	23.3	360	5	C61689 C61689 C61689 Yuji
	107	7	23.3	360	8	D35698 D35698 CELK024D2F
c	108	7	23.3	361	8	D33101 D33101 CELK026CXR
	109	7	23.3	362	1	AV191049 AV191049 AV191049
	110	7	23.3	367	9	AZ808965 AZ808965 2M0072E14
	111	7	23.3	368	8	DN910520 DN910520 Cuc5_4_H0
c	112	7	23.3	370	2	BF869438 BF869438 QV0-ET014
	113	7	23.3	371	9	AZ559339 AZ559339 RPCI-23-2
c	114	7	23.3	376	1	AW860305 AW860305 RC0-CT038
	115	7	23.3	376	5	C49304 C49304 C49304 Yuji
	116	7	23.3	377	9	BH297482 BH297482 CH230-45E
	117	7	23.3	379	1	AI858542 AI858542 wl64b01.x
c	118	7	23.3	379	1	AW374691 AW374691 MR1-CT005
c	119	7	23.3	380	1	AA339748 AA339748 EST44863
c	120	7	23.3	382	2	BE089396 BE089396 QV0-BT070
	121	7	23.3	383	1	AA244076 AA244076 nc04f09.r
c	122	7	23.3	383	1	AW374724 AW374724 MR1-CT005
	123	7	23.3	383	7	CN254924 CN254924 BIP1203 B
	124	7	23.3	385	3	BM510722 BM510722 ij49h09.x
c	125	7	23.3	386	5	BQ637572 BQ637572 he11h02.y
c	126	7	23.3	391	1	AA120928 AA120928 zn85g11.r
	127	7	23.3	399	5	BY378770 BY378770 BY378770
c	128	7	23.3	401	5	BY575085 BY575085 BY575085
c	129	7	23.3	401	8	D54696 D54696 HUM149E09B
c	130	7	23.3	403	2	BF822526 BF822526 CM2-RT000
	131	7	23.3	406	9	BH468205 BH468205 BOHHM70TF
c	132	7	23.3	407	1	AW604991 AW604991 RC0-CT038
c	133	7	23.3	407	6	CD849544 CD849544 DH0AC021Z
c	134	7	23.3	409	6	CB805097 CB805097 AMGNNUC:S
	135	7	23.3	411	9	CC411931 CC411931 PUHCX75TD
c	136	7	23.3	412	6	CD132052 CD132052 MG1-0016G
c	137	7	23.3	413	10	AG910167 AG910167 Drosophil
c	138	7	23.3	414	1	AW136178 AW136178 UI-H-BI1-
c	139	7	23.3	414	1	AW848886 AW848886 IL3-CT021
	140	7	23.3	415	6	CD122462 CD122462 ME1-0074G
	141	7	23.3	415	6	CD612884 CD612884 55114296J
	142	7	23.3	415	6	CD612885 CD612885 55114388H
c	143	7	23.3	416	6	CD612883 CD612883 55114296H
c	144	7	23.3	416	6	CD612886 CD612886 55114388J
c	145	7	23.3	416	8	D55009 D55009 HUM161H04B
	146	7	23.3	416	9	AQ110446 AQ110446 CIT-HSP-2
	147	7	23.3	417	2	BF945422 BF945422 MR0-NN019
c	148	7	23.3	419	2	BG037589 BG037589 dc53c01.y
c	149	7	23.3	419	8	D54574 D54574 HUM144F01B
	150	7	23.3	420	6	CD121530 CD121530 ME1-0068P
c	151	7	23.3	420	6	CD121590 CD121590 ME1-0068P
c	152	7	23.3	420	6	CF186048 CF186048 j4b07j2.r
	153	7	23.3	421	6	CD068446 CD068446 MA2-0001U
c	154	7	23.3	423	7	CV422585 CV422585 RC4-NN026
c	155	7	23.3	424	1	AA364259 AA364259 EST74830
	156	7	23.3	424	5	BY429713 BY429713 BY429713
c	157	7	23.3	425	2	BF325439 BF325439 su21g06.y
	158	7	23.3	425	6	CD121440 CD121440 ME1-0068G
	159	7	23.3	425	6	CF186588 CF186588 j4o18j2.f
	160	7	23.3	426	5	CA033466 CA033466 pw24a01.y
	161	7	23.3	427	2	BF634089 BF634089 NF086C07D
c	162	7	23.3	428	3	BM821667 BM821667 K-EST0090
	163	7	23.3	428	7	CV322979 CV322979 CM3-RT000
c	164	7	23.3	430	7	CN352676 CN352676 170004245
	165	7	23.3	431	10	CE405627 CE405627 tigr-gss-
c	166	7	23.3	433	6	CD132098 CD132098 MG1-0016P
	167	7	23.3	434	10	CL312700 CL312700 mth2-126J
c	168	7	23.3	435	5	BQ639784 BQ639784 he20d02.y
	169	7	23.3	435	7	CK241965 CK241965 rx03g05.y
	170	7	23.3	435	10	CW174211 CW174211 104_586_1
c	171	7	23.3	439	6	CB128198 CB128198 K-EST0177
c	172	7	23.3	440	1	AA340245 AA340245 EST45429
c	173	7	23.3	440	3	BM687546 BM687546 UI-E-CR0-
c	174	7	23.3	441	8	R99666 R99666 yq73h07.r1
	175	7	23.3	441	9	AQ210626 AQ210626 HS_2225_B
	176	7	23.3	441	9	AQ517742 AQ517742 HS_5137_B
c	177	7	23.3	442	1	AV709913 AV709913 AV709913
c	178	7	23.3	453	6	CD121489 CD121489 ME1-0068G
c	179	7	23.3	453	6	CD121608 CD121608 ME1-0068P
	180	7	23.3	455	9	CC764598 CC764598 CH240_47D
c	181	7	23.3	456	7	CN165179 CN165179 995585 MA
	182	7	23.3	456	7	CN165540 CN165540 995969 MA
	183	7	23.3	459	6	CF140573 CF140573 UI-HF-CB0
	184	7	23.3	460	1	AI940441 AI940441 CM0-CT005
	185	7	23.3	460	6	CD121532 CD121532 ME1-0068P
	186	7	23.3	460	9	AQ360939 AQ360939 HS_5036_B
c	187	7	23.3	463	3	BQ316848 BQ316848 RC0-CT038
c	188	7	23.3	463	10	CG254951 CG254951 OGVCS20TV
c	189	7	23.3	466	1	AI298268 AI298268 qm18d06.x
c	190	7	23.3	466	2	BG897704 BG897704 HOA16-1-F
	191	7	23.3	467	9	AQ985584 AQ985584 RPCI-23-3
	192	7	23.3	467	9	AQ220678 AQ220678 HS_2006_B
	193	7	23.3	470	6	CD098073 CD098073 ME1-0018T
c	194	7	23.3	471	1	AA397722 AA397722 zt80a04.r
c	195	7	23.3	474	6	CD177961 CD177961 MS1-0012P
	196	7	23.3	477	9	B43120 B43120 HS-1057-A1-
	197	7	23.3	478	11	FR0036420 AL123929 Fugu rubr
c	198	7	23.3	482	3	BM690128 BM690128 UI-E-CL0-
c	199	7	23.3	482	5	BW406290 BW406290 BW406290
c	200	7	23.3	483	2	BG875732 BG875732 CM4-CN004
c	201	7	23.3	483	3	BM827475 BM827475 K-EST0099
c	202	7	23.3	483	9	BH371911 BH371911 AG-ND-165
c	203	7	23.3	484	1	AA069319 AA069319 zf73c05.r
	204	7	23.3	484	1	AW633940 AW633940 bl14a07.w
c	205	7	23.3	484	6	CF139137 CF139137 UI-HF-CB0
	206	7	23.3	484	9	B71774 B71774 RPCI11-10M3
c	207	7	23.3	484	9	AQ701515 AQ701515 HS_2130_A
	208	7	23.3	487	2	BG609883 BG609883 324208 MA
	209	7	23.3	489	9	AQ489547 AQ489547 RPCI-11-2
	210	7	23.3	489	10	CE408643 CE408643 tigr-gss-
	211	7	23.3	490	9	BZ351373 BZ351373 hv83d06.g
	212	7	23.3	490	10	CW050549 CW050549 104_290_1
c	213	7	23.3	491	3	BQ316847 BQ316847 RC0-CT038
c	214	7	23.3	493	10	AY412737 AY412737 Homo sapi
	215	7	23.3	497	3	BI775842 BI775842 468559 MA
c	216	7	23.3	497	6	CF606721 CF606721 GEMMA01_0
	217	7	23.3	499	10	CZ781184 CZ781184 OC__Ba014
c	218	7	23.3	500	1	AW751550 AW751550 MR1-CT005
	219	7	23.3	500	2	BE026254 BE026254 db34d04.y
c	220	7	23.3	501	2	BI134002 BI134002 UI-M-BH3-
c	221	7	23.3	502	3	BI468350 BI468350 id87e02.y
c	222	7	23.3	502	3	BM510320 BM510320 ij39g12.y
c	223	7	23.3	502	3	BP423830 BP423830 BP423830
c	224	7	23.3	504	1	AW328427 AW328427 ds02e04.x
c	225	7	23.3	505	10	AG924253 AG924253 Drosophil
c	226	7	23.3	506	5	BQ639941 BQ639941 he22b06.y

	227	7	23.3	507	10	CW050010 CW050010 104_289_1
c	228	7	23.3	510	3	BM510402 BM510402 ij41a11.y
	229	7	23.3	511	3	BJ370160 BJ370160 BJ370160
	230	7	23.3	512	6	CD137743 CD137743 MG1-0049T
c	231	7	23.3	513	1	AW505812 AW505812 GE1029 G1
c	232	7	23.3	515	2	BG385407 BG385407 602454281
	233	7	23.3	518	7	CV743020 CV743020 SJAL_043_
	234	7	23.3	519	11	CR502344 CR502344 mth2-179B
c	235	7	23.3	522	3	BP425300 BP425300 BP425300
c	236	7	23.3	522	7	CK970189 CK970189 4085898 B
	237	7	23.3	522	8	DR722471 DR722471 AGENCOURT
c	238	7	23.3	522	9	BH899176 BH899176 Ots00243
	239	7	23.3	526	3	BM659972 BM659972 JCXP0112.
	240	7	23.3	526	7	CV302919 CV302919 74946.1 S
	241	7	23.3	529	10	CW022725 CW022725 104_162_1
	242	7	23.3	531	2	BG887672 BG887672 EST513523
	243	7	23.3	531	5	BW352229 BW352229 BW352229
	244	7	23.3	532	2	BE804889 BE804889 ss34d07.y
c	245	7	23.3	534	2	BG396270 BG396270 602459056
	246	7	23.3	535	10	CW097584 CW097584 104_463_1
c	247	7	23.3	537	3	BM699116 BM699116 UI-E-DX1-
c	248	7	23.3	539	5	BQ636789 BQ636789 he01d12.y
	249	7	23.3	539	7	CN434703 BE030009A
c	250	7	23.3	540	3	BQ338624 BQ338624 QV0-NN114
	251	7	23.3	541	3	BM508216 BM508216 ij41a11.x
	252	7	23.3	541	5	BU722120 SJMADH05
c	253	7	23.3	543	1	AJ706844 AJ706844
c	254	7	23.3	543	10	CW412929 CW412929 fsbb001f1
	255	7	23.3	544	2	BE665561 BE665561 154646 MA
	256	7	23.3	544	6	CD612892 CD612892 56042687J
	257	7	23.3	544	9	BH439121 BH439121 BOGVE25TR
	258	7	23.3	545	3	BQ316242 BQ316242 MR1-CT005
c	259	7	23.3	545	3	BQ338622 BQ338622 QV0-NN114
	260	7	23.3	545	6	CD612890 CD612890 56042679J
c	261	7	23.3	546	2	BB771727 BB771727 BB771727
c	262	7	23.3	546	3	BI764434 BI764434 603050707
c	263	7	23.3	547	3	BJ142201 BJ142201 BJ142201
c	264	7	23.3	547	6	CD612889 CD612889 56042679H
c	265	7	23.3	547	6	CD612891 CD612891 56042687H
	266	7	23.3	547	6	CF194901 CF194901 n1k04b3.f
c	267	7	23.3	548	3	BQ338623 BQ338623 QV0-NN114
c	268	7	23.3	549	5	BQ637952 BQ637952 hd16f04.y
c	269	7	23.3	550	3	BM511560 BM511560 ij49h09.y
	270	7	23.3	550	6	CD851584 CD851584 DH0ALL16Z
c	271	7	23.3	551	9	BH566306 BH566306 BOGDH16TF
	272	7	23.3	551	10	CW366805 CW366805 fsbb001f0
c	273	7	23.3	552	5	BQ639761 BQ639761 he19h11.y
c	274	7	23.3	553	9	AZ806209 AZ806209 2M0068B11
	275	7	23.3	555	3	BJ369149 BJ369149 BJ369149
c	276	7	23.3	555	9	AQ403233 AQ403233 HS_5051_B
c	277	7	23.3	556	10	CG328904 CG328904 OG0BA17TH
	278	7	23.3	557	5	BQ543057 BQ543057 ps84a06.y
c	279	7	23.3	557	7	CK822754 ig98a11.x
c	280	7	23.3	557	9	AQ883917 AQ883917 HS_5490_A
	281	7	23.3	558	9	AQ823849 AQ823849 HS_3234_B
	282	7	23.3	559	7	CV741535 CV741535 SJAL_033_
c	283	7	23.3	559	10	CW175439 CW175439 104_588_1
	284	7	23.3	560	9	BZ334730 BZ334730 hx93b10.b
	285	7	23.3	560	10	CZ180212 CZ180212 OA_BBa011
	286	7	23.3	561	3	BJ371142 BJ371142 BJ371142
c	287	7	23.3	561	6	CB160332 CB160332 K-EST0220
c	288	7	23.3	562	11	FR0036419 AL123928 Fugu rubr
	289	7	23.3	563	10	CW110535 CW110535 104_483_1
	290	7	23.3	564	5	BQ977762 BQ977762 QHI2P09.y
	291	7	23.3	565	9	AZ005290 AZ005290 RPCI-23-3
	292	7	23.3	565	10	CW173035 CW173035 104_584_1
c	293	7	23.3	567	5	BU086747 BU086747 Na_L3_12A
c	294	7	23.3	568	3	BJ150247 BJ150247 BJ150247
	295	7	23.3	568	10	BX983008 BX983008 Reverse s
c	296	7	23.3	569	3	BJ131441 BJ131441 BJ131441
c	297	7	23.3	569	5	CA035288 CA035288 4001088 B
c	298	7	23.3	569	7	CV100810 CV100810 FAMU_USDA
	299	7	23.3	569	9	AZ238333 AZ238333 RPCI-23-8
	300	7	23.3	574	10	CW067084 CW067084 104_314_1
	301	7	23.3	575	9	BZ626384 BZ626384 ih45e07.b
c	302	7	23.3	577	3	BJ143134 BJ143134 BJ143134
c	303	7	23.3	577	5	BU087291 BU087291 Na_L3_18G
c	304	7	23.3	578	3	BJ130670 BJ130670 BJ130670
c	305	7	23.3	578	3	BJ142926 BJ142926 BJ142926
c	306	7	23.3	579	3	BJ131358 BJ131358 BJ131358
	307	7	23.3	580	7	CV689132 CV689132 sjs4-009_
	308	7	23.3	581	10	CW139251 CW139251 104_529_1
c	309	7	23.3	582	3	BP218932 BP218932 BP218932
c	310	7	23.3	582	3	BP308895 BP308895 BP308895
	311	7	23.3	585	5	BX887224 BX887224 BX887224
	312	7	23.3	588	10	CW294951 CW294951 104_776_1
	313	7	23.3	589	5	BX393596 BX393596 BX393596
	314	7	23.3	591	10	CW865745 CW865745 she2h71-5
c	315	7	23.3	592	3	BJ527188 BJ527188 BJ527188
	316	7	23.3	592	10	CL188988 CL188988 104_405_1
c	317	7	23.3	593	2	BE382663 BE382663 601297321
c	318	7	23.3	593	3	BJ793933 BJ793933 BJ793933
c	319	7	23.3	593	5	BU783670 BU783670 in07g08.y
c	320	7	23.3	593	11	CT020766 CT020766 KBrH131O1
c	321	7	23.3	595	1	AW250342 AW250342 2821925.5
	322	7	23.3	595	3	BJ366464 BJ366464 BJ366464
c	323	7	23.3	595	3	BJ783605 BJ783605 BJ783605
	324	7	23.3	595	6	CD711666 CD711666 VVC007F09
	325	7	23.3	595	10	CW061202 CW061202 104_304_1
	326	7	23.3	596	3	BM510115 BM510115 ig98a11.x
c	327	7	23.3	596	10	CW376824 CW376824 fsbb001f0
	328	7	23.3	596	10	CW041855 CW041855 104_275_1
c	329	7	23.3	597	3	BJ146684 BJ146684 BJ146684
c	330	7	23.3	597	5	BQ635920 BQ635920 hd02a07.y
c	331	7	23.3	597	9	BH428951 BH428951 BOGFC63TF
c	332	7	23.3	598	3	BJ782008 BJ782008 BJ782008
c	333	7	23.3	599	3	BM017049 BM017049 603643749
c	334	7	23.3	599	10	AG950536 AG950536 Drosophil
c	335	7	23.3	600	3	BJ149953 BJ149953 BJ149953
	336	7	23.3	600	9	BH676789 BH676789 BOMFK40TR
	337	7	23.3	601	9	BZ602182 BZ602182 WHAAU36TF
	338	7	23.3	604	5	BQ799304 BQ799304 EST 1473
c	339	7	23.3	604	9	BZ294296 BZ294296 CG0816.f1
c	340	7	23.3	605	3	BM503970 BM503970 ig98a11.y
	341	7	23.3	605	6	CD307492 CD307492 StrPu691.
	342	7	23.3	605	10	CW096913 CW096913 104_462_1
c	343	7	23.3	606	3	BJ146006 BJ146006 BJ146006
c	344	7	23.3	606	3	BJ154817 BJ154817 BJ154817
c	345	7	23.3	606	6	CB120718 CB120718 K-EST0167
c	346	7	23.3	606	11	CR866768 CR866768 Sus scrof
	347	7	23.3	606	11	DE083571 DE083571 Oryzias l
c	348	7	23.3	607	3	BJ152114 BJ152114 BJ152114
c	349	7	23.3	608	6	CA950062 CA950062 ir86c09.y
c	350	7	23.3	609	2	BG818405 BG818405 602779953
c	351	7	23.3	609	3	BI599764 BI599764 603247894
c	352	7	23.3	609	3	BJ136787 BJ136787 BJ136787
	353	7	23.3	609	5	CA034573 CA034573 4000320 B
	354	7	23.3	609	7	CV743073 CV743073 SJAL_043_
	355	7	23.3	609	9	BZ337650 BZ337650 ia90b04.b
c	356	7	23.3	610	3	BJ142760 BJ142760 BJ142760
	357	7	23.3	610	6	CD853490 CD853490 DH0AMM18Z
c	358	7	23.3	611	3	BM690516 BM690516 UI-E-CI0-
c	359	7	23.3	612	9	BH004231 BH004231 BMBAC07K0
	360	7	23.3	612	9	CC801444 CC801444 ih14g04.b
c	361	7	23.3	613	3	BJ144454 BJ144454 BJ144454
c	362	7	23.3	613	5	BX370885 BX370885 BX370885
c	363	7	23.3	613	5	BX393597 BX393597 BX393597
	364	7	23.3	613	6	CD853562 CD853562 DH0AMM18Z
c	365	7	23.3	613	9	AZ655635 AZ655635 1M0530P07
c	366	7	23.3	615	10	CW942693 CW942693 TcB24.2_B
c	367	7	23.3	616	5	BX370884 BX370884 BX370884
	368	7	23.3	616	10	CW288982 CW288982 104_767_1
c	369	7	23.3	617	3	BP103710 BP103710 BP103710
c	370	7	23.3	617	4	CR594482 CR594482 full-leng
c	371	7	23.3	617	5	BQ639105 BQ639105 hd31d12.y
c	372	7	23.3	618	7	CN074612 CN074612 EC0CBA005

	373	7	23.3	618	7	CN583619 CN583619 USDA-FP_1
c	374	7	23.3	619	5	BQ637487 BQ637487 he10f12.y
	375	7	23.3	619	9	BZ334842 BZ334842 hx93h03.b
c	376	7	23.3	620	2	BE252817 BE252817 601112971
c	377	7	23.3	620	3	BM688357 BM688357 UI-E-CL0-
c	378	7	23.3	620	5	BQ639259 BQ639259 hd33c08.y
	379	7	23.3	620	10	CW437179 CW437179 fsbb001f1
c	380	7	23.3	621	5	BQ639090 BQ639090 hd31c04.y
c	381	7	23.3	622	10	CW116569 CW116569 104_492_1
c	382	7	23.3	623	6	CA773182 CA773182 im60g03.y
c	383	7	23.3	623	9	BZ337651 BZ337651 ia90b04.g
	384	7	23.3	623	10	CE377777 CE377777 tigr-gss-
c	385	7	23.3	625	5	BQ639971 BQ639971 he22f03.y
	386	7	23.3	625	10	CW108519 CW108519 104_480_1
	387	7	23.3	626	7	CV741275 CV741275 SJAL_032_
c	388	7	23.3	627	2	BF317056 BF317056 601903450
	389	7	23.3	627	5	BQ776627 BQ776627 il35c03.x
c	390	7	23.3	627	9	BZ334072 BZ334072 hx76e07.g
c	391	7	23.3	628	3	BM690883 BM690883 UI-E-CI1-
c	392	7	23.3	629	5	BQ639475 BQ639475 he16a09.y
	393	7	23.3	629	10	CE629126 CE629126 tigr-gss-
c	394	7	23.3	630	3	BM691251 BM691251 UI-E-CI1-
	395	7	23.3	630	9	AZ863361 AZ863361 2M0171O17
c	396	7	23.3	630	11	CNS04PZO AL301965 Tetraodon
c	397	7	23.3	632	10	CW341558 CW341558 104_843_1
c	398	7	23.3	633	5	BX429972 BX429972 BX429972
	399	7	23.3	633	10	CW222786 CW222786 104_658_1
	400	7	23.3	633	10	CNS02R7X AL210246 Tetraodon
c	401	7	23.3	634	6	CB919659 CB919659 VVD054B12
	402	7	23.3	634	10	CW464365 CW464365 fsbb001f2
c	403	7	23.3	635	5	BQ637969 BQ637969 hd16h03.y
c	404	7	23.3	635	6	CB005060 CB005060 VVC007F09
c	405	7	23.3	636	1	AI055508 AI055508 coau0004C
	406	7	23.3	636	2	BE617959 BE617959 601442188
	407	7	23.3	636	9	BZ204263 BZ204263 CH230-474
c	408	7	23.3	638	1	AL846120 AL846120 AL846120
c	409	7	23.3	638	7	CK962285 CK962285 4076831 B
c	410	7	23.3	639	10	CW147631 CW147631 104_542_1
	411	7	23.3	639	10	CW210688 CW210688 104_641_1
c	412	7	23.3	640	6	CB921460 CB921460 VVD071D05
	413	7	23.3	640	10	CW181513 CW181513 104_596_1
	414	7	23.3	641	9	AZ380806 AZ380806 1M0136J22
	415	7	23.3	641	9	CE262051 CE262051 tigr-gss-
	416	7	23.3	642	1	AW644971 AW644971 cm47e04.w
c	417	7	23.3	643	1	AJ817105 AJ817105 AJ817105
c	418	7	23.3	643	1	AL967701 AL967701 AL967701
	419	7	23.3	643	3	BM980710 BM980710 UI-CF-EN1
	420	7	23.3	644	2	BF435460 BF435460 nac31b01.
c	421	7	23.3	644	2	BB665682 BB665682 BB665682
c	422	7	23.3	644	5	BX915065 BX915065 BX915065
	423	7	23.3	644	10	CW281492 CW281492 104_757_1
	424	7	23.3	645	2	BE618820 BE618820 601462694
c	425	7	23.3	645	5	BU072826 BU072826 il35c03.y
c	426	7	23.3	645	8	CV896786 CV896786 PA045D11
	427	7	23.3	645	10	CW341559 CW341559 104_843_1
c	428	7	23.3	646	2	BF528606 BF528606 602041214
c	429	7	23.3	646	5	BQ637836 BQ637836 hd15b12.y
c	430	7	23.3	646	11	DE084808 DE084808 Oryzias l
	431	7	23.3	647	1	AA608630 AA608630 ae55a04.s
c	432	7	23.3	647	5	BX450341 BX450341 BX450341
	433	7	23.3	647	8	DN087483 DN087483 JGI_CABE1
	434	7	23.3	647	10	CZ862684 CZ862684 OC__Ba025
	435	7	23.3	648	2	BG775456 BG775456 602649937
	436	7	23.3	648	10	CE269742 CE269742 tigr-gss-
c	437	7	23.3	649	3	BM083354 BM083354 imageqc_6
	438	7	23.3	649	9	BZ068364 BZ068364 ljt09e01.
	439	7	23.3	649	10	CW070603 CW070603 104_321_1
	440	7	23.3	649	10	CW341557 CW341557 104_843_1
	441	7	23.3	650	7	CV756230 CV756230 sj16-006_
	442	7	23.3	650	10	CW864558 CW864558 sh2a11-1.
c	443	7	23.3	651	5	BX313720 BX313720 BX313720
	444	7	23.3	651	6	CB891151 CB891151 EST648120
c	445	7	23.3	653	7	CK946925 CK946925 4071583 B
	446	7	23.3	655	10	CW280670 CW280670 104_756_1
c	447	7	23.3	656	7	CK966179 CK966179 4081332 B
c	448	7	23.3	656	11	CR299927 CR299927 mtel-18C1
c	449	7	23.3	657	2	BF316388 BF316388 601901957
c	450	7	23.3	657	7	CN352670 CN352670 170004243
	451	7	23.3	657	9	CC396542 CC396542 PUHCW47TD
c	452	7	23.3	657	10	CW204191 CW204191 104_632_1
c	453	7	23.3	657	11	CR866654 CR866654 Sus scrof
c	454	7	23.3	657	11	CR913394 CR913394 Sus scrof
c	455	7	23.3	658	7	CK004735 CK004735 AGENCOURT
c	456	7	23.3	659	3	BM728605 BM728605 UI-E-EJ0-
	457	7	23.3	659	6	CF572324 CF572324 MCSA036G0
c	458	7	23.3	659	10	CW189570 CW189570 104_610_1
c	459	7	23.3	660	6	CA355394 CA355394 627268 NC
c	460	7	23.3	660	9	AZ571034 AZ571034 281PvH07
	461	7	23.3	662	1	AA126454 AA126454 zn85g11.s
c	462	7	23.3	662	6	CB002599 CB002599 VVB018F09
c	463	7	23.3	662	7	CN352672 CN352672 170006000
	464	7	23.3	664	1	AW693993 AW693993 NF071D10S
c	465	7	23.3	664	2	BF680862 BF680862 602156119
	466	7	23.3	664	9	AZ280502 AZ280502 RPCI-23-1
c	467	7	23.3	665	3	BJ153465 BJ153465 BJ153465
	468	7	23.3	665	10	CW313207 CW313207 104_803_1
c	469	7	23.3	666	10	CW095044 CW095044 104_459_1
	470	7	23.3	667	3	BJ616966 BJ616966 BJ616966
	471	7	23.3	667	10	CW427267 CW427267 fsbb001f1
c	472	7	23.3	669	2	BG818826 BG818826 602779184
c	473	7	23.3	669	8	DR759990 DR759990 HESC4_110
	474	7	23.3	669	10	CW210712 CW210712 104_641_1
	475	7	23.3	670	9	AZ880991 AZ880991 RPCI-23-2
	476	7	23.3	670	9	BZ345684 BZ345684 hs87h07.b
c	477	7	23.3	671	2	BF348176 BF348176 602022081
c	478	7	23.3	671	10	CW245396 CW245396 104_706_1
c	479	7	23.3	672	2	BG913689 BG913689 602811020
	480	7	23.3	672	3	BM671974 BM671974 UI-E-EO0-
	481	7	23.3	672	6	CD762720 CD762720 GGEZSM102
c	482	7	23.3	673	5	BQ794011 BQ794011 EST 2949
	483	7	23.3	676	6	CA427782 CA427782 UI-H-DF0-
	484	7	23.3	677	10	CW185257 CW185257 104_602_1
c	485	7	23.3	678	5	BX429999 BX429999 BX429999
c	486	7	23.3	678	7	CN352664 CN352664 170006000
c	487	7	23.3	679	2	BG570286 BG570286 602590706
	488	7	23.3	679	5	BX461899 BX461899 BX461899
c	489	7	23.3	679	7	CN352667 CN352667 170006000
	490	7	23.3	679	11	CR169579 CR169579 Reverse s
c	491	7	23.3	681	10	CW168790 CW168790 104_578_1
c	492	7	23.3	682	10	CW084123 CW084123 104_426_1
	493	7	23.3	682	10	CW578049 CW578049 OA_ABa010
	494	7	23.3	683	2	BE293477 BE293477 600942920
c	495	7	23.3	683	3	BI334953 BI334953 602998832
c	496	7	23.3	683	5	BX425798 BX425798 BX425798
	497	7	23.3	683	8	DR927683 DR927683 EST111922
	498	7	23.3	683	10	CW427678 CW427678 fsbb001f1
c	499	7	23.3	685	1	AW813699 AW813699 RC3-ST019
c	500	7	23.3	685	3	BI333755 BI333755 602999232
	501	7	23.3	685	8	DN909766 DN909766 Cuc2_3_E0
c	502	7	23.3	686	9	BZ519663 BZ519663 BOMRE89TR
c	503	7	23.3	686	10	CW430025 CW430025 fsbb001f1
c	504	7	23.3	687	7	CK002911 CK002911 AGENCOURT
c	505	7	23.3	687	10	CW370871 CW370871 fsbb001f0
	506	7	23.3	687	10	CG027641 CG027641 CHGAM03TR
c	507	7	23.3	687	10	CW011242 CW011242 ZMMBLc000
c	508	7	23.3	688	10	CW079839 CW079839 104_404_1
	509	7	23.3	688	10	CL187984 CL187984 104_404_1
c	510	7	23.3	689	5	BU425228 BU425228 603959441
c	511	7	23.3	689	5	BU595359 BU595359 AGENCOURT
c	512	7	23.3	689	5	BX452797 BX452797 BX452797
	513	7	23.3	689	10	CW397230 CW397230 fsbb001f0
c	514	7	23.3	690	3	BJ779207 BJ779207 BJ779207
c	515	7	23.3	690	5	BW098468 BW098468 BW098468
c	516	7	23.3	690	10	CW320675 CW320675 104_813_1
c	517	7	23.3	690	10	CW345002 CW345002 104_847_1
c	518	7	23.3	691	4	CR608393 CR608393 full-leng

c	519	7	23.3	691	5	BX450568	BX450568 BX450568
c	520	7	23.3	691	5	BX452796	BX452796 BX452796
	521	7	23.3	691	10	CW167128	CW167128 104_576_1
	522	7	23.3	691	10	AG349450	AG349450 Mus muscu
	523	7	23.3	691	11	CR486081	CR486081 mth2-155E
	524	7	23.3	692	10	CW078811	CW078811 104_397_1
	525	7	23.3	692	10	CW497087	CW497087 fsbb001f2
	526	7	23.3	693	10	CW151892	CW151892 104_552_1
c	527	7	23.3	693	10	CW371206	CW371206 fsbb001f0
	528	7	23.3	693	10	CW380748	CW380748 fsbb001f0
	529	7	23.3	693	10	AG349452	AG349452 Mus muscu
	530	7	23.3	694	1	AW157045	AW157045 au91c01.x
c	531	7	23.3	694	6	CD068021	CD068021 MA1-0051P
c	532	7	23.3	694	7	CN352661	CN352661 170004243
	533	7	23.3	694	10	CW190318	CW190318 104_611_1
c	534	7	23.3	696	3	BQ108726	BQ108726 imageqc_9
c	535	7	23.3	697	1	AI300086	AI300086 qn59f04.x
c	536	7	23.3	697	10	CW245395	CW245395 104_706_1
	537	7	23.3	698	10	CW229703	CW229703 104_671_1
c	538	7	23.3	699	3	BI760095	BI760095 603044579
	539	7	23.3	699	9	BZ823949	BZ823949 PUFGS35TB
c	540	7	23.3	700	10	CW280626	CW280626 104_755_1
	541	7	23.3	700	10	CW352138	CW352138 fsbb001f0
c	542	7	23.3	701	6	CB914402	CB914402 VVD006D09
	543	7	23.3	701	6	CF511947	CF511947 CAbud0004
c	544	7	23.3	701	10	CW181514	CW181514 104_596_1
c	545	7	23.3	702	6	CF664961	CF664961 RTCNT1_13
c	546	7	23.3	702	10	CW372098	CW372098 fsbb001f0
c	547	7	23.3	702	10	CE328118	CE328118 tigr-gss-
	548	7	23.3	703	10	CW254933	CW254933 104_719_1
	549	7	23.3	704	9	AZ571877	AZ571877 299PvG02
	550	7	23.3	706	7	CN062973	CN062973 Ag2_p39_L
	551	7	23.3	707	9	BH125376	BH125376 RPCI-24-2
c	552	7	23.3	707	10	CW280671	CW280671 104_756_1
c	553	7	23.3	708	5	BX325832	BX325832 BX325832
	554	7	23.3	708	7	CV743049	CV743049 SJAL_043_
	555	7	23.3	712	9	BH564787	BH564787 BOHHX19TF
c	556	7	23.3	713	10	CL598791	CL598791 OB__Ba006
c	557	7	23.3	714	5	BU557161	BU557161 AGENCOURT
	558	7	23.3	714	6	CF542173	CF542173 CsC558F c
	559	7	23.3	716	8	CX861217	CX861217 SJMAUG01.
c	560	7	23.3	716	10	CW300090	CW300090 104_783_1
	561	7	23.3	716	10	CW361607	CW361607 fsbb001f0
c	562	7	23.3	718	10	CW077316	CW077316 104_379_1
	563	7	23.3	718	10	CW168152	CW168152 104_577_1
c	564	7	23.3	719	2	BE798646	BE798646 601582096
	565	7	23.3	719	10	CW080202	CW080202 104_408_1
c	566	7	23.3	719	10	CW086759	CW086759 104_430_1
	567	7	23.3	720	1	AW633854	AW633854 bl13a06.w
	568	7	23.3	721	8	DN909981	DN909981 Cuc3_2_H0
	569	7	23.3	721	10	CE735276	CE735276 tigr-gss-
	570	7	23.3	722	1	AI573104	AI573104 tr69e10.x
c	571	7	23.3	722	9	BH941131	BH941131 odf16h12.
	572	7	23.3	722	10	CW202227	CW202227 104_628_1
c	573	7	23.3	723	7	CN352663	CN352663 170004706
	574	7	23.3	723	10	CW476903	CW476903 fsbb001f2
c	575	7	23.3	724	2	BG474334	BG474334 602517017
	576	7	23.3	724	7	CK847607	CK847607 970265 MA
	577	7	23.3	724	10	CW078812	CW078812 104_397_1
c	578	7	23.3	724	10	CW229067	CW229067 104_670_1
c	579	7	23.3	725	5	BW170038	BW170038 BW170038
	580	7	23.3	725	10	CW256753	CW256753 104_722_1
c	581	7	23.3	726	1	AV895894	AV895894 AV895894
	582	7	23.3	726	10	CW399786	CW399786 fsbb001f0
	583	7	23.3	727	5	BU633835	BU633835 UI-H-FL1-
	584	7	23.3	727	10	CW162906	CW162906 104_570_1
	585	7	23.3	727	10	CW347358	CW347358 fsbb001f0
	586	7	23.3	727	10	CW359260	CW359260 fsbb001f0
c	587	7	23.3	728	3	BI824130	BI824130 603039278
	588	7	23.3	728	10	CW149787	CW149787 104_549_1
	589	7	23.3	729	5	BU620622	BU620622 UI-H-FL1-
	590	7	23.3	729	6	CD367046	CD367046 UI-H-FT2-
c	591	7	23.3	729	6	CF454712	CF454712 AGENCOURT
	592	7	23.3	729	9	BH958843	BH958843 odi42a12.
c	593	7	23.3	730	2	BI257141	BI257141 602973128
c	594	7	23.3	730	3	BM043129	BM043129 603619277
	595	7	23.3	730	10	CW075951	CW075951 104_363_1
	596	7	23.3	730	10	CL163639	CL163639 104_357_1
	597	7	23.3	731	8	CX458005	CX458005 JGI_XZG54
	598	7	23.3	731	10	CW556005	CW556005 OA_ABa007
c	599	7	23.3	732	9	BH263867	BH263867 CH230-161
c	600	7	23.3	732	10	CZ883334	CZ883334 OC__Ba028
c	601	7	23.3	733	9	CE007388	CE007388 tigr-gss-
c	602	7	23.3	734	3	BM045782	BM045782 603624749
	603	7	23.3	734	10	CL174925	CL174925 104_379_1
	604	7	23.3	735	5	BU617943	BU617943 UI-H-DF0-
c	605	7	23.3	735	10	CL154996	CL154996 104_340_1
c	606	7	23.3	736	6	CF457286	CF457286 AGENCOURT
	607	7	23.3	736	8	DR715336	DR715336 AGENCOURT
c	608	7	23.3	736	10	CW492293	CW492293 fsbb001f2
c	609	7	23.3	737	7	CV174462	CV174462 EUCLIDIA2
	610	7	23.3	738	3	BM684665	BM684665 UI-E-EO1-
	611	7	23.3	739	7	CV743223	CV743223 SJAL_044_
	612	7	23.3	739	10	CW369217	CW369217 fsbb001f0
c	613	7	23.3	741	6	CA061278	CA061278 ssalrgb50
	614	7	23.3	741	10	CW179210	CW179210 104_593_1
	615	7	23.3	742	10	CE355097	CE355097 tigr-gss-
	616	7	23.3	743	10	CW204192	CW204192 104_632_1
c	617	7	23.3	744	10	CW473671	CW473671 fsbb001f2
c	618	7	23.3	745	2	BF343070	BF343070 602017190
	619	7	23.3	745	9	BZ424330	BZ424330 id59f07.g
c	620	7	23.3	745	9	CE261280	CE261280 tigr-gss-
c	621	7	23.3	746	3	BM011310	BM011310 603635480
c	622	7	23.3	746	10	CW151893	CW151893 104_552_1
	623	7	23.3	747	2	BG648871	BG648871 EST510490
c	624	7	23.3	747	8	DR847027	DR847027 JGI_CABE1
	625	7	23.3	748	5	BQ448008	BQ448008 UI-H-EU1-
c	626	7	23.3	748	9	BH263917	BH263917 CH230-161
	627	7	23.3	748	10	CG136399	CG136399 PUILV05TB
	628	7	23.3	749	1	AI660492	AI660492 we67g12.x
c	629	7	23.3	749	5	BX408354	BX408354 BX408354
c	630	7	23.3	749	9	AQ748010	AQ748010 HS_5537_A
c	631	7	23.3	750	6	CB970790	CB970790 CAB10004_
c	632	7	23.3	750	9	BH116494	BH116494 RPCI-24-2
c	633	7	23.3	750	10	CW341556	CW341556 104_843_1
c	634	7	23.3	750	10	CW495485	CW495485 fsbb001f2
c	635	7	23.3	751	2	BF337746	BF337746 602037524
c	636	7	23.3	751	2	BG472957	BG472957 602514893
c	637	7	23.3	751	8	CV987977	CV987977 IpCGFr1_1
	638	7	23.3	752	6	CB454941	CB454941 711769 MA
c	639	7	23.3	752	10	CW408070	CW408070 fsbb001f1
	640	7	23.3	752	10	AG097209	AG097209 Pan trogl
c	641	7	23.3	754	5	BX408016	BX408016 BX408016
	642	7	23.3	754	10	CL154995	CL154995 104_340_1
	643	7	23.3	756	10	AG440405	AG440405 Mus muscu
	644	7	23.3	757	5	BU906893	BU906893 AGENCOURT
	645	7	23.3	757	7	CO878155	CO878155 BovGen_06
	646	7	23.3	757	9	CC058899	CC058899 ii17a08.b
c	647	7	23.3	757	10	CW079835	CW079835 104_404_1
c	648	7	23.3	759	2	BF346274	BF346274 602018467
	649	7	23.3	760	10	CW164809	CW164809 104_573_1
c	650	7	23.3	761	3	BJ809262	BJ809262 BJ809262
c	651	7	23.3	761	9	AQ291912	AQ291912 nbxb0040I
	652	7	23.3	762	10	CW084122	CW084122 104_426_1
c	653	7	23.3	763	6	CD579287	CD579287 EST_PSF00
c	654	7	23.3	763	8	CX749028	CX749028 JGI_ANHP1
	655	7	23.3	763	10	AG585275	AG585275 Mus muscu
c	656	7	23.3	763	10	CW028413	CW028413 104_255_1
c	657	7	23.3	764	2	BG820251	BG820251 602780329
c	658	7	23.3	764	5	BX367744	BX367744 BX367744
	659	7	23.3	764	10	CW879971	CW879971 she2h50-5
c	660	7	23.3	766	10	CW352858	CW352858 fsbb001f0
c	661	7	23.3	769	2	BF339980	BF339980 602036910
c	662	7	23.3	771	2	BE973865	BE973865 601680674
	663	7	23.3	771	5	BU417917	BU417917 603233341
c	664	7	23.3	771	6	CF270373	CF270373 AGENCOURT

c	665	7	23.3	772	3	BM048857 BM048857 603625231
c	666	7	23.3	772	7	CN352678 CN352678 170006001
c	667	7	23.3	772	10	CZ713986 CZ713986 OC__Ba003
	668	7	23.3	772	10	CL176765 CL176765 104_383_1
	669	7	23.3	774	3	BJ615547 BJ615547
c	670	7	23.3	774	8	DR879486 DR879486 JGI_CABJ7
c	671	7	23.3	776	6	CB951149 CB951149 AGENCOURT
	672	7	23.3	776	10	CW409052 CW409052 fsbb001f1
	673	7	23.3	777	5	BU213891 BU213891 603755685
c	674	7	23.3	777	8	DT084719 DT084719 JGI_AIZU5
	675	7	23.3	778	8	CX751170 CX751170 AGENCOURT
c	676	7	23.3	780	2	BF311248 BF311248 601898514
	677	7	23.3	781	8	DR932598 DR932598 EST112413
c	678	7	23.3	781	9	CC439968 CC439968 PUHLN52TD
c	679	7	23.3	782	6	CF209750 CF209750 CAB20005_
c	680	7	23.3	783	6	CF355672 CF355672 V-B-130H0
c	681	7	23.3	783	8	DN087484 DN087484 JGI_CABE1
c	682	7	23.3	784	10	CZ864707 CZ864707 OC__Ba025
	683	7	23.3	785	7	CK465964 CK465964 937126 MA
c	684	7	23.3	785	7	CK468065 CK468065 939430 MA
c	685	7	23.3	786	8	CV993359 CV993359 IpCGFr2_1
	686	7	23.3	787	9	BH705258 BH705258 BOMPQ18TR
	687	7	23.3	787	9	CC398202 CC398202 PUHIA75TB
	688	7	23.3	787	10	CW407387 CW407387 fsbb001f1
c	689	7	23.3	788	8	CX950038 CX950038 UMC-bcl_0
c	690	7	23.3	790	2	BG866687 BG866687 602785679
	691	7	23.3	790	10	DU032845 DU032845 14489 Tom
c	692	7	23.3	791	9	BZ116208 BZ116208 CH230-422
	693	7	23.3	792	10	AG541166 AG541166 Mus muscu
c	694	7	23.3	793	2	BG831070 BG831070 602766613
	695	7	23.3	793	6	CB893336 CB893336 EST646128
c	696	7	23.3	794	7	CO087564 CO087564 GR__Ea06B
	697	7	23.3	794	9	BZ445134 BZ445134 BONIM25TR
	698	7	23.3	794	9	CC921594 CC921594 t055d22ba
c	699	7	23.3	796	3	BJ145095 BJ145095
c	700	7	23.3	796	5	BQ438306 BQ438306 AGENCOURT
	701	7	23.3	796	7	CK456727 CK456727 920970 MA
c	702	7	23.3	797	6	CB979231 CB979231 CAB40007_
	703	7	23.3	797	7	CN039505 CN039505 nm_32h_g1
c	704	7	23.3	798	2	BI115994 BI115994 602866575
	705	7	23.3	798	3	BP699115 BP699115 BP699115
	706	7	23.3	798	8	DR916885 DR916885 EST110842
c	707	7	23.3	798	10	CW692448 CW692448 OP__Ba005
	708	7	23.3	798	11	CR824972 CR824972 GR0AAA55D
c	709	7	23.3	800	6	CB942320 CB942320 AGENCOURT
	710	7	23.3	801	6	CB893579 CB893579 EST646371
	711	7	23.3	801	10	CZ726218 CZ726218 OC__Ba005
c	712	7	23.3	802	8	DR760142 DR760142 HESC4_112
	713	7	23.3	803	2	BE293760 BE293760 601186720
c	714	7	23.3	804	3	BM043734 BM043734 603620548
	715	7	23.3	804	7	CO502604 CO502604 59873.1 I
c	716	7	23.3	805	3	BI763087 BI763087 603047894
c	717	7	23.3	806	2	BG707552 BG707552 602670601
c	718	7	23.3	807	3	BI771445 BI771445 603059492
c	719	7	23.3	809	6	CF456807 CF456807 AGENCOURT
	720	7	23.3	811	9	AQ866214 AQ866214 nbeb0027M
c	721	7	23.3	811	10	CW369218 CW369218 fsbb001f0
	722	7	23.3	812	3	BM112256 BM112256 EST559792
c	723	7	23.3	813	8	CX401110 CX401110 JGI_XZT48
c	724	7	23.3	813	10	CZ748529 CZ748529 OC__Ba009
c	725	7	23.3	815	3	BM043371 BM043371 603619708
c	726	7	23.3	817	10	CZ292423 CZ292423 cp81c08.f
c	727	7	23.3	818	7	CK086146 CK086146 RG12_B10
	728	7	23.3	818	8	DN910764 DN910764 Cuc6_1_E0
c	729	7	23.3	819	8	DR771355 DR771355 ILLUMIGEN
	730	7	23.3	819	9	BZ963342 BZ963342 PUGEV86TB
c	731	7	23.3	822	2	BG108431 BG108431 602278372
	732	7	23.3	822	9	BZ603536 BZ603536 WHABU82TR
	733	7	23.3	822	10	CZ275000 CZ275000 ZMMBF0056
	734	7	23.3	823	2	BG683419 BG683419 602651244
c	735	7	23.3	823	7	CK774209 CK774209 962945 MA
c	736	7	23.3	824	5	BX343563 BX343563 BX343563
c	737	7	23.3	826	7	CO080800 CO080800 GR__Ea44H
c	738	7	23.3	826	10	CG330438 CG330438 OG4AT33TC
	739	7	23.3	828	10	CW370845 CW370845 fsbb001f0
	740	7	23.3	830	6	CF514861 CF514861 CAP0001_I
c	741	7	23.3	830	7	CK720357 CK720357 20782 Swo
c	742	7	23.3	831	7	CO452647 CO452647 MZCCL1018
c	743	7	23.3	831	8	CX376429 CX376429 JGI_XZT33
c	744	7	23.3	832	3	BM048740 BM048740 603625362
c	745	7	23.3	832	5	BU962103 BU962103 AGENCOURT
	746	7	23.3	832	7	CK353300 CK353300 AGENCOURT
c	747	7	23.3	833	6	CF515040 CF515040 CAP0001_I
c	748	7	23.3	834	2	BI194079 BI194079 602945765
	749	7	23.3	834	2	BE915489 BE915489 601664990
c	750	7	23.3	834	3	BM044084 BM044084 603621154
	751	7	23.3	835	7	CK289724 CK289724 EST752446
c	752	7	23.3	838	7	CN802981 CN802981 ILLUMIGEN
c	753	7	23.3	838	7	CO077745 CO077745 GR__Ea39K
	754	7	23.3	838	8	CX788629 CX788629 HESC3_100
c	755	7	23.3	839	8	CX998529 CX998529 JGI_CAAQ1
	756	7	23.3	840	7	CV302921 CV302921 74949.1 S
c	757	7	23.3	841	6	CF515381 CF515381 CAP0001_I
	758	7	23.3	841	10	CG070766 CG070766 PUILI96TB
c	759	7	23.3	842	8	DR158667 DR158667 HESC2_93_
c	760	7	23.3	844	8	DN057533 DN057533 JGI_CABA1
	761	7	23.3	845	9	AZ738116 AZ738116 RPCI-24-1
c	762	7	23.3	845	11	CR230347 CR230347 Forward s
c	763	7	23.3	847	9	CC417982 CC417982 PUHBT14TD
c	764	7	23.3	847	10	CL992239 CL992239 ZMMBHf000
c	765	7	23.3	848	8	DN035362 DN035362 JGI_CAAR1
c	766	7	23.3	849	5	BU594748 BU594748 AGENCOURT
c	767	7	23.3	849	9	CC545223 CC545223 CH240_427
	768	7	23.3	850	7	CO071797 CO071797 GR__Ea30H
c	769	7	23.3	851	3	BM043345 BM043345 603619659
	770	7	23.3	851	9	CC735676 CC735676 PUJAD86TD
c	771	7	23.3	855	3	BM043668 BM043668 603620257
	772	7	23.3	855	8	CX998528 CX998528 JGI_CAAQ1
	773	7	23.3	857	8	CX828126 CX828126 JGI_CAAK6
c	774	7	23.3	857	10	CL665895 CL665895 PRI0151a_
c	775	7	23.3	857	10	CW019446 CW019446 ZMMBLc001
	776	7	23.3	858	2	BI084832 BI084832 602869378
c	777	7	23.3	858	5	BX450359 BX450359 BX450359
c	778	7	23.3	859	5	BX450155 BX450155 BX450155
c	779	7	23.3	860	6	CA987235 CA987235 AGENCOURT
	780	7	23.3	861	5	BX463364 BX463364 BX463364
c	781	7	23.3	862	2	BF038095 BF038095 601461313
	782	7	23.3	863	6	CF704001 CF704001 CCAC983TF
c	783	7	23.3	864	5	BQ949309 BQ949309 AGENCOURT
	784	7	23.3	864	5	BX413801 BX413801 BX413801
c	785	7	23.3	865	8	DR916612 DR916612 EST110815
c	786	7	23.3	867	2	BI116768 BI116768 602868461
	787	7	23.3	867	8	DN910205 DN910205 Cuc4_3_D0
c	788	7	23.3	868	8	DR157381 DR157381 HESC2_77_
	789	7	23.3	872	10	AG903518 AG903518 Oryza sat
	790	7	23.3	873	5	BX436258 BX436258 BX436258
	791	7	23.3	873	7	CK296429 CK296429 EST759143
c	792	7	23.3	873	8	CX838203 CX838203 JGI_CAAK8
c	793	7	23.3	873	9	AZ669988 AZ669988 ENTKG90TF
	794	7	23.3	874	5	BU916894 BU916894 AGENCOURT
	795	7	23.3	874	7	CO084617 CO084617 GR__Ea01F
c	796	7	23.3	876	5	BU542223 BU542223 AGENCOURT
c	797	7	23.3	877	6	CD513554 CD513554 AGENCOURT
c	798	7	23.3	877	10	CG116045 CG116045 PUIEV46TD
c	799	7	23.3	878	5	BU541183 BU541183 AGENCOURT
c	800	7	23.3	879	3	BI765826 BI765826 603047468
c	801	7	23.3	880	2	BG820857 BG820857 602780925
c	802	7	23.3	880	5	BQ923280 BQ923280 AGENCOURT
c	803	7	23.3	880	8	DR943785 DR943785 EST113532
	804	7	23.3	881	6	CF660961 CF660961 CcLL10a33
c	805	7	23.3	881	9	BH163824 BH163824 ENTRT32TF
	806	7	23.3	882	6	CB564681 CB564681 AGENCOURT
	807	7	23.3	885	6	CF515470 CF515470 CAP0001_I
c	808	7	23.3	885	7	CO077743 CO077743 GR__Ea39K
c	809	7	23.3	886	5	BQ927643 BQ927643 AGENCOURT
c	810	7	23.3	886	5	BQ961801 BQ961801 AGENCOURT

	811	7	23.3	886	10	CZ716299 CZ716299 OC__Ba004
c	812	7	23.3	887	3	BM046124 BM046124 603625857
c	813	7	23.3	890	5	BX450411 BX450411 BX450411
c	814	7	23.3	890	6	CD580510 CD580510 EST_PSF01
c	815	7	23.3	891	3	BM562968 BM562968 AGENCOURT
c	816	7	23.3	892	6	CD580426 CD580426 EST_PSF01
	817	7	23.3	892	7	CK291746 CK291746 EST754460
c	818	7	23.3	893	5	BQ943624 BQ943624 AGENCOURT
c	819	7	23.3	895	2	BE740676 BE740676 601593636
c	820	7	23.3	897	5	BQ958567 BQ958567 AGENCOURT
c	821	7	23.3	897	5	BU542487 BU542487 AGENCOURT
	822	7	23.3	897	9	BZ815746 BZ815746 PUGCV39TB
	823	7	23.3	901	5	BU393469 BU393469 603511668
c	824	7	23.3	902	2	BF984658 BF984658 602309723
	825	7	23.3	902	9	CC007845 CC007845 PUDHI02TD
c	826	7	23.3	906	5	BU154502 BU154502 AGENCOURT
c	827	7	23.3	907	5	BU932063 BU932063 AGENCOURT
c	828	7	23.3	907	7	CK085802 CK085802 RG7_E06 C
c	829	7	23.3	907	9	CC402419 CC402419 PUHEG63TD
	830	7	23.3	909	2	BF100728 BF100728 601754353
c	831	7	23.3	909	5	BU850228 BU850228 AGENCOURT
c	832	7	23.3	911	10	CG950221 CG950221 MBELM28TR
	833	7	23.3	912	10	AG889810 AG889810 Oryza sat
	834	7	23.3	914	2	BF181395 BF181395 601807281
	835	7	23.3	914	6	CA974676 CA974676 AGENCOURT
	836	7	23.3	914	7	CK298590 CK298590 EST761304
c	837	7	23.3	915	5	BX449930 BX449930 BX449930
	838	7	23.3	916	9	CC587562 CC587562 CH240_385
c	839	7	23.3	916	10	AG865370 AG865370 Oryza sat
c	840	7	23.3	917	5	BX408347 BX408347 BX408347
c	841	7	23.3	919	5	BU541279 BU541279 AGENCOURT
	842	7	23.3	920	5	BX764749 BX764749 BX764749
c	843	7	23.3	921	2	BG766114 BG766114 602738303
	844	7	23.3	922	10	CG108588 CG108588 PUIIE09TD
c	845	7	23.3	923	7	CK278844 CK278844 EST724922
	846	7	23.3	925	5	BU916353 BU916353 AGENCOURT
c	847	7	23.3	925	9	CC405076 CC405076 PUHSQ61TB
	848	7	23.3	926	5	BX374351 BX374351 BX374351
c	849	7	23.3	926	6	CF511872 CF511872 CAbud0004
	850	7	23.3	927	6	CD360901 CD360901 AGENCOURT
c	851	7	23.3	929	5	BX354155 BX354155 BX354155
c	852	7	23.3	930	5	BQ670797 BQ670797 AGENCOURT
	853	7	23.3	931	5	BX354154 BX354154 BX354154
c	854	7	23.3	933	10	CG111346 CG111346 PUFLB55TB
c	855	7	23.3	934	5	BQ924706 BQ924706 AGENCOURT
c	856	7	23.3	940	5	BQ943465 BQ943465 AGENCOURT
	857	7	23.3	946	5	BX442866 BX442866 BX442866
c	858	7	23.3	946	5	BX461044 BX461044 BX461044
	859	7	23.3	948	9	CC430500 CC430500 PUHBQ53TD
c	860	7	23.3	950	5	BQ884346 BQ884346 AGENCOURT
	861	7	23.3	953	5	BX449994 BX449994 BX449994
c	862	7	23.3	955	2	BI220623 BI220623 602938719
c	863	7	23.3	955	10	CG077981 CG077981 PUJFR40TB
	864	7	23.3	957	5	BX432909 BX432909 BX432909
	865	7	23.3	966	10	CG143922 CG143922 PUFNT79TB
	866	7	23.3	966	10	CL868162 CL868162 Gma_02_B2
c	867	7	23.3	967	5	BX449985 BX449985 BX449985
	868	7	23.3	968	5	BX353029 BX353029 BX353029
c	869	7	23.3	969	5	BQ943681 BQ943681 AGENCOURT
	870	7	23.3	969	10	CG111348 CG111348 PUFLB55TD
c	871	7	23.3	971	5	BQ717761 BQ717761 AGENCOURT
	872	7	23.3	972	5	BX418082 BX418082 BX418082
c	873	7	23.3	973	3	BQ217664 BQ217664 AGENCOURT
c	874	7	23.3	975	2	BG026841 BG026841 602294111
c	875	7	23.3	975	2	BE795188 BE795188 601592444
	876	7	23.3	976	5	BX420909 BX420909 BX420909
	877	7	23.3	978	5	BX450119 BX450119 BX450119
c	878	7	23.3	978	10	CZ949796 CZ949796 263187 To
c	879	7	23.3	980	10	CZ965360 CZ965360 168611 To
c	880	7	23.3	987	5	BX449971 BX449971 BX449971
	881	7	23.3	989	10	CG168310 CG168310 PUKCR31TB
	882	7	23.3	991	6	CD513514 CD513514 AGENCOURT
	883	7	23.3	1005	5	BX340658 BX340658 BX340658
c	884	7	23.3	1012	5	BX425353 BX425353 BX425353
	885	7	23.3	1016	2	BF966696 BF966696 602286851
c	886	7	23.3	1021	5	BX422944 BX422944 BX422944
c	887	7	23.3	1023	5	BX331847 BX331847 BX331847
	888	7	23.3	1024	5	BX428956 BX428956 BX428956
c	889	7	23.3	1030	3	BM910805 BM910805 AGENCOURT
	890	7	23.3	1030	9	CC305174 CC305174 CH261-189
c	891	7	23.3	1038	5	BX418084 BX418084 BX418084
c	892	7	23.3	1042	5	BX449219 BX449219 BX449219
c	893	7	23.3	1049	3	BM552282 BM552282 AGENCOURT
	894	7	23.3	1050	5	BX442560 BX442560 BX442560
c	895	7	23.3	1052	3	BM451759 BM451759 AGENCOURT
	896	7	23.3	1057	1	AL527978 AL527978 AL527978
c	897	7	23.3	1059	3	BQ070054 BQ070054 AGENCOURT
c	898	7	23.3	1060	2	BF141893 BF141893 601791376
	899	7	23.3	1062	5	BX331846 BX331846 BX331846
	900	7	23.3	1076	2	BG775909 BG775909 602650315
c	901	7	23.3	1084	4	CR592666 CR592666 full-leng
c	902	7	23.3	1086	5	BX444524 BX444524 BX444524
c	903	7	23.3	1089	5	BX419119 BX419119 BX419119
	904	7	23.3	1096	10	CL240135 CL240135 ZMMBBb058
	905	7	23.3	1102	5	BX442343 BX442343 BX442343
c	906	7	23.3	1107	5	BX442344 BX442344 BX442344
	907	7	23.3	1125	6	CF223020 CF223020 AGENCOURT
c	908	7	23.3	1129	3	BI763101 BI763101 603050013
	909	7	23.3	1135	8	DR736242 DR736242 FGAS02242
c	910	7	23.3	1143	8	DN733527 DN733527 CNB70-E08
c	911	7	23.3	1145	2	BE795029 BE795029 601592819
c	912	7	23.3	1146	4	CR609423 CR609423 full-leng
c	913	7	23.3	1147	2	BF205980 BF205980 601869423
c	914	7	23.3	1150	9	CC295548 CC295548 CH261-64F
c	915	7	23.3	1153	2	BG112976 BG112976 602283606
c	916	7	23.3	1167	9	BZ692366 BZ692366 SP__Ba001
	917	7	23.3	1186	8	DR121831 DR121831 49350200
c	918	7	23.3	1231	3	BM922084 BM922084 AGENCOURT
c	919	7	23.3	1239	4	CR617409 CR617409 full-leng
c	920	7	23.3	1314	4	CR618760 CR618760 full-leng
c	921	7	23.3	1325	5	BQ923354 BQ923354 AGENCOURT
c	922	7	23.3	1342	4	CR604078 CR604078 full-leng
	923	7	23.3	1347	8	DN696113 DN696113 CLJ05-A01
c	924	7	23.3	1348	4	CR618535 CR618535 full-leng
c	925	7	23.3	1350	4	CR599533 CR599533 full-leng
	926	7	23.3	1358	10	AG429865 AG429865 Mus muscu
c	927	7	23.3	1374	4	CR625533 CR625533 full-leng
c	928	7	23.3	1376	4	CR602935 CR602935 full-leng
c	929	7	23.3	1376	4	CR604715 CR604715 full-leng
c	930	7	23.3	1376	4	CR614656 CR614656 full-leng
c	931	7	23.3	1385	4	CR595016 CR595016 full-leng
c	932	7	23.3	1387	4	CR602332 CR602332 full-leng
c	933	7	23.3	1390	4	CR614187 CR614187 full-leng
c	934	7	23.3	1391	4	CR618341 CR618341 full-leng
c	935	7	23.3	1395	4	CR604286 CR604286 full-leng
c	936	7	23.3	1404	4	CR593337 CR593337 full-leng
c	937	7	23.3	1404	4	CR620989 CR620989 full-leng
	938	7	23.3	2007	10	CL964658 CL964658 OsIFCC038
	939	7	23.3	2047	4	AY814882 AY814882 Schistoso
c	940	7	23.3	2438	4	AK053940 AK053940 Mus muscu
	941	7	23.3	4000	4	AK032482 AK032482 Mus muscu
	942	6	20.0	66	9	CC199739 CC199739 XH307 Bay
c	943	6	20.0	67	9	BH810661 BH810661 SALK_0510
c	944	6	20.0	68	7	CN873833 CN873833 001207AAR
c	945	6	20.0	69	3	BP028932 BP028932 BP028932
c	946	6	20.0	69	9	BZ763023 BZ763023 SALK_1117
	947	6	20.0	87	9	AZ311298 AZ311298 1M0026I12
	948	6	20.0	97	8	W62306 W62306 md96h04.r1
	949	6	20.0	101	2	BE755157 BE755157 208904 MA
	950	6	20.0	101	10	CZ294364 CZ294364 P066D10 G
	951	6	20.0	105	8	CX290859 CX290859 C02027H11
	952	6	20.0	106	10	CG594150 CG594150 OST251972
c	953	6	20.0	107	9	BH463965 BH463965 BOGOC36TF
	954	6	20.0	108	1	AI925590 AI925590 wo34a03.x
	955	6	20.0	108	3	BP739707 BP739707 BP739707
c	956	6	20.0	109	3	BM056100 BM056100 952008F09

c 957	6	20.0	109	8	DR038269	DR038269 BNE000001
958	6	20.0	110	2	BG010433	BG010433 MR1-GN017
959	6	20.0	110	2	BE089398	BE089398 QV0-BT070
960	6	20.0	112	9	BH074942	BH074942 RPCI-24-3
c 961	6	20.0	112	9	BH723841	BH723841 BOHVM91TR
c 962	6	20.0	113	10	CG265790	CG265790 OGVCO01TH
c 963	6	20.0	116	1	AF110071	AF110071 AF110071
964	6	20.0	116	2	BE425589	BE425589 WHE0320_F
c 965	6	20.0	116	4	CNS09O1K	BX067236 Single re
c 966	6	20.0	116	10	CZ273157	CZ273157 ZMMBF0053
c 967	6	20.0	116	10	AG397683	AG397683 Mus muscu
c 968	6	20.0	117	2	BF809304	BF809304 QV0-CI019
c 969	6	20.0	121	1	AW541978	AW541978 C0153C07-
970	6	20.0	121	2	BE814684	BE814684 PM1-BN008
c 971	6	20.0	121	3	BP561413	BP561413 BP561413
c 972	6	20.0	124	7	CN076674	CN076674 EC2BBA12B
c 973	6	20.0	124	7	CN079105	CN079105 EC2BBA16A
c 974	6	20.0	124	9	BH199916	BH199916 Sm1-48G5.
c 975	6	20.0	126	6	CA813485	CA813485 CA48LN10I
c 976	6	20.0	128	2	BG458969	BG458969 947052A12
977	6	20.0	130	1	AI749258	AI749258 at41d08.x
c 978	6	20.0	132	3	BP707441	BP707441 BP707441
979	6	20.0	132	5	BX779154	BX779154 BX779154
980	6	20.0	132	7	CF965400	CF965400 10495rsic
c 981	6	20.0	132	9	BH810662	BH810662 SALK_0510
982	6	20.0	134	1	AA172677	AA172677 ms56g08.r
c 983	6	20.0	136	2	BG234593	BG234593 dab67f02.
984	6	20.0	136	9	BH336980	BH336980 CH230-154
985	6	20.0	139	2	BF806001	BF806001 MR1-CI018
986	6	20.0	140	11	CR805319	CR805319 GR0AAA26D
987	6	20.0	141	10	CW039728	CW039728 104_272_1
988	6	20.0	143	2	BG409252	BG409252 gb88g04.y
989	6	20.0	143	10	AG248627	AG248627 Lotus cor
c 990	6	20.0	144	1	AA196658	AA196658 zq08c01.r
c 991	6	20.0	144	2	BG433527	BG433527 602497826
992	6	20.0	144	10	BX948564	BX948564 Arabidops
993	6	20.0	145	2	BF878274	BF878274 CM2-ET012
c 994	6	20.0	145	9	AQ112896	AQ112896 CIT-HSP-2
c 995	6	20.0	147	1	AJ717035	AJ717035 AJ717035
996	6	20.0	147	5	BW337108	BW337108 BW337108
997	6	20.0	148	1	AA860434	AA860434 aj80c10.s
c 998	6	20.0	149	1	AA095578	AA095578 l5021.seq
c 999	6	20.0	149	6	CF582493	CF582493 AGENCOURT
c1000	6	20.0	152	2	BF245134	BF245134 601863976

ALIGNMENTS

RESULT 1
BX849231/c
LOCUS BX849231 720 bp mRNA linear EST 11-DEC-2003
DEFINITION BX849231 NICHD_XGC_O01 Xenopus laevis cDNA clone IMAGp998M0614215 ; IMAGE:6637806 5', mRNA sequence.
ACCESSION BX849231
VERSION BX849231.1 GI:39738015
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 720)
AUTHORS Heil,O., Neubert,P., Peters,M., Radelof,U., Schneider,D., Schroth,A., Korn,B. and Landgrebe,J.
TITLE Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998M0614215.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB No.998) http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer: SP6, 5' ATTTAGGTGACACTATAG 3'.
FEATURES Location/Qualifiers
source 1. .720
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGp998M0614215 ; IMAGE:6637806"
/tissue_type="oocytes"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_O01"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Life Technologies."
ORIGIN

Alignment Scores:

Pred. No.:	17.2	Length:	720
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	30.0%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-1 (1-30) x BX849231 (1-720)

```
Qy         18 IleGlnAspLeuArgAsnGluLeuAla 26
              |||||||||||||||||||||||||||
Db        199 ATTCAGGATTTGAGAAATGAGTTGGCA 173
```

RESULT 2
BU911748/c
LOCUS BU911748 909 bp mRNA linear EST 17-OCT-2002
DEFINITION AGENCOURT_10463950 NICHD_XGC_O01 Xenopus laevis cDNA clone IMAGE:6637806 5', mRNA sequence.
ACCESSION BU911748
VERSION BU911748.1 GI:24093662
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 909)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14215 row: m column: 06
High quality sequence start: 35
High quality sequence stop: 669.
FEATURES Location/Qualifiers
source 1. .909
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"

/clone="IMAGE:6637806"
/tissue_type="oocytes"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_OO1"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	21.5	Length:	909
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	30.0%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-1 (1-30) x BU911748 (1-909)

```
Qy         18 IleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||||||||||
Db        213 ATTCAGGATTTGAGAAATGAGTTGGCA 187
```

RESULT 3
AA328059
LOCUS AA328059 225 bp mRNA linear EST 20-APR-1997
DEFINITION EST31482 Embryo, 12 week I Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA328059
VERSION AA328059.1 GI:1980303
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 225)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
PUBMED 7566098
COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .225
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):129689"
/db_xref="taxon:9606"
/dev_stage="embryo, 12 wks"
/clone_lib="Embryo, 12 week I"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	65.9	Length:	225
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	1	Gaps:	0

US-10-758-902-1 (1-30) x AA328059 (1-225)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        170 ACAGTGTCATTTAATTTGGGAGAG 193
```

RESULT 4
BF352328/c
LOCUS BF352328 246 bp mRNA linear EST 22-NOV-2000
DEFINITION RC6-HT0594-180500-011-G06 HT0594 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF352328
VERSION BF352328.1 GI:11311402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC6&t2=RC6-HT0594-
180500-011-G06&t3=2000-05-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 246.
FEATURES Location/Qualifiers
source 1. .246
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0594"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```
ORIGIN

Alignment Scores:
Pred. No.:              71.8          Length:         246
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
DB:                     2             Gaps:           0

US-10-758-902-1 (1-30) x BF352328 (1-246)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db         69 ACAGTGTCATTTAATTTGGGAGAG 46

RESULT 5
AW887063
LOCUS       AW887063                264 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  RC1-OT0086-130400-022-h06 OT0086 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW887063
VERSION     AW887063.1  GI:8049076
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 264)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC1-OT0086-130
            400-022-h06&t3=2000-04-13&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 264.
FEATURES             Location/Qualifiers
     source          1. .264
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="OT0086"
                     /note="Organ: ovary; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No.
                     196,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              76.9          Length:         264
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
DB:                     1             Gaps:           0

US-10-758-902-1 (1-30) x AW887063 (1-264)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        178 ACAGTGTCATTTAATTTGGGAGAG 201

RESULT 6
BY550514
LOCUS       BY550514                415 bp    mRNA    linear   EST 14-DEC-2002
DEFINITION  BY550514 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730214I08 3', mRNA sequence.
ACCESSION   BY550514
VERSION     BY550514.1  GI:26884893
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
```

genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .415
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F730214I08"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells"

ORIGIN

Alignment Scores:

Pred. No.:	119	Length:	415
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-1 (1-30) x BY550514 (1-415)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        131 ACTGTATCTTTTAATTTAGGGGAA 154
```

RESULT 7
DN507933
LOCUS DN507933 420 bp mRNA linear EST 10-MAR-2005
DEFINITION HL020003000_PLATE_H06_48_048 Equine placenta cDNA Library Equus caballus cDNA clone HL020003000_PLATE_H06_48_048, mRNA sequence.
ACCESSION DN507933
VERSION DN507933.1 GI:60718123
KEYWORDS EST.
SOURCE Equus caballus (horse)
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 420)
AUTHORS Antczak,D.F.
TITLE Expressed sequence tags from a normalized equine placenta library
JOURNAL Unpublished (2005)
COMMENT Contact: Antczak DF
Baker Institute for Animal Health, College of Veterinary Medicine Cornell University
Hungerford Hill Rd., Ithaca, NY 14853, USA
Tel: 607.256.5633
Fax: 607.256.5608
Email: dfa1@cornell.edu
High quality sequence stop: 420.

FEATURES Location/Qualifiers
source 1. .420
/organism="Equus caballus"
/mol_type="mRNA"
/strain="Thoroughbred, Standardbred, & Pony breeds"
/db_xref="taxon:9796"
/clone="HL020003000_PLATE_H06_48_048"
/tissue_type="Invasive [Chorionic Girdle (Tag-(polyA)TGCGT)] and Non-invasive [Allantochorion (Tag-(polyA)TCGGT)] trophoblast"
/dev_stage="Pooled day 34 equine conceptuses"
/lab_host="DH12S E. coli cells (Invitrogen)"
/clone_lib="Equine placenta cDNA Library"
/note="Vector: pGEM11Zf(+) (Promega); Site_1: EcoR1; Site_2: Not1"

ORIGIN

Alignment Scores:

Pred. No.:	120	Length:	420
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x DN507933 (1-420)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        143 ACAGTGTCATTTAATTTGGGAGAG 166
```

RESULT 8
BF451736/c
LOCUS BF451736 445 bp mRNA linear EST 29-DEC-2000
DEFINITION uz78f04.y1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3675199 5', mRNA sequence.
ACCESSION BF451736
VERSION BF451736.1 GI:11517905
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 445)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other_ESTs: uz78f04.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml

MGI:1435967
Seq primer: -40RP from Gibco
High quality sequence stop: 444.

FEATURES Location/Qualifiers
source 1. .445
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:3675199"
/tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

```
ORIGIN

Alignment Scores:
Pred. No.:              127             Length:         445
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-1 (1-30) x BF451736 (1-445)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        145 ACTGTATCTTTTAATTTAGGGGAA 122

RESULT 9
BF807534
LOCUS       BF807534                452 bp    mRNA    linear   EST 12-JAN-2001
DEFINITION  RC2-CI0090-111100-015-a08 CI0090 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF807534
VERSION     BF807534.1  GI:12136523
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC2&t2=RC2-CI0090-
            111100-015-a08&t3=2000-11-11&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 5
            High quality sequence stop: 452.
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="CI0090"
                     /note="Organ: colon_ins; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              129             Length:         452
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-1 (1-30) x BF807534 (1-452)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        380 ACAGTGTCATTTAATTTGGGAGAG 403

RESULT 10
AJ653060
LOCUS       AJ653060                454 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  AJ653060 KN277 Sus scrofa cDNA clone C0005182_N21, mRNA sequence.
ACCESSION   AJ653060
VERSION     AJ653060.1  GI:49335506
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
            R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
            from pooled early embryos, from 8- cell stage to blastocysts.
            Clones available from UK Centre for Functional Genomics in Farm
            Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS,
            www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="C0005182_N21"
                     /tissue_type="embryo"
                     /clone_lib="KN277"
                     /note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from pooled early embryos, from 8-cell stage
                     to blastocysts."
ORIGIN

Alignment Scores:
Pred. No.:              130             Length:         454
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     1               Gaps:           0

US-10-758-902-1 (1-30) x AJ653060 (1-454)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        270 ACAGTGTCATTTAATTTGGGAGAG 293

RESULT 11
AW748411
LOCUS       AW748411                501 bp    mRNA    linear   EST 28-APR-2000
DEFINITION  RC4-BT0256-151099-031-e12 BT0256 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW748411
```

```
VERSION     AW748411.1  GI:7663343
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC4&t2=RC4-BT0256-
            151099-031-e12&t3=1999-10-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 14
            High quality sequence stop: 501.
FEATURES             Location/Qualifiers
     source          1. .501
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="BT0256"
                     /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No.
                     196,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                143             Length:         501
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.7%           Indels:         0
DB:                       1               Gaps:           0

US-10-758-902-1 (1-30) x AW748411 (1-501)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db         80 ACAGTGTCATTTAATTTGGGAGAG 103

RESULT 12
CC383551/c
LOCUS       CC383551                506 bp    DNA     linear   GSS 19-MAY-2003
DEFINITION  PUHHN58TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa452J20,
            genomic survey sequence.
ACCESSION   CC383551
VERSION     CC383551.1  GI:30862752
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUHHN58TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa452J20"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

Alignment Scores:
Pred. No.:                144             Length:         506
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.7%           Indels:         0
DB:                       9               Gaps:           0

US-10-758-902-1 (1-30) x CC383551 (1-506)

Qy         19 GlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||||||
Db         49 CAAGACCTTAGAAATGAGTTAGCA 26

RESULT 13
BG037734
LOCUS       BG037734                517 bp    mRNA    linear   EST 24-JAN-2001
DEFINITION  dc67d08.y1 NICHD_XGC_Emb1 Xenopus laevis cDNA clone IMAGE:3402278
            5', mRNA sequence.
ACCESSION   BG037734
VERSION     BG037734.1  GI:12480319
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: Xenopus clones from this library are available
            through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
            Seq primer: -40RP from Gibco
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
```

```
     source          1. .517
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:3402278"
                     /tissue_type="embryo (stage 10)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Emb1"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 1.55 kb. Constructed by Life Technologies. Note: This
                     is a Xenopus Gene Collection (XGC) library."
ORIGIN

Alignment Scores:
Pred. No.:              147           Length:         517
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
DB:                     2             Gaps:           0

US-10-758-902-1 (1-30) x BG037734 (1-517)

Qy         22 ArgAsnGluLeuAlaLysGlyThr 29
              |||||||||||||||||||||||
Db        327 CGAAATGAACTGGCAAAAGGAACC 350

RESULT 14
AI035950/c
LOCUS       AI035950                520 bp    mRNA    linear   EST 26-JUN-1998
DEFINITION  ub50a10.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
            IMAGE:1381146 5', mRNA sequence.
ACCESSION   AI035950
VERSION     AI035950.1  GI:3259641
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 520)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:903614
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .520
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1381146"
                     /sex="male"
                     /tissue_type="mammary gland"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_mammary_gland_NbMMG"
                     /note="Organ: mammary gland; Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
ORIGIN

Alignment Scores:
Pred. No.:              148           Length:         520
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
DB:                     1             Gaps:           0

US-10-758-902-1 (1-30) x AI035950 (1-520)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        161 ACTGTATCTTTTAATTTAGGGGAA 138

RESULT 15
CZ658046/c
LOCUS       CZ658046                567 bp    DNA     linear   GSS 07-JUL-2005
DEFINITION  OM__Ba0209D02.r OM__Ba Oryza minuta genomic clone OM__Ba0209D02 3',
            genomic survey sequence.
ACCESSION   CZ658046
VERSION     CZ658046.1  GI:70227225
KEYWORDS    GSS.
SOURCE      Oryza minuta
  ORGANISM  Oryza minuta
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 567)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            Plate: 0209  row: D  column: 02
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .567
                     /organism="Oryza minuta"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:63629"
                     /clone="OM__Ba0209D02"
                     /tissue_type="leaves"
                     /lab_host="DH10B"
                     /clone_lib="OM__Ba"
                     /note="Vector: pCUGIBAC1; Site_1: HindIII; Site_2:
                     HindIII"
ORIGIN

Alignment Scores:
Pred. No.:              161           Length:         567
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
```

```
DB:                    10            Gaps:          0

US-10-758-902-1 (1-30) x CZ658046 (1-567)

Qy         15 ProThrPheIleGlnAspLeuArg 22
              ||||||||||||||||||||||||
Db        532 CCCACGTTCATTCAGGACCTGCGT 509

RESULT 16
CN775134
LOCUS       CN775134                582 bp    mRNA    linear   EST 20-MAY-2004
DEFINITION  tae69h10.y1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 5'
            similar to TR:Q9VB28 Q9VB28 CG13972 PROTEIN. ;, mRNA sequence.
ACCESSION   CN775134
VERSION     CN775134.1  GI:47545768
KEYWORDS    EST.
SOURCE      Hydra magnipapillata
  ORGANISM  Hydra magnipapillata
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
            Hydridae; Hydra.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
            Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,
            Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
            Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,
            Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
  TITLE     WashU Hydra EST Project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hans Bode
            WashU Hydra EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library was constructed by Corina Guder / GATC Konstanz, Germany
            Library materials provided by Thomas Holstein / Molecular Cell
            Biology, TUD, Darmstadt DNA sequencing by: Washington University
            Genome Sequencing Center For information on obtaining a clone
            please contact: Hans Bode (hrbode@uci.edu)
            Seq primer: -40UP
            High quality sequence stop: 582.
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Hydra magnipapillata"
                     /mol_type="mRNA"
                     /strain="sf-1 mutant of Hydra magnipapillata"
                     /db_xref="taxon:6085"
                     /lab_host="TransforMax EC100 (Epicentre), T1 Phage
                     resistant electrocompetent cells"
                     /clone_lib="Hydra EST Darmstadt I"
                     /note="Vector: pBluescript II SK (+); Site_1: NotI;
                     Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              165           Length:        582
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     7             Gaps:          0

US-10-758-902-1 (1-30) x CN775134 (1-582)

Qy         19 GlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||||||
Db        163 CAAGATCTAAGAAATGAATTGGCA 186

RESULT 17
BE131785
LOCUS       BE131785                585 bp    mRNA    linear   EST 29-JUN-2000
DEFINITION  db38b02.y1 Blackshear/Soares normalized Xenopus egg library Xenopus
            laevis cDNA clone IMAGE:3300747 5', mRNA sequence.
ACCESSION   BE131785
VERSION     BE131785.1  GI:8579148
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
            Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
            Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Xenopus EST project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Sandy Clifton, Ph.D.
            WashU Xenopus EST project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library constructed by Bento Soares and M. Fatima Bonaldo
            (University of Iowa). DNA Sequencing by: Washington University
            Genome Sequencing Center
             Clone distribution: Xenopus clones from this library are available
            through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
            Seq primer: -40RP from Gibco
            High quality sequence stop: 473.
FEATURES             Location/Qualifiers
     source          1. .585
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:3300747"
                     /sex="female"
                     /tissue_type="unfertilized egg"
                     /cell_type="unfertilized egg"
                     /dev_stage="unfertilized egg"
                     /lab_host="DH10B"
                     /clone_lib="Blackshear/Soares normalized Xenopus egg
                     library"
                     /note="Vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
                     PolyA-selected mRNA was prepared from unfertilized Xenopus
                     laevis eggs.  The library was constructed in the vector
                     pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
                     Soares, M.B. 'Normalization and subtraction:  two
                     approaches to facilitate gene discovery',  Genome Research
                     6:791-806, 1996.  The first strand synthesis used a
                     NotI-dT18 primer; double stranded cDNAs were ligated to
                     EcoRI adapters, digested with NotI, and directionally
                     cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
                     The library contained approximately 7.2 X 10^5
                     recombinants, with average insert sizes of 1-1.5 kb."
ORIGIN

Alignment Scores:
Pred. No.:              166           Length:        585
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x BE131785 (1-585)

Qy         22 ArgAsnGluLeuAlaLysGlyThr 29
              |||||||||||||||||||||||
Db        121 CGAAATGAACTGGCAAAAGGAACC 144

RESULT 18
CN773487
```

```
LOCUS       CN773487               601 bp    mRNA    linear   EST 20-MAY-2004
DEFINITION  tae61d03.y1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 5',
            mRNA sequence.
ACCESSION   CN773487
VERSION     CN773487.1  GI:47544121
KEYWORDS    EST.
SOURCE      Hydra magnipapillata
  ORGANISM  Hydra magnipapillata
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
            Hydridae; Hydra.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
            Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,
            Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
            Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,
            Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
  TITLE     WashU Hydra EST Project
  JOURNAL   Unpublished (2002)
COMMENT     Other_ESTs: tae61d03.x1
            Contact: Hans Bode
            WashU Hydra EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library was constructed by Corina Guder / GATC Konstanz, Germany
            Library materials provided by Thomas Holstein / Molecular Cell
            Biology, TUD, Darmstadt DNA sequencing by: Washington University
            Genome Sequencing Center For information on obtaining a clone
            please contact: Hans Bode (hrbode@uci.edu)
            Seq primer: -40UP.
FEATURES             Location/Qualifiers
     source          1. .601
                     /organism="Hydra magnipapillata"
                     /mol_type="mRNA"
                     /strain="sf-1 mutant of Hydra magnipapillata"
                     /db_xref="taxon:6085"
                     /lab_host="TransforMax EC100 (Epicentre), T1 Phage
                     resistant electrocompetent cells"
                     /clone_lib="Hydra EST Darmstadt I"
                     /note="Vector: pBluescript II SK (+); Site_1: NotI;
                     Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              170             Length:         601
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-1 (1-30) x CN773487 (1-601)

Qy         19 GlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||||||||
Db        552 CAAGATCTTAGAAATGAATTGGCA 575

RESULT 19
BX668613
LOCUS       BX668613               603 bp    mRNA    linear   EST 07-MAY-2004
DEFINITION  BX668613 Sus Scrofa library (scac) Sus scrofa cDNA clone
            scac0031i.l.02 5prim, mRNA sequence.
ACCESSION   BX668613
VERSION     BX668613.1  GI:37977340
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 603)
  AUTHORS   Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S.,
            Soares,M., Bonaldo,F. and Hatey,F.
  TITLE     A Pig Normalised Multi-Tissue cDNA Library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tosser-Klopp G
            Genetique Animale
            Institut National de la Recherche Agronomique
            Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
            cedex, FRANCE
            Tel: 33 (0) 5.61.28.51.14
            Fax: 33 (0) 5.61.28.53.08
            Email: tosser@toulouse.inra.fr
            Sequence cleaned of vector, adaptator and repetitions. Contact us
            at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0031  row: l  column: 2.
FEATURES             Location/Qualifiers
     source          1. .603
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="scac0031i.l.02"
                     /tissue_type="mixed"
                     /clone_lib="Sus Scrofa library (scac)"
                     /note="Vector: pT7T3D-pac vector; tissues: adipose tissue,
                     brain, kidney, liver, muscle, ovary, testis,  heart,
                     hypothalamus, pancreas, skin, spleen, thymus, placenta,
                     pituitary  gland, seminal vesicle, small intestine,
                     uterus, adrenals, bulbo uretral  gland, cerebral trunk,
                     epididymis, female gonad, gall-bladder,  hippocampus,
                     large intestine, male gonad, melanocytes, stomach, udder"
ORIGIN

Alignment Scores:
Pred. No.:              170             Length:         603
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     5               Gaps:           0

US-10-758-902-1 (1-30) x BX668613 (1-603)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db          6 ACAGTGTCATTTAATTTGGGAGAG 29

RESULT 20
BG924897
LOCUS       BG924897               612 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC38-1-E10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BG924897
VERSION     BG924897.1  GI:14319420
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 612)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
   PUBMED   11597177
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
```

```
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES              Location/Qualifiers
     source           1. .612
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="cartilage"
                      /lab_host="E.coli DH10 B"
                      /clone_lib="HNC (Human Normal Cartilage)"
                      /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                      Directional"
ORIGIN

Alignment Scores:
Pred. No.:              173           Length:         612
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
DB:                     2             Gaps:           0

US-10-758-902-1 (1-30) x BG924897 (1-612)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db        459 ACAGTGTCATTTAATTTGGGAGAG 482

RESULT 21
CD354962/c
LOCUS       CD354962                617 bp    mRNA    linear   EST 15-JUL-2003
DEFINITION  UI-M-GM0-cge-b-14-0-UI.r1 NIH_BMAP_GM0 Mus musculus cDNA clone
            IMAGE:30361477 5', mRNA sequence.
ACCESSION   CD354962
VERSION     CD354962.1  GI:31147463
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES              Location/Qualifiers
     source           1. .617
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:30361477"
                      /tissue_type="whole brain"
                      /dev_stage="1, 5 and 15 days newborn"
                      /lab_host="DH10B (T1 phage resistant)"
                      /clone_lib="NIH_BMAP_GM0"
                      /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                      Site_2: Not I; The library was constructed according
                      Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                      1996. Denatured RNA was size fractionated on a 1% agarose
                      gel.First strand cDNA synthesis was primed with oligo-dT
                      primer containing a Not I site.Double strand cDNA was size
                      selected according to mRNA size fraction,ligated with EcoR
                      I adaptor, digested with NotI and then cloned
                      directionally into pYX-Asc vector. The library tag
                      sequence located between the Not I site and the polyA tail
                      is CGAACTGAAT. This library was created for the University
                      Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                      Developing Mouse Nervous System', supported by National
                      Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                      program coordinator."
ORIGIN

Alignment Scores:
Pred. No.:              174           Length:         617
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            26.7%         Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-1 (1-30) x CD354962 (1-617)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db        308 ACTGTATCTTTAATTTAGGGGAA 285

RESULT 22
CZ874300
LOCUS       CZ874300                623 bp    DNA     linear   GSS 27-JUL-2005
DEFINITION  OC__Ba0273P13.r OC__Ba Oryza coarctata genomic clone OC__Ba0273P13
            3', genomic survey sequence.
ACCESSION   CZ874300
VERSION     CZ874300.1  GI:71350056
KEYWORDS    GSS.
SOURCE      Oryza coarctata (Porteresia coarctata)
  ORGANISM  Oryza coarctata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 623)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0273  row: P  column: 13
            Seq primer: CAC TCA TTA GGC ACC CCA
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .623
                      /organism="Oryza coarctata"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:77588"
                      /clone="OC__Ba0273P13"
                      /tissue_type="leaves"
                      /dev_stage="mature"
                      /lab_host="DH10B"
                      /clone_lib="OC__Ba"
                      /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Alignment Scores:
```

```
Pred. No.:              176             Length:         623
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-1 (1-30) x CZ874300 (1-623)

Qy         20 AspLeuArgAsnGluLeuAlaLys 27
              ||||||||||||||||||||||||||
Db        416 GATCTGAGAAATGAATTGGCTAAA 439

RESULT 23
CN770424/c
LOCUS       CN770424                626 bp    mRNA    linear   EST 20-MAY-2004
DEFINITION  tae69h10.x1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 3'
            similar to TR:Q9VB28 Q9VB28 CG13972 PROTEIN. ;, mRNA sequence.
ACCESSION   CN770424
VERSION     CN770424.1  GI:47541058
KEYWORDS    EST.
SOURCE      Hydra magnipapillata
  ORGANISM  Hydra magnipapillata
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
            Hydridae; Hydra.
REFERENCE   1  (bases 1 to 626)
  AUTHORS   Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
            Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,
            Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
            Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,
            Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
  TITLE     WashU Hydra EST Project
  JOURNAL   Unpublished (2002)
COMMENT     Other_ESTs: tae69h10.y1
            Contact: Hans Bode
            WashU Hydra EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library was constructed by Corina Guder / GATC Konstanz, Germany
            Library materials provided by Thomas Holstein / Molecular Cell
            Biology, TUD, Darmstadt DNA sequencing by: Washington University
            Genome Sequencing Center For information on obtaining a clone
            please contact: Hans Bode (hrbode@uci.edu)
            Putative full length read
            vector to vector length is
            Seq primer: degenerate primer.
FEATURES             Location/Qualifiers
     source          1. .626
                     /organism="Hydra magnipapillata"
                     /mol_type="mRNA"
                     /strain="sf-1 mutant of Hydra magnipapillata"
                     /db_xref="taxon:6085"
                     /lab_host="TransforMax EC100 (Epicentre), T1 Phage
                     resistant electrocompetent cells"
                     /clone_lib="Hydra EST Darmstadt I"
                     /note="Vector: pBluescript II SK (+); Site_1: NotI;
                     Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              177             Length:         626
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-1 (1-30) x CN770424 (1-626)

Qy         19 GlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||||||||
Db        463 CAAGATCTAAGAAATGAATTGGCA 440

RESULT 24
CN768873/c
LOCUS       CN768873                628 bp    mRNA    linear   EST 20-MAY-2004
DEFINITION  taf20d12.x1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 3'
            similar to TR:Q9VB28 Q9VB28 CG13972 PROTEIN. ;, mRNA sequence.
ACCESSION   CN768873
VERSION     CN768873.1  GI:47539507
KEYWORDS    EST.
SOURCE      Hydra magnipapillata
  ORGANISM  Hydra magnipapillata
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
            Hydridae; Hydra.
REFERENCE   1  (bases 1 to 628)
  AUTHORS   Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
            Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,
            Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
            Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,
            Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
  TITLE     WashU Hydra EST Project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hans Bode
            WashU Hydra EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library was constructed by Corina Guder / GATC Konstanz, Germany
            Library materials provided by Thomas Holstein / Molecular Cell
            Biology, TUD, Darmstadt DNA sequencing by: Washington University
            Genome Sequencing Center For information on obtaining a clone
            please contact: Hans Bode (hrbode@uci.edu)
            Putative full length read
            vector to vector length is
            Seq primer: degenerate primer.
FEATURES             Location/Qualifiers
     source          1. .628
                     /organism="Hydra magnipapillata"
                     /mol_type="mRNA"
                     /strain="sf-1 mutant of Hydra magnipapillata"
                     /db_xref="taxon:6085"
                     /lab_host="TransforMax EC100 (Epicentre), T1 Phage
                     resistant electrocompetent cells"
                     /clone_lib="Hydra EST Darmstadt I"
                     /note="Vector: pBluescript II SK (+); Site_1: NotI;
                     Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              177             Length:         628
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-1 (1-30) x CN768873 (1-628)

Qy         19 GlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||||||||
Db        465 CAAGATCTTAGAAATGAATTGGCA 442

RESULT 25
DN373796
LOCUS       DN373796                630 bp    mRNA    linear   EST 07-MAR-2005
DEFINITION  LIB38527_001_E07_T7_1 LIB38527 Canis familiaris cDNA clone
            LIB38527_001_E07, mRNA sequence.
ACCESSION   DN373796
VERSION     DN373796.1  GI:60555016
KEYWORDS    EST.
```

```
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 630)
  AUTHORS   Staten,N.R.
  TITLE     Direct Submission (Staten,N.R.)
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Nick Staten
            Tel: 636 247 6855
            Email: nicholas.r.staten@pfizer.com.
FEATURES             Location/Qualifiers
     source          1. .630
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /clone="LIB38527_001_E07"
                     /tissue_type="kidney"
                     /lab_host="DH10B"
                     /clone_lib="LIB38527"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI"
ORIGIN

Alignment Scores:
Pred. No.:                178             Length:         630
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.7%           Indels:         0
DB:                       8               Gaps:           0

US-10-758-902-1 (1-30) x DN373796 (1-630)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db        397 ACAGTGTCATTTAATTTGGGAGAG 420

RESULT 26
CB844714/c
LOCUS       CB844714                642 bp    mRNA    linear   EST 01-SEP-2003
DEFINITION  M2PN-0266 MOUSE POST-NATAL DAY 2 EYE Mus musculus cDNA 5', mRNA
            sequence.
ACCESSION   CB844714
VERSION     CB844714.1  GI:34375666
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   Yu,J., Farjo,R., MacNee,S.P., Baehr,W., Stambolian,D.E. and
            Swaroop,A.
  TITLE     Annotation and analysis of 10,000 expressed sequence tags from
            developing mouse eye and adult retina
  JOURNAL   Genome Biol. 4 (10), R65 (2003)
   PUBMED   14519200
COMMENT     Contact: Swaroop, A.
            Department of Ophthalmology and Visual Sciences
            Kellogg Eye Center, University of Michigan
            540 KEC, 1000 Wall St., Ann Arbor, MI 48105, USA
            Tel: 734 615 2246
            Fax: 734 647 0228
            Email: swaroop@umich.edu.
FEATURES             Location/Qualifiers
     source          1. .642
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="eye"
                     /clone_lib="MOUSE POST-NATAL DAY 2 EYE"
                     /note="Vector: pSPORT1"
ORIGIN

Alignment Scores:
Pred. No.:                181             Length:         642
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.7%           Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-1 (1-30) x CB844714 (1-642)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db        276 ACTGTATCTTTTAATTTAGGGGAA 253

RESULT 27
BJ109333
LOCUS       BJ109333                646 bp    mRNA    linear   EST 23-JAN-2002
DEFINITION  BJ109333 unpublished oligo-capped cDNA library, C. elegans L1 stage
            Caenorhabditis elegans cDNA clone yk1118b10 5', mRNA sequence.
ACCESSION   BJ109333
VERSION     BJ109333.1  GI:18269362
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .646
                     /organism="Caenorhabditis elegans"
                     /mol_type="mRNA"
                     /strain="N2"
                     /db_xref="taxon:6239"
                     /clone="yk1118b10"
                     /sex="hermaphrodite"
                     /tissue_type="whole animal"
                     /dev_stage="L1"
                     /clone_lib="unpublished oligo-capped cDNA library, C.
                     elegans L1 stage"
ORIGIN

Alignment Scores:
Pred. No.:                182             Length:         646
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.7%           Indels:         0
DB:                       3               Gaps:           0

US-10-758-902-1 (1-30) x BJ109333 (1-646)

Qy         17 PheIleGlnAspLeuArgAsnGlu 24
              ||||||||||||||||||||||||
Db        295 TTTATTCAAGACCTCCGAAACGAA 318

RESULT 28
CW374967
LOCUS       CW374967                654 bp    DNA     linear   GSS 01-NOV-2004
DEFINITION  fsbb001f052b17f0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fsbb001f052b17, genomic survey
```

```
            sequence.
ACCESSION   CW374967
VERSION     CW374967.1  GI:55093411
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 654)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: fsbb001f052  row: b  column: 17
            Seq primer: f Forward
            Class: methylation filtered
            High quality sequence stop: 654.
FEATURES             Location/Qualifiers
     source          1. .654
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="fsbb001f052b17"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:                184           Length:        654
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              26.7%         Indels:        0
DB:                       10            Gaps:          0

US-10-758-902-1 (1-30) x CW374967 (1-654)

Qy         20 AspLeuArgAsnGluLeuAlaLys 27
              |||||||||||||||||||||||||
Db         37 GATTTAAGAAATGAGTTAGCAAAA 60

RESULT 29
CD469335
LOCUS       CD469335                 676 bp    mRNA    linear   EST 04-JUN-2003
DEFINITION  LeukoS2_3_H05.b1_A024 Stimulated peripheral blood leukocytes S2
            Equus caballus cDNA clone LeukoS2_3_H05_A024 3', mRNA sequence.
ACCESSION   CD469335
VERSION     CD469335.1  GI:31390603
KEYWORDS    EST.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 676)
  AUTHORS   Vandenplas,M., Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S.,
            Moore,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.
  TITLE     An EST database from equine (Equus caballus) stimulated peripheral
            blood leukocytes
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: LeukoS2_3_H05.g1_A024
            Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
            the Human Genome Center, University of Tokyo Institute of Medical
            Science; tissue and RNA were prepared in the Department of Large
            Animal Medicine, University of Georgia; sequencing done in the
            Laboratory for Genomics and Bioinformatics, University of Georgia.
            Sequence ends have been trimmed to exclude vector and regions below
            Phred quality 16. Three-prime sequences are presented as their
            reverse complement and have been trimmed to exclude polyA.
            Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .676
                     /organism="Equus caballus"
                     /mol_type="mRNA"
                     /strain="thoroughbred"
                     /db_xref="taxon:9796"
                     /clone="LeukoS2_3_H05_A024"
                     /sex="male"
                     /tissue_type="blood"
                     /cell_type="leukocytes"
                     /lab_host="DH10B-T1 phage-resistant E. coli"
                     /clone_lib="Stimulated peripheral blood leukocytes S2"
                     /note="Organ: circulatory system; Vector: pME18S-FL3;
                     Site_1: XhoI; Site_2: XhoI; The library was prepared from
                     polyA+ RNA from equine peripheral blood leukocytes
                     isolated from a healthy adult horse. The leukocytes were
                     stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.
                     Double-stranded cDNA was cloned unidirectionally into
                     different DraIII sites of the pME18S-FL3 vector (5-prime
                     DraIII site is CACTGTGTG, 3-prime DraIII site is
                     CACCATGTG). XhoI excises the cDNA insert."
ORIGIN

Alignment Scores:
Pred. No.:                190           Length:        676
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              26.7%         Indels:        0
DB:                       6             Gaps:          0

US-10-758-902-1 (1-30) x CD469335 (1-676)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db         43 ACAGTGTCATTTAATTTGGGAGAG 66

RESULT 30
CN773154/c
LOCUS       CN773154                 690 bp    mRNA    linear   EST 20-MAY-2004
DEFINITION  tae61d03.x1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 3',
            mRNA sequence.
ACCESSION   CN773154
VERSION     CN773154.1  GI:47543788
KEYWORDS    EST.
SOURCE      Hydra magnipapillata
  ORGANISM  Hydra magnipapillata
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
            Hydridae; Hydra.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
```

Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R., Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
TITLE WashU Hydra EST Project
JOURNAL Unpublished (2002)
COMMENT Contact: Hans Bode
WashU Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell Biology, TUD, Darmstadt DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrbode@uci.edu)
Seq primer: degenerate primer.

FEATURES Location/Qualifiers
source 1. .690
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="sf-1 mutant of Hydra magnipapillata"
/db_xref="taxon:6085"
/lab_host="TransforMax EC100 (Epicentre), T1 Phage resistant electrocompetent cells"
/clone_lib="Hydra EST Darmstadt I"
/note="Vector: pBluescript II SK (+); Site_1: NotI; Site_2: EcoRI"

ORIGIN

Alignment Scores:

Pred. No.:	194	Length:	690
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	7	Gaps:	0

US-10-758-902-1 (1-30) x CN773154 (1-690)

```
Qy         19 GlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||||||||
Db        467 CAAGATCTTAGAAATGAATTGGCA 444
```

RESULT 31
CB469308/c
LOCUS CB469308 694 bp mRNA linear EST 26-MAR-2003
DEFINITION sn05_H01.f sn Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CB469308
VERSION CB469308.1 GI:29275693
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 694)
AUTHORS Neilan,J.G., Kutish,G.F., Lu,Z., Zsak,A. and Rock,D.L.
TITLE Sequence analysis of African swine fever virus infected and non-infected porcine macrophage cDNA libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Neilan JG
Plum Island Animal Disease Center
US Department of Agriculture, Agricultural Research Service
PO Box 848, Greenport, NY 11944-848, USA
Tel: 631 323 3133
Fax: 631 323 3044
Email: jneilan@piadc.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified by cross_match v0.990329 and lucy v1.17p.
Seq primer: M13 Forward.

FEATURES Location/Qualifiers
source 1. .694
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="lymphoid"
/cell_type="macrophage"
/lab_host="DH10B"
/clone_lib="sn"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Library made from pools of polyA selected RNA, isolated at different times post-infection (0 to 16 hrs) from African swine fever virus (isolate Pretorisuskop/96/4) infected swine macrophages. Macrophages were derived from peripheral blood mononuclear cells cultured for 48 hrs on plastic in the presence of 30% L929 supernatant."

ORIGIN

Alignment Scores:

Pred. No.:	195	Length:	694
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.7%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x CB469308 (1-694)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        660 ACAGTGTCATTTAATTTGGGAGAG 637
```

RESULT 32
BY764463
LOCUS BY764463 704 bp mRNA linear EST 17-DEC-2002
DEFINITION BY764463 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730030B04 3', mRNA sequence.
ACCESSION BY764463
VERSION BY764463.1 GI:27201928
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 704)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

```
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .704
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="F730030B04"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
ORIGIN

Alignment Scores:
Pred. No.:                198             Length:         704
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.7%           Indels:         0
DB:                       5               Gaps:           0

US-10-758-902-1 (1-30) x BY764463 (1-704)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db        420 ACTGTATCTTTTAATTTAGGGGAA 443

RESULT 33
CW084955/c
LOCUS       CW084955                 716 bp    DNA     linear   GSS 28-OCT-2004
DEFINITION  104_428_10946110_116_32564_095 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10946110, genomic survey
            sequence.
ACCESSION   CW084955
VERSION     CW084955.1  GI:54761685
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 716)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 428  row: b  column: 22
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 716.
FEATURES             Location/Qualifiers
     source          1. .716
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10946110"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:                201             Length:         716
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.7%           Indels:         0
DB:                       10              Gaps:           0

US-10-758-902-1 (1-30) x CW084955 (1-716)

Qy         20 AspLeuArgAsnGluLeuAlaLys 27
              |||||||||||||||||||||||
Db        369 GATTTAAGAAATGAGTTAGCAAAA 346

RESULT 34
BP677084
LOCUS       BP677084                 736 bp    mRNA    linear   EST 07-MAY-2004
DEFINITION  BP677084 Osada Taira anterior neuroectoderm (ANE) pCS105 cDNA
            library Xenopus laevis cDNA clone XL424m18ex 5', mRNA sequence.
ACCESSION   BP677084
VERSION     BP677084.1  GI:46025039
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
```

```
REFERENCE   1  (bases 1 to 736)
  AUTHORS   Osada,S., Kitayama,A., Ueno,N. and Taira,M.
  TITLE     Expression analysis of genes which are expressed in the anterior
            neuroectoderm of Xenopus embryos
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Masanori Taira
            Department of Biological Sciences
            Graduate School of Science, University of Tokyo; CREST, Japan
            Science and Technology Corporation, Japan
            7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
            Tel: 81-03-5841-4434
            Fax: 81-03-5841-4434
            Email: m_taira@biol.s.u-tokyo.ac.jp,
            URL:http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.
FEATURES             Location/Qualifiers
     source          1. .736
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL424m18ex"
                     /tissue_type="anterior neuroectoderm"
                     /dev_stage="late gastrula (stage 12.5)"
                     /clone_lib="Osada Taira anterior neuroectoderm (ANE)
                     pCS105 cDNA library"
ORIGIN

Alignment Scores:
Pred. No.:                207             Length:         736
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.7%           Indels:         0
DB:                       3               Gaps:           0

US-10-758-902-1 (1-30) x BP677084 (1-736)

Qy          22 ArgAsnGluLeuAlaLysGlyThr 29
               |||||||||||||||||||||||||
Db         141 CGAAATGAACTGGCAAAAGGAACC 164

RESULT 35
AJ820130
LOCUS       AJ820130                740 bp    mRNA    linear   EST 12-MAY-2005
DEFINITION  AJ820130 KN206 Bos sp. cDNA clone C0006017i09, mRNA sequence.
ACCESSION   AJ820130
VERSION     AJ820130.1  GI:51887606
KEYWORDS    EST.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 740)
  AUTHORS   McGuire,K. and Glass,E.J.
  TITLE     The expanding role of microarrays in the investigation of
            macrophage responses to pathogens
  JOURNAL   Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT     Contact: McGuire K
            Genomics and Genetics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
            1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
            constructed from pooled monocytes from Bos taurus (Holstein) and
            Bos indicus (Sahiwals) cattle subjected to various stimuli,
            including infection with the protozoan parasite Theileria annulata.
FEATURES             Location/Qualifiers
     source          1. .740
                     /organism="Bos sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:29061"
                     /clone="C0006017i09"
                     /tissue_type="blood"
                     /cell_type="bovine monocyte"
                     /clone_lib="KN206"
                     /note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
                     Site_2: NotI; Normalised library constructed from pooled
                     monocytes from Bos taurus (Holstein) and Bos indicus
                     (Sahiwals) cattle subjected to various stimuli, including
                     infection with the protozoan parasite Theileria annulata"
ORIGIN

Alignment Scores:
Pred. No.:                208             Length:         740
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.7%           Indels:         0
DB:                       1               Gaps:           0

US-10-758-902-1 (1-30) x AJ820130 (1-740)

Qy           1 TyrAsnThrValSerPheAsnLeu 8
                ||||||||||||||||||||||||
Db         346 TATAACACTGTGTCATTTAACCTT 369

RESULT 36
CW373064
LOCUS       CW373064                746 bp    DNA     linear   GSS 01-NOV-2004
DEFINITION  fsbb001f049e01f0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fsbb001f049e01, genomic survey
            sequence.
ACCESSION   CW373064
VERSION     CW373064.1  GI:55091508
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: fsbb001f049  row: e  column: 01
            Seq primer: f Forward
            Class: methylation filtered
            High quality sequence stop: 746.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="fsbb001f049e01"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
```

```
ORIGIN

Alignment Scores:
Pred. No.:              209           Length:        746
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     10            Gaps:          0

US-10-758-902-1 (1-30) x CW373064 (1-746)

Qy         20 AspLeuArgAsnGluLeuAlaLys 27
              ||||||||||||||||||||||||
Db        586 GATTTAAGAAATGAGTTAGCAAAA 609

RESULT 37
BI089654
LOCUS       BI089654                758 bp    mRNA    linear   EST 20-JUN-2001
DEFINITION  602854348F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996066 5',
            mRNA sequence.
ACCESSION   BI089654
VERSION     BI089654.1  GI:14507984
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 758)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11020  row: o  column: 11
            High quality sequence start: 8
            High quality sequence stop: 622.
FEATURES             Location/Qualifiers
     source          1. .758
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4996066"
                     /cell_line="MGC36"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_10"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5 kb. Library prepared by Life
                     Technologies."
ORIGIN

Alignment Scores:
Pred. No.:              213           Length:        758
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x BI089654 (1-758)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        532 ACAGTGTCATTTAATTTGGGAGAG 555

RESULT 38
DR103654
LOCUS       DR103654                771 bp    mRNA    linear   EST 13-JUN-2005
DEFINITION  JHU040H05L771 Canine cardiovascular system biased cDNA Canis
            familiaris cDNA similar to Hs Wilms tumor 1 associated protein
            (WTAP), transcript variant 1, mRNA sequence.
ACCESSION   DR103654
VERSION     DR103654.1  GI:67563009
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   DiSilvestre,D., Yung,C., Gao,Z., Farukhi,Y., Winslow,R.L. and
            Tomaselli,G.F.
  TITLE     Canine cardiovascular system biased cDNA sequences
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Gordon F. Tomaselli
            Johns Hopkins University
            720 Rutland Avenue/Ross 844, Baltimore, MD 21205, USA
            Tel: 4109552774
            Fax: 4105022096
            Email: gtomasel@jhmi.edu.
FEATURES             Location/Qualifiers
     source          1. .771
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /strain="Mixed"
                     /db_xref="taxon:9615"
                     /sex="Mixed"
                     /clone_lib="Canine cardiovascular system biased cDNA"
                     /note="Organ: Mixed; Vector: PCDNA3.1; Site_1: EcoRI;
                     Site_2: XhoI; Adult tissue from eye, lung, aorta,
                     pulmonary artery and brain; neonatal tissue from liver,
                     spleen, thymus, lung, kidney, aorta and brain; 50% is from
                     cardiac tissues."
ORIGIN

Alignment Scores:
Pred. No.:              216           Length:        771
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.7%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x DR103654 (1-771)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        698 ACAGTGTCATTTAATTTGGGAGAG 721

RESULT 39
CO430592/c
LOCUS       CO430592                773 bp    mRNA    linear   EST 06-JUL-2004
DEFINITION  UI-M-HX0-csb-m-15-0-UI.r1 NIH_BMAP_HX0 Mus musculus cDNA clone
            IMAGE:30684110 5', mRNA sequence.
ACCESSION   CO430592
VERSION     CO430592.1  GI:49676886
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 773)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

```
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES              Location/Qualifiers
     source           1. .773
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:30684110"
                      /tissue_type="whole eye"
                      /dev_stage="newborn (1, 5, 15 days) and embryonic (15, 16,
                      17, 18 dpc)"
                      /lab_host="DH10B (T1 phage resistant)"
                      /clone_lib="NIH_BMAP_HX0"
                      /note="Organ: Eye; Vector: pYX-Asc; Site_1: EcoR I;
                      Site_2: Not I; The library was constructed according
                      Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                      1996. Denatured RNA was size fractionated on a 1% agarose
                      gel.First strand cDNA synthesis was primed with oligo-dT
                      primer containing a Not I site .Double strand cDNA was
                      size selected according to mRNA size fraction, ligated
                      with EcoR I adaptor, digested with NotI and then cloned
                      directionally into pYX-Asc vector. The library tag
                      sequence located between the Not I site and the polyA tail
                      is AATAATTACG. This library was created for the University
                      Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                      Developing Mouse Nervous System', supported by National
                      Institute of Mental Health (NIMH)."
ORIGIN

Alignment Scores:
Pred. No.:              217             Length:         773
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-1 (1-30) x CO430592 (1-773)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||||
Db        353 ACTGTATCTTTTAATTTAGGGGAA 330

RESULT 40
CO386739
LOCUS       CO386739                789 bp    mRNA    linear   EST 30-JUN-2004
DEFINITION  AGENCOURT_26185782 Blumberg_Cho dorsal blastopore lip Xenopus
            laevis cDNA clone IMAGE:7297475 5', mRNA sequence.
ACCESSION   CO386739
VERSION     CO386739.1  GI:49494330
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 789)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Bruce Blumberg
             cDNA Library Preparation: B. Blumberg
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15322  row: o  column: 09
            High quality sequence start: 3
            High quality sequence stop: 698.
FEATURES              Location/Qualifiers
     source           1. .789
                      /organism="Xenopus laevis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8355"
                      /clone="IMAGE:7297475"
                      /sex="both"
                      /tissue_type="dorsal blastopore lip"
                      /lab_host="TOP10"
                      /clone_lib="Blumberg_Cho dorsal blastopore lip"
                      /note="Organ: embryo; Vector: pBluescript SK-; Site_1:
                      EcoRI; Site_2: XhoI; Library was prepared from 50 ug of
                      total RNA by oligo-dT priming and AMV reverse
                      transcriptase. After addition of EcoRI linkers and
                      EcoRI-XhoI digestion, the cDNA was size selected by
                      chromatography on Sepharose CL-4B columns and fractions
                      containing cDNAs larger than 500 bp were ligated into
                      EcoRI-XhoI-digested lambda ZAPII (UniZAP-XR) and packaged
                      in vitro. Average insert size is 1.4 kb. The original
                      library contained 6 x 106 recombinants, of which 3 x 106
                      were amplified and stored at -70 C in SM buffer containing
                      7% DMSO. 3 x 106 pfu were mass excised and the resulting
                      phagemids used to infect Top10F. References: Science 253,
                      196-196 and Methods in Molecular Biology 97, 555-574.
                      Additional sequences from this library have been deposited
                      under the name Xenopus laevis dorsal blastopore lip.
                      Library constructed by Bruce Blumberg (University of
                      California, Irvine, Department of Developmental and Cell
                      Biology)."
ORIGIN

Alignment Scores:
Pred. No.:              221             Length:         789
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-1 (1-30) x CO386739 (1-789)

Qy         18 IleGlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||||||
Db        418 ATTCAGGATTTGAGAAATGAGTTG 441


Search completed: February 20, 2006, 02:52:56
Job time : 1091.92 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2006, 23:43:27 ; Search time 6014.94 Seconds
(without alignments)
1408.107 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160759_3676/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10758902_@CGN_1_1_5142_@runat_17022006_160759_3676 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	747	97.3	1387	15	AF445416	AF445416 Bougainvi
2	739	96.2	1085	15	AY437531	AY437531 Bougainvi
3	609	79.3	363	6	A82773	A82773 Sequence 8
4	609	79.3	363	6	AR454123	AR454123 Sequence
5	329.5	42.9	1364	15	DQ013264	DQ013264 Bougainvi
6	225	29.3	1286	15	AB070925	AB070925 Spinacia
7	221.5	28.8	756	6	E02511	E02511 DNA encodin
8	221.5	28.8	765	11	SYNMIJAVP	J04707 M.jalapa sy
9	221.5	28.8	1015	15	MJLATVP	D10569 M.jalapa ge
10	220.5	28.7	913	6	AR003723	AR003723 Sequence
11	220.5	28.7	913	6	AR010059	AR010059 Sequence
12	220.5	28.7	913	6	AR055265	AR055265 Sequence
13	220.5	28.7	913	6	AR141194	AR141194 Sequence
14	220.5	28.7	913	6	AR141431	AR141431 Sequence
15	220.5	28.7	913	6	I11903	I11903 Sequence 13
16	220.5	28.7	913	6	I40476	I40476 Sequence 13
17	220.5	28.7	913	6	AR367960	AR367960 Sequence
18	220.5	28.7	913	6	AR430941	AR430941 Sequence
19	220.5	28.7	914	15	MBMOMORII	Z12175 M.balsamina
20	219.5	28.6	756	6	E02815	E02815 DNA sequenc
21	218.5	28.5	795	15	MCH294541	AJ294541 Momordica
22	217.5	28.3	1066	15	MJLMAP	D10227 M. jalapa L
23	215.5	28.1	795	15	AY523412	AY523412 Momordica
24	215.5	28.1	795	15	AJ748278	AJ748278 Momordica
25	215.5	28.1	861	15	AY817142	AY817142 Momordica
26	215.5	28.1	861	15	AF284811	AF284811 Momordica
27	215.5	28.1	919	15	S79450	S79450 Map30=anti-
28	211.5	27.5	762	6	E03954	E03954 DNA encodin
29	194.5	25.3	1932	15	AF259548	AF259548 Cinnamomu
30	193.5	25.2	2010	15	AY039803	AY039803 Cinnamomu
31	193.5	25.2	2024	15	AY039801	AY039801 Cinnamomu
32	191.5	24.9	2020	15	AY039802	AY039802 Cinnamomu
33	191	24.9	1692	15	AF409135	AF409135 Sambucus
34	191	24.9	1879	15	SNU41299	U41299 Sambucus ni
35	191	24.9	1906	15	AF249280	AF249280 Sambucus
36	190.5	24.8	962	6	I34238	I34238 Sequence 14
37	190.5	24.8	1129	15	AY148091	AY148091 Mirabilis
38	187.5	24.4	1809	15	AY082349	AY082349 Trichosan
39	187	24.3	1892	15	SEB400822	AJ400822 Sambucus
40	186.5	24.3	741	15	AY669811	AY669811 Trichosan
41	184	24.0	1042	15	AB045560	AB045560 Cucumis f
42	183.5	23.9	741	15	AB039324	AB039324 Trichosan
43	183.5	23.9	886	6	AR032228	AR032228 Sequence
44	183.5	23.9	886	6	BD165859	BD165859 Transgeni
45	183.5	23.9	886	6	I32881	I32881 Sequence 3
46	183.5	23.9	886	6	AR228702	AR228702 Sequence
47	183.5	23.9	886	6	BD011600	BD011600 Recombina
48	183.5	23.9	1010	15	TRHTCSA	M34858 T.kirilowii
49	183.5	23.9	1134	15	S70176	S70176 trichosanth
50	183.5	23.9	1194	15	AB000666	AB000666 Trichosan
51	183.5	23.9	1227	15	TRHTCS	J05434 T.kirilowii
52	183	23.8	1584	15	ABRIABRD	M98346 Abrus preca
53	183	23.8	2743	15	APAB	X55667 A.precatori
54	180.5	23.5	1799	15	AF367252	AF367252 Trichosan
55	179.5	23.4	758	6	AR117133	AR117133 Sequence
56	179.5	23.4	762	6	AX019439	AX019439 Sequence
57	179.5	23.4	762	6	AX019442	AX019442 Sequence
58	179.5	23.4	768	6	AX019440	AX019440 Sequence
59	179.5	23.4	768	6	AX019443	AX019443 Sequence
60	179.5	23.4	1084	15	BYNBD1	L42298 Bryonia dio
61	179.5	23.4	1094	6	I24020	I24020 Sequence 1
62	179.5	23.4	1499	6	AR117137	AR117137 Sequence
63	176.5	23.0	756	6	A90900	A90900 Sequence 7
64	176.5	23.0	762	6	A90894	A90894 Sequence 1
65	176.5	23.0	774	6	AR164303	AR164303 Sequence
66	176.5	23.0	810	15	AY584242	AY584242 Trichosan
67	176.5	23.0	855	6	AX798190	AX798190 Sequence
68	176.5	23.0	1433	15	AY082348	AY082348 Trichosan
69	176.5	23.0	1596	6	AX019438	AX019438 Sequence
70	176.5	23.0	1596	6	AX019441	AX019441 Sequence
71	176.5	23.0	1602	15	AY081149	AY081149 Viscum al
72	176.5	23.0	1692	15	DQ011864	DQ011864 Viscum al
73	176.5	23.0	1882	15	AY377890	AY377890 Viscum al
74	176.5	23.0	1923	6	A58957	A58957 Sequence 1
75	176.5	23.0	1923	6	AR164305	AR164305 Sequence
76	176.5	23.0	1958	6	AX798194	AX798194 Sequence

77	175	22.8	2079	15	SNU76524	U76524 Sambucus ni
78	174.5	22.7	747	15	AY081148	AY081148 Viscum al
79	174.5	22.7	837	6	AR633329	AR633329 Sequence
80	174.5	22.7	1044	15	MCAMC	X57682 M.charantia
81	174.5	22.7	1756	15	AY377892	AY377892 Viscum al
82	174.5	22.7	1873	15	AF369961	AF369961 Viscum al
83	174.5	22.7	1944	15	AY377893	AY377893 Viscum al
84	174	22.7	756	15	APRICA72	X54872 Abrus preca
85	172	22.4	1581	15	ABRIABRB	M98345 Abrus preca
86	171.5	22.3	747	15	AF508915	AF508915 Viscum al
87	171.5	22.3	762	6	AR633323	AR633323 Sequence
88	171.5	22.3	762	6	AX139573	AX139573 Sequence
89	170.5	22.2	810	15	TKU25675	U25675 Trichosanth
90	169.5	22.1	705	6	AR164307	AR164307 Sequence
91	169	22.0	600	6	I09063	I09063 Sequence 46
92	169	22.0	848	6	CS070403	CS070403 Sequence
93	169	22.0	848	11	SYNRICA	M32614 Synthetic r
94	169	22.0	1050	6	I02107	I02107 Sequence 3
95	169	22.0	1050	6	I07418	I07418 Sequence 30
96	169	22.0	1050	6	I08353	I08353 Sequence 9
97	169	22.0	1140	6	A23903	A23903 partial seq
98	169	22.0	1140	6	A23989	A23989 pICI 1102 p
99	169	22.0	1140	6	AR059851	AR059851 Sequence
100	169	22.0	1140	6	I25094	I25094 Sequence 15

ALIGNMENTS

```
RESULT 1
AF445416
LOCUS       AF445416                1387 bp    mRNA    linear   PLN 29-NOV-2001
DEFINITION  Bougainvillea spectabilis bouganin mRNA, complete cds.
ACCESSION   AF445416
VERSION     AF445416.1  GI:17149253
KEYWORDS    .
SOURCE      Bougainvillea spectabilis
  ORGANISM  Bougainvillea spectabilis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE   1  (bases 1 to 1387)
  AUTHORS   den Hartog,M.T., Lubelli,C., Boon,L., Heerkens,S., Ortiz
            Buijsse,A.P., de Boer,M. and Stirpe,F.
  TITLE     Cloning and expression of cDNA coding for bouganin: A type I
            ribosome-inactivating protein from Bougainvillea spectabilis Willd
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1387)
  AUTHORS   den Hartog,M.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-NOV-2001) Meibergdreef 45, Amsterdam 1105 BA, The
            Netherlands
FEATURES             Location/Qualifiers
     source          1. .1387
                     /organism="Bougainvillea spectabilis"
                     /mol_type="mRNA"
                     /db_xref="taxon:146096"
                     /note="authority: Bougainvillea spectabilis Willd"
     CDS             238. .1155
                     /note="ribosome-inactivating protein"
                     /codon_start=1
                     /product="bouganin"
                     /protein_id="AAL35962.1"
                     /db_xref="GI:17149254"
                     /translation="MGWWAIIVEPMLVMPSIVNKETTSLGYNTVSFNLGEAYEYPTFI
                     QDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQD
                     KWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYK
                     LEFSIEAIHGKTINGQEIAKFFLIVIQMVSEAARFKYIETEVVDRGLYGSFKPNFKVL
                     NLENNWGDISDAIHKSSPQCTTINPALQLISPSNDPWVVNKVSQISPDMGILKFKSSK
                     LTQFATMIRSAIVEDLDGDELEILEPNIA"
ORIGIN

Alignment Scores:
Pred. No.:              4.21e-72        Length:         1387
```

```
Score:                  747.00          Matches:        147
Percent Similarity:     98.7%           Conservative:   0
Best Local Similarity:  98.7%           Mismatches:     2
Query Match:            97.3%           Indels:         0
DB:                     15              Gaps:           0

US-10-758-902-9 (1-149) x AF445416 (1-1387)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 375

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 435

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 495

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 555

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 615

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 675

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 GCCAAAGTGGATAGAAAGGATCTCGAACTGGGGGTTTACAAATTGGAATTTTCCATTGAA 735

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||  |||||||||  ||||||
Db        736 GCAATCCATGGTAAAACGATAAATGGT 762
```

```
RESULT 2
AY437531
LOCUS       AY437531                1085 bp    mRNA    linear   PLN 20-JAN-2005
DEFINITION  Bougainvillea spectabilis antiviral protein (Ap1) mRNA, complete
            cds.
ACCESSION   AY437531
VERSION     AY437531.1  GI:40890052
KEYWORDS    .
SOURCE      Bougainvillea spectabilis
  ORGANISM  Bougainvillea spectabilis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE   1  (bases 1 to 1085)
  AUTHORS   Balasaraswathi,R., Suguna Rani,K. and Bansal,V.
  TITLE     A full length antiviral cDNA sequence from Bougainvillea
            spectabilis Willd.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1085)
  AUTHORS   Balasaraswathi,R., Suguna Rani,K. and Bansal,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-OCT-2003) Centre For Plant Molecular Biology, Tamil
            Nadu Agricultural University, Lawley Road, Coimbatore, Tamil Nadu
            641003, India
FEATURES             Location/Qualifiers
     source          1. .1085
                     /organism="Bougainvillea spectabilis"
                     /mol_type="mRNA"
                     /db_xref="taxon:146096"
                     /ecotype="Coimbatore region"
                     /country="India"
                     /note="biotype: red flower trait; authority: Bougainvillea
                     spectabilis Willd."
```

```
     gene            1. .1085
                     /gene="Ap1"
     5'UTR           1. .25
                     /gene="Ap1"
     CDS             26. .943
                     /gene="Ap1"
                     /note="crop antiviral and ribosome-inactivating protein;
                     BAP; BAP1; antiviral activity against tospo group of crop
                     viruses"
                     /codon_start=1
                     /product="antiviral protein"
                     /protein_id="AAR97371.1"
                     /db_xref="GI:40890053"
                     /translation="MGWWAIIVEPMLVMPSIVNKETTSLGYNTVSFNLGEAYEYPTFI
                     QDLRNELAKGTPVCQLPVTLQTIADAKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQD
                     KWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYK
                     LEFSIEAIHGKTINGQEIAKFFLITIQMVSEAARFKYIETEVVDRGLYGSFKPNFKVL
                     NLENNWGDISDAIHKSSPQCTTINPALQLISPSNDPWVVNKVSQISPDMGILKFKSSK
                     LTQFATMIRSAIAEDLDGDELEILEPNIA"
     3'UTR           944. .1085
                     /gene="Ap1"
     polyA_signal    984. .989
                     /gene="Ap1"
ORIGIN

Alignment Scores:
Pred. No.:              2.39e-71        Length:         1085
Score:                  739.00          Matches:        146
Percent Similarity:     98.0%           Conservative:   0
Best Local Similarity:  98.0%           Mismatches:     3
Query Match:            96.2%           Indels:         0
DB:                     15              Gaps:           0

US-10-758-902-9 (1-149) x AY437531 (1-1085)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 TACAACACTGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 163

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 223

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 ATAGCCGATGCCAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 283

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 343

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 403

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 463

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GCCAAAGTGGATAGAAAGGATCTCGAACTGGGGGTTTACAAATTGGAATTTTCCATTGAA 523

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||  |||||||||   ||||||
Db        524 GCAATCCATGGTAAAACGATAAATGGT 550

RESULT 3
A82773
LOCUS       A82773                   363 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 8 from Patent WO9855623.
ACCESSION   A82773
VERSION     A82773.1  GI:6732463
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     TYPE-1 RIBOSOME-INACTIVATING PROTEIN
  JOURNAL   Patent: WO 9855623-A 8 10-DEC-1998;
            STIRPE FIORENZO (IT); BOLOGNESI ANDREA (IT)
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.21e-57        Length:         363
Score:                  609.00          Matches:        120
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            79.3%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x A82773 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361

RESULT 4
AR454123
LOCUS       AR454123                 363 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 8 from patent US 6680296.
ACCESSION   AR454123
VERSION     AR454123.1  GI:42687052
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     Type-1 ribosome-inactivating protein
  JOURNAL   Patent: US 6680296-A 8 20-JAN-2004;
            Tanox Pharma B.V.; Amsterdam;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
```

```
Pred. No.:              1.21e-57        Length:         363
Score:                  609.00          Matches:        120
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            79.3%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x AR454123 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361

RESULT 5
DQ013264
LOCUS       DQ013264               1364 bp    mRNA    linear   PLN 20-JUL-2005
DEFINITION  Bougainvillea x buttiana antiviral protein 1 mRNA, complete cds.
ACCESSION   DQ013264
VERSION     DQ013264.2  GI:68342547
KEYWORDS    .
SOURCE      Bougainvillea x buttiana
  ORGANISM  Bougainvillea x buttiana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Choudhary,N. and Lodha,M.L.
  TITLE     cDNA Sequence of Bougainvillea Antiviral Protein (BAP1)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1364)
  AUTHORS   Choudhary,N. and Lodha,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2005) Division of Biochemistry, Indian
            Agricultural Research Institute, Pusa, New Delhi 110012, India
REFERENCE   3  (bases 1 to 1364)
  AUTHORS   Choudhary,N. and Lodha,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-2005) Division of Biochemistry, Indian
            Agricultural Research Institute, Pusa, New Delhi 110012, India
  REMARK    Sequence update by submitter
COMMENT     On Jun 30, 2005 this sequence version replaced gi:63147983.
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="Bougainvillea x buttiana"
                     /mol_type="mRNA"
                     /cultivar="Mahara"
                     /db_xref="taxon:328062"
                     /tissue_type="leaves"
     5'UTR           1. .120
     CDS             121. .1080
                     /note="BAP1"
                     /codon_start=1
                     /product="antiviral protein 1"
                     /protein_id="AAY34283.2"
                     /db_xref="GI:68342548"
                     /translation="MKPLGGLVITCIWWAIIVELVVIKPSIITKETASLGHNTVSFNL
                     EDATEQVYRSVIKSLRNELQTSTLVCKIPVTPQSLAVDKNQFVVVSLTWKSKEVQLGI
                     DVTNAYVVGYQDKLKNQDYRAPLLKDAPPLAKDKLFPGVKSETLPFGGTYPNLVKAGN
                     VDRREQFELGVEKLGHAIDSIFGKPKNDQNVARFFLNAIQIVSEAARFKYIENEVVRG
                     GLNSGLSKPNGKMLNLENSWGHISDAIHNSNQKYKCETISPALELQNADYSKWVVNKV
                     SEISPDLGILKYKSSKLTQSTTIMRSIVVEDSDELEKLETIIG"
     3'UTR           1081. .1364
ORIGIN

Alignment Scores:
Pred. No.:              2.34e-26        Length:         1364
Score:                  329.50          Matches:        79
Percent Similarity:     68.6%           Conservative:   26
Best Local Similarity:  51.6%           Mismatches:     41
Query Match:            42.9%           Indels:         7
DB:                     15              Gaps:           6

US-10-758-902-9 (1-149) x DQ013264 (1-1364)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIle 18
              :::||||||||||||||||||||||   :::|||   |||       |||   :::   |||
Db        229 CACAACACTGTGTCATTTAACCTGGAAGATGCTACTGAACAAGTGTACCGCTCTGTTATA 288

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeu 38
              :::   ||||||||||||||||          |||   |||||::::::|||||||||
Db        289 AAATCTTTGCGCAACGAATTACAAACTAGCACACTAGTATGTAAAATTCCAGTGACACCA 348

Qy         39 GlnThrIleAlaAspAspLys---ArgPheValLeuValAspIleThrThrThrSerLys 57
              |||::::::|||   ||||||   :::|||||||:::|||   :::|||       ||||||
Db        349 CAAAGCCTAGCCGTTGATAAAAACCAATTTGTTGTGGTTAGTCTCACTTGGAAGTCAAAG 408

Qy         58 LysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLys 77
              :::   |||::::::   |||||||||||:::   ||||||||||||||||||||||||
Db        409 GAA---GTTCAACTTGGTATAGATGTGACGAATGCGTATGTGGTGGGTTATCAAGACAAA 465

Qy         78 TrpAspGlyLysAsp---ArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
                    :::|||   ||||||        |||       |||   :::|||
Db        466 TTGAAGAACCAAGATTATCGAGCCTTTTTGCTTAAAGATGCTCCTCCACTTGCAAAAGAT 525

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||   :::      ||||||   |||   |||:::|||
Db        526 AAACTTTTCCCTGGAGTGAAAAGTGAA---ACATTACCGTTTGGAGGCACCTATCCAAAC 582

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAsp---LeuGluLeuGlyValTyrLysLeu 135
              ||||||   |||       ||||||||:::::       ||||||||||||   ||||||
Db        583 CTTGTAAAAGCTGGCAATGTCGATCGTAGAGAACAATTCGAACTGGGTGTTGAAAAACTC 642

Qy        136 GluPheSerIleGluAlaIleTrpGlyLysThrGlnAsn 148
                 :::|||::::::|||:::||||||   :::|||
Db        643 GGACATGCCATTGATTCAATTTTTGGTAAACCAAAAAAT 681

RESULT 6
AB070925
LOCUS       AB070925               1286 bp    mRNA    linear   PLN 05-JAN-2002
DEFINITION  Spinacia oleracea mRNA for ribosome-inactivatin protein, complete
            cds.
ACCESSION   AB070925
VERSION     AB070925.1  GI:18149180
KEYWORDS    .
SOURCE      Spinacia oleracea (spinach)
  ORGANISM  Spinacia oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Amaranthaceae; Spinacia.
REFERENCE   1
  AUTHORS   Megumi,C., Masuda,K. and Shirai,K.
  TITLE     Ribosome-inactivating protein from the embryogenic callus of
            Spinach(Spinacia oleracea)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1286)
  AUTHORS   Megumi,C. and Masuda,K.
```

```
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-2001) Chiaki Megumi, Hokkaido University,
            Laboratory of Horticultural Science; Nishi 9 Kita 9, Kita-ku,
            Sapporo, Hokkaido 060-8589, Japan
            (E-mail:tanechan@res.agr.hokudai.ac.jp, Tel:81-11-706-3875,
            Fax:81-11-706-4937)
FEATURES             Location/Qualifiers
     source          1. .1286
                     /organism="Spinacia oleracea"
                     /mol_type="mRNA"
                     /db_xref="taxon:3562"
                     /tissue_type="embryogenic callus"
     CDS             100. .1059
                     /function="ribosome-inactivating"
                     /note="haurensin"
                     /codon_start=1
                     /product="ribosome-inactivating protein"
                     /protein_id="BAB83507.1"
                     /db_xref="GI:18149181"
                     /translation="MKLSATTIWVLRWCMMMVVVVAVAVVPPSLAVVEDEEMIENLRY
                     TTVTFELTNGVTGYSSFMTRLRNAVEAPTRACGLQSTRSTPLPGAEYIHVDLKISNTQ
                     WVTLGIDVKDFYVWGYQDNVRYNGNYRASFLNDAPQAAKNNLFRGSTIRTTRFGGNYN
                     SLEPAAGITRRNLVLGIQNLDGAIRTVYGKQESELNKGNAEARFFLIAIQMVAEAARF
                     KFMEEAIVRNDNTPDFKRKMVAFQNDWDPISTAIHRAEAATPKCTRITPTLVISNTEY
                     RQEVNTVAEIKDDMGLLKYRSTTLSSIASSILDDDEFLESALI"
ORIGIN

Alignment Scores:
Pred. No.:              6.2e-15       Length:         1286
Score:                  225.00        Matches:        55
Percent Similarity:     54.3%         Conservative:   27
Best Local Similarity:  36.4%         Mismatches:     65
Query Match:            29.3%         Indels:         4
DB:                     15            Gaps:           3

US-10-758-902-9 (1-149) x AB070925 (1-1286)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu---TyrProThrPheIleGln 19
              |||  ||||||:::|||   |||           |||   :::|||:::
Db        229 TACACCACTGTAACATTTGAACTAACAAATGGTGTTACAGGCTACTCAAGTTTCATGACA 288

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGln 39
                |||||||||   :::         |||      |||  |||      |||
Db        289 AGGTTGCGCAACGCTGTGGAAGCCCCAACTAGAGCGTGCGGGTTACAATCAACACGAAGC 348

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
              |||           :::::::   ||||||:::     ::::::   :::
Db        349 ACACCATTACCAGGAGCCGAATACATTCACGTAGACCTCAAAATCAGCAACACACAATGG 408

Qy         60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp------Lys 77
              |||   :::   |||||||||   |||   ||||||   ||||||||||||      :::
Db        409 GTTACTTTAGGAATAGATGTCAAAGACTTCTATGTTTGGGGTTATCAAGACAATGTTAGA 468

Qy         78 TrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys 97
              ::::::|||      ||||||   ||||||:::     |||      |||   :::
Db        469 TATAACGGCAATTATAGAGCAAGTTTCCTTAATGATGCCCCTCAAGCTGCTAAGAACAAC 528

Qy         98 LeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
              ||||||   |||   |||   |||   |||      |||   |||:::|||      |||
Db        529 CTTTTCCGTGGTTCAACAATTAGAACCACT---AGGTTCGGAGGTAACTATAACAGTCTT 585

Qy        118 ValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPhe 137
                 ||||||   :::   |||::::::|||   ||||||:::     |||:::
Db        586 GAGCCGGCTGCCGGTATTACTCGAAGGAACCTTGTGCTAGGAATTCAGAACCTTGACGGG 645

Qy        138 SerIleGluAlaIleTrpGlyLysThrGlnAsn 148
              :::|||      ::::::||||||   ::::::
Db        646 GCTATAAGAACGGTGTACGGGAAACAAGAAAGT 678

RESULT 7
E02511
LOCUS       E02511                   756 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA encoding mirabilis antiviral protein.
ACCESSION   E02511
VERSION     E02511.1  GI:2170741
KEYWORDS    JP 1990186988-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   Habuka,N., Horikoshi,K., Kudo,T. and Murakami,Y.
  TITLE     PRODUCTION OF ANTIVIRAL PROTEIN
  JOURNAL   Patent: JP 1990186988-A 1 23-JUL-1990;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1990186988-A/1
            PD   23-JUL-1990
            PF   18-APR-1988 JP 1988093494
            PR   14-APR-1988 JP 88P    90166
            PI   HABUKA NORIYUKI, HORIKOSHI KOKI, KUDO TOSHIAKI, MURAKAMI YUJI
            PC   C12N15/29,C12N1/21,C12P21/02,(C12N1/21,C12R1:19),(C12P21/02,
            PC   C12R1:19);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   CDS             1. .756
            FT                   /product='Mirabilis antiviral protein'.
FEATURES             Location/Qualifiers
     source          1. .756
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              8.18e-15      Length:         756
Score:                  221.50        Matches:        54
Percent Similarity:     55.9%         Conservative:   27
Best Local Similarity:  37.2%         Mismatches:     55
Query Match:            28.8%         Indels:         9
DB:                     6             Gaps:           4

US-10-758-902-9 (1-149) x E02511 (1-756)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||              |||   :::||||||   ::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 84

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||      |||      |||            |||:::|||   |||:::
Db         85 GTCGCAGACAAAACCGAACAGTGT-----------ACCATCCAGAAAATCTCTAAAACC 132

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                    :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              ||||||||:::   |||:::||||||:::||||||   |||      :::      |||
Db        193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
              ||||||   |||          |||                :::      |||||||||
Db        253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||       |||
Db        313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                   :::   |||||||||      ||||||::::::::::||||||   ||||||
Db        373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429
```

```
Qy        141 AlaIleTrpGlyLys 145
                  |||:::||||||
Db        430 AACATTTATGGCAAA 444

RESULT 8
SYNMIJAVP
LOCUS       SYNMIJAVP               765 bp    DNA     linear   SYN 27-APR-1993
DEFINITION  M.jalapa synthetic antiviral protein gene, complete cds.
ACCESSION   J04707
VERSION     J04707.1  GI:208832
KEYWORDS    antiviral protein; artificial gene.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   Habuka,N., Murakami,Y., Noma,M., Kudo,T. and Horikoshi,K.
  TITLE     Amino acid sequence of Mirabilis antiviral protein, total synthesis
            of its gene and expression in Escherichia coli
  JOURNAL   J. Biol. Chem. 264 (12), 6629-6637 (1989)
   PUBMED   2708328
COMMENT     Original source text: Synthetic DNA.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by N.Habuka, 16-FEB-1989, for release after publication.
FEATURES             Location/Qualifiers
     source          1. .765
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     CDS             1. .756
                     /note="Mirabilis antiviral protein"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA72213.1"
                     /db_xref="GI:208833"
                     /translation="MAPTLETIASLDLNNPTTYLSFITNIRTKVADKTEQCTIQKISK
                     TFTQRYSYIDLIVSSTQKITLAIDMADLYVLGYSDIANNKGRAPFFKDVTEAVANNFF
                     PGATGTNRIKLTFTGSYGDLEKNGGLRKDNPLGIFRLENSIVNIYGKAGDVKKQAKFF
                     LLAIQMVSEAARFKYISDKIPSEKYEEVTVDEYMTALENNWAKLSTAVYNSKPSTTTA
                     TKCQLATSPVTISPWIFKTVEEIKLVMGLLKSS"
ORIGIN

Alignment Scores:
Pred. No.:              8.29e-15      Length:         765
Score:                  221.50        Matches:        54
Percent Similarity:     55.9%         Conservative:   27
Best Local Similarity:  37.2%         Mismatches:     55
Query Match:            28.8%         Indels:         9
DB:                     11            Gaps:           4

US-10-758-902-9 (1-149) x SYNMIJAVP (1-765)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||               |||   :::||||||   ::::::|||   :::
Db         28 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 87

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||      |||      |||           |||:::|||   |||:::
Db         88 GTCGCAGACAAAACCGAACAGTGT-----------ACCATCCAGAAAATCTCTAAAACC 135

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                  :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        136 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 195

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||:::   |||:::||||||:::||||||   |||      :::   |||
Db        196 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 255

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
              ||||||   |||         |||                :::      |||||||||
Db        256 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 315

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||      |||

Db        316 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 375

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                  :::   ||||||||        ||||||::::::::::||||||   ||||||
Db        376 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 432

Qy        141 AlaIleTrpGlyLys 145
                  |||:::||||||
Db        433 AACATTTATGGCAAA 447

RESULT 9
MJLATVP
LOCUS       MJLATVP                 1015 bp    DNA     linear   PLN 14-APR-2000
DEFINITION  M.jalapa gene for antiviral protein.
ACCESSION   D10569
VERSION     D10569.1  GI:217953
KEYWORDS    antiviral protein.
SOURCE      Mirabilis jalapa (garden four-o'clock)
  ORGANISM  Mirabilis jalapa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Mirabilis.
REFERENCE   1  (bases 1 to 1015)
  AUTHORS   Kataoka,J., Miyano,M., Habuka,N., Masuta,C. and Koiwai,A.
  TITLE     A genomic gene for MAP, a ribosome-inactivating protein from
            Mirabilis jalapa, contains an intron
  JOURNAL   Nucleic Acids Res. 21 (4), 1035 (1993)
   PUBMED   8451171
REFERENCE   2  (bases 1 to 1015)
  AUTHORS   Kataoka,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1992) Jiro Kataoka, Japan Tabacco Inc., Life
            Science Research Laboratory; 6-2 Umegaoka, Midori-ku, Yokohama,
            Kanagawa 227, Japan (Tel:045-972-5901, Fax:045-972-6205)
COMMENT     Submitted (24-FEB-1992) to DDBJ by:
            Jiro Kataoka
            Life Science Research Laboratory
            Japan Tobacco Inc.
            6-2 Umegaoka
            Midori-ku, Yokohama
            Kanagawa, 227
            Japan
            Phone:  81-45-972-5901
            Fax:    81-45-972-620.
FEATURES             Location/Qualifiers
     source          1. .1015
                     /organism="Mirabilis jalapa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3538"
     CDS             join(1. .618,781. .999)
                     /codon_start=1
                     /product="antiviral protein"
                     /protein_id="BAA01425.1"
                     /db_xref="GI:217954"
                     /translation="MLTTTKVFFLLLTTWITWYAIVNPQSRAAPTLETIASLDLNNPT
                     TYLSFITNIRTKVADKTEQCTIQKISKTFTQRYSYIDLIVSSTQKITLAIDMADLYVL
                     GYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKNGGLRKDNP
                     LGIFRLENSIVNIYGKAGDVKKQAKFFLLAIQMVSEAARFKYISDKIPSEKYEEVTVD
                     EYMTALENNWAKLSTAVYNSKPSTTTATKCQLATSPVTISPWIFKTVEEIKLVMGLLK
                     SS"
     exon            <1. .618
                     /number=1
     intron          619. .780
                     /number=1
     exon            781. .>1015
                     /number=2
ORIGIN

Alignment Scores:
Pred. No.:              1.14e-14      Length:         1015
Score:                  221.50        Matches:        54
Percent Similarity:     55.9%         Conservative:   27
Best Local Similarity:  37.2%         Mismatches:     55
```

```
Query Match:            28.8%       Indels:        9
DB:                     15          Gaps:          4

US-10-758-902-9 (1-149) x MJLATVP (1-1015)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||                |||   :::||||||   :::::::|||   :::
Db        109 TCTTTGGACCTAAATAATCCCACCACATATCTATCATTTATCACAAATATAAGAACAAAA 168

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||     |||     |||          |||:::|||   |||:::
Db        169 GTTGCTGATAAAACCGAGCAATGT-----------ACAATTCAGAAAATAAGCAAAACA 216

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                    :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        217 TTTACTCAAAGATATTCATACATCGACTTGATAGTCTCAAGCACTCAAAAGATTACATTA 276

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||:::   |||:::||||||:::||||||   |||      :::   |||
Db        277 GCAATAGATATGGCTGATCTGTATGTGCTTGGATATAGCGATATAGCGAATAACAAAGGG 336

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              ||||||   |||      |||                :::      |||||||||
Db        337 CGTGCTTTCTTCTTTAAAGATGTCACCGAGGCAGTCGCAAACAACTTTTTCCCTGGTGCA 396

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||      |||
Db        397 ACCGGAACTAATCGAATTAAGTTAACATTCACAGGAAGTTATGGTGACCTTGAAAAAAAT 456

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                   :::   |||||||||      ||||||:::::::::||||||   ||||||
Db        457 GGTGGTTTA---CGAAAAGATAATCCATTAGGAATATTCAGACTGGAGAATAGCATAGTT 513

Qy        141 AlaIleTrpGlyLys 145
              |||:::|||||||
Db        514 AACATATATGGTAAA 528

RESULT 10
AR003723
LOCUS       AR003723                913 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 13 from patent US 5744580.
ACCESSION   AR003723
VERSION     AR003723.1  GI:3964982
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 5744580-A 13 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:          1.31e-14       Length:        913
Score:              220.50         Matches:       52
Percent Similarity: 59.9%          Conservative:  33
Best Local Similarity: 36.6%       Mismatches:    50
Query Match:        28.7%          Indels:        7
DB:                 6              Gaps:          3

US-10-758-902-9 (1-149) x AR003723 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||            |||      |||      |||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::               :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                       |||:::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 11
AR010059
LOCUS       AR010059                913 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 13 from patent US 5756699.
ACCESSION   AR010059
VERSION     AR010059.1  GI:3968864
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 5756699-A 13 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:          1.31e-14       Length:        913
Score:              220.50         Matches:       52
Percent Similarity: 59.9%          Conservative:  33
Best Local Similarity: 36.6%       Mismatches:    50
Query Match:        28.7%          Indels:        7
DB:                 6              Gaps:          3

US-10-758-902-9 (1-149) x AR010059 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||            |||      |||      |||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::               :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
```

```
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
Db        487 TTGTTT 492

RESULT 12
AR055265
LOCUS       AR055265                913 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 13 from patent US 5837491.
ACCESSION   AR055265
VERSION     AR055265.1  GI:5980842
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Polynucleotides encoding gelonin sequences
  JOURNAL   Patent: US 5837491-A 13 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.31e-14        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     6               Gaps:           3

US-10-758-902-9 (1-149) x AR055265 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
Db        487 TTGTTT 492

RESULT 13
AR141194
LOCUS       AR141194                913 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 13 from patent US 6146631.
ACCESSION   AR141194
VERSION     AR141194.1  GI:15100711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 6146631-A 13 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.31e-14        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     6               Gaps:           3

US-10-758-902-9 (1-149) x AR141194 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
Db        487 TTGTTT 492

RESULT 14
AR141431
LOCUS       AR141431                913 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 13 from patent US 6146850.
ACCESSION   AR141431
VERSION     AR141431.1  GI:15100947
KEYWORDS    .
```

```
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Better,M.D. and Carroll,S.F.
  TITLE     Proteins encoding gelonin sequences
  JOURNAL   Patent: US 6146850-A 13 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                 1.31e-14       Length:          913
Score:                     220.50         Matches:         52
Percent Similarity:        59.9%          Conservative:    33
Best Local Similarity:     36.6%          Mismatches:      50
Query Match:               28.7%          Indels:          7
DB:                        6              Gaps:            3

US-10-758-902-9 (1-149) x AR141431 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||           |||       |||       ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||               |||      :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::::||||||:::       |||       :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 15
I11903
LOCUS       I11903                  913 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 13 from Patent US 5416202.
ACCESSION   I11903
VERSION     I11903.1  GI:909346
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Bernhard,S.L., Better,M.D., Carroll,S.F., Lane,J.A. and Lei,S.-P.
  TITLE     Materials comprising and methods of preparation and use for
            ribosome-inactivating proteins
  JOURNAL   Patent: US 5416202-A 13 16-MAY-1995;
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                 1.31e-14       Length:          913
Score:                     220.50         Matches:         52
Percent Similarity:        59.9%          Conservative:    33
Best Local Similarity:     36.6%          Mismatches:      50
Query Match:               28.7%          Indels:          7
DB:                        6              Gaps:            3

US-10-758-902-9 (1-149) x I11903 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||           |||       |||       ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||               |||      :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::::||||||:::       |||       :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 16
I40476
LOCUS       I40476                  913 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 13 from patent US 5621083.
ACCESSION   I40476
VERSION     I40476.1  GI:2082768
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 5621083-A 13 15-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                 1.31e-14       Length:          913
Score:                     220.50         Matches:         52
Percent Similarity:        59.9%          Conservative:    33
Best Local Similarity:     36.6%          Mismatches:      50
Query Match:               28.7%          Indels:          7
DB:                        6              Gaps:            3
```

```
US-10-758-902-9 (1-149) x I40476 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||         |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||     |||           |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              |||||||||||||||:::||||||||||||   |||:::                 :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||::::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 17
AR367960
LOCUS       AR367960                913 bp    mRNA    linear   PAT 12-SEP-2003
DEFINITION  Sequence 13 from patent US 6376217.
ACCESSION   AR367960
VERSION     AR367960.1  GI:34601471
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Better,M.D. and Carroll,S.F.
  TITLE     Fusion proteins and polynucleotides encoding gelonin sequences
  JOURNAL   Patent: US 6376217-A 13 23-APR-2002;
            Xoma Technology Ltd.;;
            BMX;
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.31e-14      Length:         913
Score:                  220.50        Matches:        52
Percent Similarity:     59.9%         Conservative:   33
Best Local Similarity:  36.6%         Mismatches:     50
Query Match:            28.7%         Indels:         7
DB:                     6             Gaps:           3

US-10-758-902-9 (1-149) x AR367960 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||         |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||     |||           |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              |||||||||||||||:::||||||||||||   |||:::                 :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||::::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 18
AR430941
LOCUS       AR430941                913 bp    mRNA    linear   PAT 18-DEC-2003
DEFINITION  Sequence 13 from patent US 6649742.
ACCESSION   AR430941
VERSION     AR430941.1  GI:40192772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 6649742-A 13 18-NOV-2003;
            XOMA Technology Ltd.;;
            BEX;
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.31e-14      Length:         913
Score:                  220.50        Matches:        52
Percent Similarity:     59.9%         Conservative:   33
Best Local Similarity:  36.6%         Mismatches:     50
Query Match:            28.7%         Indels:         7
DB:                     6             Gaps:           3

US-10-758-902-9 (1-149) x AR430941 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||         |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||     |||           |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              |||||||||||||||:::||||||||||||   |||:::                 :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309
```

```
Qy          82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
               |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db         310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy         102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  |||   :::::|||||   :::   |||:::|||:::   |||       ||||||
Db         370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                     |||:::::::::::|||||:::       |||       :::|||
Db         427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy         142 IleTrp 143
               ::::::
Db         487 TTGTTT 492
```

```
RESULT 19
MBMOMORII
LOCUS       MBMOMORII                914 bp    DNA     linear   PLN 18-APR-2005
DEFINITION  M.balsamina mRNA for momordin II.
ACCESSION   Z12175
VERSION     Z12175.1  GI:19525
KEYWORDS    momordin II.
SOURCE      Momordica balsamina (balsam apple)
  ORGANISM  Momordica balsamina
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Ortigao,M. and Better,M.
  TITLE     Momordin II, a ribosome inactivating protein from Momordica
            balsamina, is homologous to other plant proteins
  JOURNAL   Nucleic Acids Res. 20 (17), 4662 (1992)
   PUBMED   1408771
REFERENCE   2  (bases 1 to 914)
  AUTHORS   Ortigao,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAY-1992) Marcelo Ortigao, Molecular Genetics, Xoma
            Corporation, 1545 17th., street, Santa Monica, CA, 90404, USA
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Momordica balsamina"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3672"
     CDS             10. .870
                     /codon_start=1
                     /product="momordin II"
                     /protein_id="CAA78166.1"
                     /db_xref="GI:19526"
                     /db_xref="GOA:P29339"
                     /db_xref="InterPro:IPR001574"
                     /db_xref="UniProt/Swiss-Prot:P29339"
                     /translation="MVKCLLLSFLIIAIFIGVPTAKGDVNFDLSTATAKTYTKFIEDF
                     RATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETISVAIDVTNVYVVAYRTRDV
                     SYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIRENIDLGLPALSSAITTL
                     FYYNAQSAPSALLVLIQTTAEAARFKYIERHVAKYVATNFKPNLAIISLENQWSALSK
                     QIFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSDVVKGNIKLLLNSRASTADENFITT
                     MTLLGESVVN"
     mat_peptide     79. .867
                     /product="momordin II"
ORIGIN

Alignment Scores:
Pred. No.:              1.31e-14        Length:         914
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     15              Gaps:           3

US-10-758-902-9 (1-149) x MBMOMORII (1-914)

Qy           4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
```

```
                |||:::|||:::|||            |||       |||      ||||||:::|||
Db          82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy          22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
               |||       |||             |||      :::|||:::          ||||||
Db         142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy          42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
               :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db         202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy          62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
               ||||||||||||||||||:::||||||||||||   |||:::                :::
Db         262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC------------CGC 309

Qy          82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
               |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db         310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy         102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  |||   :::::|||||   :::   |||:::|||:::   |||       ||||||
Db         370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                     |||:::::::::::|||||:::       |||       :::|||
Db         427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy         142 IleTrp 143
               ::::::
Db         487 TTGTTT 492
```

```
RESULT 20
E02815
LOCUS       E02815                   756 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence coding for Mirabilis antiviral protein.
ACCESSION   E02815
VERSION     E02815.1  GI:2171043
KEYWORDS    JP 1991076580-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   Habuka,N., Akiyama,K., Tsushimo,H., Matsumoto,T. and Noma,M.
  TITLE     ESCHERICHIA COLI MANIFESTATION VECTOR AND PRODUCTION OF ANTIVIRAL
            PROTEIN USING THE SAME
  JOURNAL   Patent: JP 1991076580-A 2 02-APR-1991;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            OS   Mirabilis jalapa (Four O'clock)
            PN   JP 1991076580-A/2
            PD   02-APR-1991
            PF   17-AUG-1989 JP 1989210767
            PI   HABUKA NORIYUKI, AKIYAMA KIYOTAKA, TSUSHIMO HIDEAKI, PI
            MATSUMOTO TAKASHI,
            PI   NOMA MASAKATA
            PC   C12N15/29,C12M1/21,C12N15/73,C12P21/02,(C12P21/02,C12R1:19);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: library=pMHI;
            FH   Key             Location/Qualifiers
            FH
            FT   CDS             >1. .756
            FT                   /product='Mirabilis antiviral protein'.
FEATURES             Location/Qualifiers
     source          1. .756
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN
```

```
Alignment Scores:
Pred. No.:              1.35e-14        Length:         756
Score:                  219.50          Matches:        54
Percent Similarity:     55.2%           Conservative:   26
Best Local Similarity:  37.2%           Mismatches:     56
Query Match:            28.6%           Indels:         9
DB:                     6               Gaps:           4

US-10-758-902-9 (1-149) x E02815 (1-756)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||                |||      ||||||   ::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTGTTTCATAACGAATATCCGTACGAAA 84

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||      |||      |||            |||:::|||   |||:::
Db         85 GTCGCAGACAAAACCGAACAGTGT-----------ACCATCCAGAAAATCTCTAAAACC 132

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                  :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||||:::   |||:::||||||:::||||||   |||      :::    |||
Db        193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
              ||||||   |||         |||                 :::      |||||||||
Db        253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||      |||
Db        313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              :::   |||||||||      ||||||:::::::::||||||   ||||||
Db        373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429

Qy        141 AlaIleTrpGlyLys 145
                 |||:::||||||
Db        430 AACATTTATGGCAAA 444

RESULT 21
MCH294541
LOCUS       MCH294541               795 bp    DNA     linear   PLN 11-SEP-2000
DEFINITION  Momordica charantia partial RIP gene for ribosome inactivating
            protein, type I.
ACCESSION   AJ294541
VERSION     AJ294541.1  GI:10129817
KEYWORDS    ribosome inactivating protein; RIP; RIP gene; type I.
SOURCE      Momordica charantia (balsam pear)
  ORGANISM  Momordica charantia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
REFERENCE   1
  AUTHORS   Nguyen Huy,H., Nghiem Ngoc,M., Dao Huy,P., Le Tran,B. and Nong
            Van,H.
  TITLE     Expression of a RIP gene from Momordica charantia in E. coli
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 795)
  AUTHORS   Nong Van,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2000) Nong Van H., Applied DNA Technology Lab,
            Institute of Biotechnology (IBT), NCST, Hoang Quoc Viet Rd.,
            Nghiado, Caugiay, Hanoi 10,000, VIET NAM
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Momordica charantia"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3673"
     gene            1. .792
                     /gene="RIP"
     CDS             <1. .>792
                     /gene="RIP"
                     /function="unknown"
                     /codon_start=1
                     /evidence=experimental
                     /product="ribosome inactivating protein, RIP, type I"
                     /protein_id="CAC08217.1"
                     /db_xref="GI:10129818"
                     /db_xref="GOA:Q9FSH2"
                     /db_xref="UniProt/TrEMBL:Q9FSH2"
                     /translation="MDVNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD
                     SRRFILLNLTSYAYETISVAIDVTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKI
                     TLPYTGNYENLQTAAHKIRENIELGLPALSSAITTLFYYNAQSAPSALLVLIQTTAEA
                     ARFKYIERHVAKYVATNFKPNLAIISLENQWSALSKQIFLAQNQGAKFRNPVDLIKPT
                     GERFQVTNVDSDVVKGNIKLLLNSRASTADENFITTMTLLGESVVN"
     mat_peptide     <4. .>792
                     /gene="RIP"
                     /product="ribosome inactivating protein, RIP. type I"
                     /evidence=experimental
ORIGIN

Alignment Scores:
Pred. No.:              1.85e-14        Length:         795
Score:                  218.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.5%           Indels:         7
DB:                     15              Gaps:           3

US-10-758-902-9 (1-149) x MCH294541 (1-795)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||            |||      |||      ||||||:::|||
Db          7 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 66

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::         ||||||
Db         67 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 126

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::::::::|||:::   :::   :::|||:::
Db        127 TCCGACTCCAGACGTTTCATACTCCTCAATCTCACAAGTTATGCATATGAAACCATCTCG 186

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||:::||||||||||   |||:::          :::
Db        187 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCCTATCGCACC-----------CGC 234

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        235 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 294

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        295 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 351

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                   |||:::::::::||||||||:::      |||      :::|||
Db        352 CACAAAATAAGAGAGAATATTGAGCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 411

Qy        142 IleTrp 143
              ::::::
Db        412 TTGTTT 417

RESULT 22
MJLMAP
LOCUS       MJLMAP                  1066 bp    mRNA    linear   PLN 01-FEB-2000
DEFINITION  M. jalapa L. mRNA for Mirabilis antiviral protein (MAP), complete
            cds.
ACCESSION   D10227 D90347
VERSION     D10227.1  GI:217955
KEYWORDS    RNA N-glycosidase activity; antiviral protein;
            ribosome-inactivating protein.
SOURCE      Mirabilis jalapa (garden four-o'clock)
```

```
  ORGANISM  Mirabilis jalapa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Mirabilis.
REFERENCE   1  (bases 1 to 1066)
  AUTHORS   Kataoka,J., Habuka,N., Furuno,M., Miyano,M., Takanami,Y. and
            Koiwai,A.
  TITLE     DNA sequence of Mirabilis antiviral protein (MAP), a
            ribosome-inactivating protein with an antiviral property, from
            mirabilis jalapa L. and its expression in Escherichia coli
  JOURNAL   J. Biol. Chem. 266 (13), 8426-8430 (1991)
   PUBMED   2022657
REFERENCE   2  (bases 1 to 1066)
  AUTHORS   Kataoka,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAR-1991) Jiro Kataoka, Japan Tabacco Inc., Life
            Science Research Laboratory; 6-2 Umegaoka, Midori-ku, Yokohama,
            Kanagawa 227, Japan (Tel:045-972-5901, Fax:045-972-6205)
COMMENT     Submitted (06-Mar-1991) to DDBJ by:
            Jiro Kataoka
            Life Science Research Laboratory
            Japan Tabcco Inc.
            6-2 Umegaoka, Midori-ku
            Yokohama, Kanagawa 227
            Japan
            Phone:  045-972-5901
            Fax:    045-972-6205.
FEATURES             Location/Qualifiers
     source          1. .1066
                     /organism="Mirabilis jalapa"
                     /mol_type="mRNA"
                     /db_xref="taxon:3538"
                     /tissue_type="root"
     gene            1. .1066
                     /gene="MAP"
     CDS             50. .886
                     /gene="MAP"
                     /codon_start=1
                     /evidence=experimental
                     /product="MAP precursor"
                     /protein_id="BAA01079.1"
                     /db_xref="GI:217956"
                     /translation="MLTTTKVFFLLLTTWITWYAIVNPQSRAAPTLETLASLDLNNPT
                     TYLSFITNIRTKVVDKTEQCTIQKISKTFTQRYSYIDLIVSSTQKITLAIDMADLYVL
                     GYSDIANNKGRAFFPKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKNGGLRKDNP
                     LGIFRLENSIVNIYGKAGDCKKQAKFFLLAIQMVSEAARFKYISDKIPSEKYEEVTVG
                     EYMTALENNWAKLSTAVYNSKPSTTTATKCQLATSPVTISPWIFKTVEEIKLVMGLLK
                     SS"
     sig_peptide     50. .133
                     /gene="MAP"
     mat_peptide     134. .883
                     /gene="MAP"
                     /product="MAP mature peptide"
     polyA_signal    954. .959
                     /gene="MAP"
     stem_loop       966. .1014
                     /gene="MAP"
     repeat_region   1015. .1047
                     /rpt_type=tandem
                     /rpt_unit="1015. .1020"
                     /rpt_unit="1021. .1027"
                     /rpt_unit="1028. .1034"
                     /rpt_unit="1035. .1041"
                     /rpt_unit="1042. .1047"
     polyA_signal    1050. .1055
                     /gene="MAP"
ORIGIN

Alignment Scores:
Pred. No.:              3.32e-14        Length:         1066
Score:                  217.50          Matches:        53
Percent Similarity:     55.2%           Conservative:   27
Best Local Similarity:  36.6%           Mismatches:     56

Query Match:            28.3%           Indels:         9
DB:                     15              Gaps:           4

US-10-758-902-9 (1-149) x MJLMAP (1-1066)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||           |||   :::||||||   :::::::|||   :::
Db        158 TCTTTGGACCTAAATAATCCCACCACATATCTATCATTTATCACAAATATAAGAACAAAA 217

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::         |||      |||            |||:::|||   |||:::
Db        218 GTTGTTGATAAAACCGAGCAATGT-----------ACAATTCAGAAAATAAGCAAAACA 265

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                 :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        266 TTTACTCAAAGATATTCATATATCGACTTGATAGTCTCAAGCACTCAAAAGATTACATTA 325

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||||:::   |||:::||||||:::||||||   |||      :::   |||
Db        326 GCAATAGATATGGCTGATCTGTATGTGCTTGGATATAGCGATATAGCGAATAACAAAGGG 385

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              ||||||   |||          |||                 :::      |||||||||
Db        386 CGTGCTTTCTTCTTTAAAGATGTCACCGAGGCAGTCGCAAACAACTTTTTCCCTGGTGCA 445

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||      |||
Db        446 ACCGGAACTAATCGAATTAAGTTAACATTCACAGGAAGTTATGGTGACCTTGAAAAAAAT 505

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                 :::   |||||||||      ||||||:::::::::||||||   ||||||
Db        506 GGTGGTTTA---CGAAAAGATAATCCATTAGGAATATTCAGACTGGAGAATAGCATAGTT 562

Qy        141 AlaIleTrpGlyLys 145
                 |||:::||||||
Db        563 AACATATATGGTAAA 577

RESULT 23
AY523412
LOCUS       AY523412                795 bp    mRNA    linear   PLN 15-FEB-2004
DEFINITION  Momordica charantia Rip (rip) mRNA, complete cds.
ACCESSION   AY523412
VERSION     AY523412.1  GI:42491749
KEYWORDS    .
SOURCE      Momordica charantia (balsam pear)
  ORGANISM  Momordica charantia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   Wei,Y.-F., Cai,L.-B. and Zhuang,W.
  TITLE     Cloning rip gene and identification of its resistance to
            Aspergillus flavus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 795)
  AUTHORS   Zhuang,W. and Wei,Y.-F.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-2004) College of Crop Sciences, Fujian
            Agriculture and Forestry University, Fuzhou, Fujian 350002, China
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Momordica charantia"
                     /mol_type="mRNA"
                     /db_xref="taxon:3673"
     gene            1. .795
                     /gene="rip"
     CDS             1. .795
                     /gene="rip"
                     /note="type I"
                     /codon_start=1
                     /product="Rip"
                     /protein_id="AAS17014.1"
                     /db_xref="GI:42491750"
```

```
                     /translation="MDVNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD
                     SRRFILLNLTSYAYETISVAIDVTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKI
                     TLPYTGNYENLQTAAHKIRENIDLGLPALSSAITTLFYYNAQSAPSALLVLIQTTAEA
                     ARFKYIERHVAKYVATNFKPNLAIISLENQWSALSKQIFLAQNQGGKFRNPVDLIKPT
                     GERFQVTNVDSDVVKGNIKLLLNSRASTADENFITTMTLLGESVVN"
ORIGIN

Alignment Scores:
Pred. No.:              3.94e-14        Length:         795
Score:                  215.50          Matches:        51
Percent Similarity:     59.9%           Conservative:   34
Best Local Similarity:  35.9%           Mismatches:     50
Query Match:            28.1%           Indels:         7
DB:                     15              Gaps:           3

US-10-758-902-9 (1-149) x AY523412 (1-795)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||            |||      |||      ||||||:::|||
Db          7 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 66

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::         ||||||
Db         67 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 126

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::::::::|||:::   :::   :::|||:::
Db        127 TCCGACTCCAGACGTTTCATACTCCTCAATCTCACAAGTTATGCATATGAAACCATCTCG 186

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||:::||||||||||||   |||:::                :::
Db        187 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCCTATCGCACC-----------CGC 234

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        235 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 294

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        295 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 351

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                   |||::::::::::::||||||:::      |||      :::|||
Db        352 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 411

Qy        142 IleTrp 143
              ::::::
Db        412 TTGTTT 417

RESULT 24
AJ748278
LOCUS       AJ748278                795 bp    DNA     linear   PLN 27-AUG-2004
DEFINITION  Momordica charantia partial rip gene for type I ribosome
            inactivating protein precursor, variant allele.
ACCESSION   AJ748278
VERSION     AJ748278.1  GI:51587347
KEYWORDS    rip gene; rRNA N-glycosylase; type I ribosome inactivating protein.
SOURCE      Momordica charantia (balsam pear)
  ORGANISM  Momordica charantia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
REFERENCE   1
  AUTHORS   Nguyen Dinh,C., Nguyen Thuy,D., Le Thi Thu,H., Nguyen Huy,H., Tran
            Thi Phuong,L. and Nong Van,H.
  TITLE     Expression of a gene encoding ribosome inactivating protein from
            bitter melon (Momordica charantia)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 795)
  AUTHORS   Nong,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUN-2004) Nong V., Applied DNA Technology Laboratory,
            Institute of Biotechnology (IBT), VAST, 18 Hoang Quoc Viet Rd.,
            Hanoi, 10000, VIET NAM
COMMENT     Related sequence:AJ294541.
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Momordica charantia"
                     /mol_type="genomic DNA"
                     /isolate="HN1"
                     /db_xref="taxon:3673"
                     /clone="2"
                     /country="Viet Nam:Hanoi"
     gene            1. .795
                     /gene="rip"
     CDS             <1. .795
                     /gene="rip"
                     /codon_start=1
                     /allele="rip variant"
                     /product="type I ribosome inactivating protein precursor"
                     /protein_id="CAH19208.1"
                     /db_xref="GI:51587348"
                     /translation="MDVNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD
                     SRRFILLNLTSYAYETISVAIDVTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKI
                     TLPYTGNYENLQTAAHKIRENIDLGLPALSSAITTLFYYNAQSAPSALLVLIQTTAEA
                     ARFKYIERHVAKYVATNFKPNLAIISLENQWSALSKQIFLAQNQGGKFRNPVDLIKPT
                     GERFQVTNVDSDVVKGNIKLLLNSRASTADENFITTMTLRGESVVN"
     sig_peptide     <1. .3
                     /gene="rip"
     mat_peptide     4. .792
                     /gene="rip"
                     /product="type I ribosome inactivating protein"
                     /EC_number="3.2.2.22"
                     /function="ribosome inactivation"
     variation       375
                     /gene="rip"
                     /citation=[1]
                     /replace="g"
     variation       438
                     /gene="rip"
                     /citation=[1]
                     /replace="g"
     variation       617
                     /gene="rip"
                     /citation=[1]
                     /replace="c"
ORIGIN

Alignment Scores:
Pred. No.:              3.94e-14        Length:         795
Score:                  215.50          Matches:        51
Percent Similarity:     59.9%           Conservative:   34
Best Local Similarity:  35.9%           Mismatches:     50
Query Match:            28.1%           Indels:         7
DB:                     15              Gaps:           3

US-10-758-902-9 (1-149) x AJ748278 (1-795)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||            |||      |||      ||||||:::|||
Db          7 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 66

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::         ||||||
Db         67 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 126

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::::::::|||:::   :::   :::|||:::
Db        127 TCCGACTCCAGACGTTTCATACTCCTCAATCTCACAAGTTATGCATATGAAACCATCTCG 186

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||:::||||||||||||   |||:::                :::
Db        187 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCCTATCGCACC-----------CGC 234

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
```

```
Db        235 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 294

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db        295 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 351

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||::::::::::::|||||:::       |||       :::|||
Db        352 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 411

Qy        142 IleTrp 143
                 ::::::
Db        412 TTGTTT 417

RESULT 25
AY817142
LOCUS       AY817142                 861 bp    DNA     linear   PLN 29-NOV-2004
DEFINITION  Momordica charantia ribosomal inactivating protein gene, complete
            cds.
ACCESSION   AY817142
VERSION     AY817142.1  GI:55977577
KEYWORDS    .
SOURCE      Momordica charantia (Thai bitter melon)
  ORGANISM  Momordica charantia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Leelamanit,W. and Watthanachaiyingcharoen,R.
  TITLE     Genetic variation of type I ribosomal inactivating protein from
            Momordica species: sequence comparison with related proteins
  JOURNAL   Warasan Phesatchasat 27, 27-39 (2000)
REFERENCE   2  (bases 1 to 861)
  AUTHORS   Leelamanit,W., Boonchoy,C., Luetrakul,T., Prapaitrakul,S.,
            Tanaka,H. and Shoyama,Y.
  TITLE     A novel Thai bitter melon protein possesses potent anti-tumor and
            anti-HSV activities
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 861)
  AUTHORS   Leelamanit,W. and Boonchoy,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-2004) Biochemistry, Mahidol University, 447
            Sri-Ayudhaya Rd., Bangkok 10400, Thailand
FEATURES             Location/Qualifiers
     source          1. .861
                     /organism="Momordica charantia"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3673"
                     /note="common: Thai bitter melon"
     mRNA            <1. .>861
                     /product="ribosomal inactivating protein"
     CDS             1. .861
                     /note="glycosidase; TBMP-II"
                     /codon_start=1
                     /product="ribosomal inactivating protein"
                     /protein_id="AAV68558.1"
                     /db_xref="GI:55977578"
                     /translation="MVKCLLLSFLIIAIFIGVPTAKGDVNFDLSTATAKTYTKFIEDF
                     RATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETISVAIDVTNVYVVAYRTRDV
                     SYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIRENIDLGLPALSSAITTL
                     FYYNAQSAPSALLVLIQTTAEAARFKYIERHVAKYVATNFKPNLAIISLENQWSALSK
                     QIFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSDVVKGNIKLLLNSRASTADENFITT
                     MTLLGESVVN"
ORIGIN

Alignment Scores:
Pred. No.:              4.31e-14       Length:        861
Score:                  215.50         Matches:       51
Percent Similarity:     59.9%          Conservative:  34
Best Local Similarity:  35.9%          Mismatches:    50
Query Match:            28.1%          Indels:        7
DB:                     15             Gaps:          3
```

```
US-10-758-902-9 (1-149) x AY817142 (1-861)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||          |||       |||       ||||||:::|||
Db         73 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 132

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||             |||       :::|||:::         ||||||
Db        133 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 192

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::::::::|||:::   :::   :::|||:::
Db        193 TCCGACTCCAGACGTTTCATACTCCTCAATCTCACAAGTTATGCATATGAAACCATCTCG 252

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                :::
Db        253 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCCTATCGCACC------------CGC 300

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db        301 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 360

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db        361 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 417

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||::::::::::::|||||:::       |||       :::|||
Db        418 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 477

Qy        142 IleTrp 143
                 ::::::
Db        478 TTGTTT 483

RESULT 26
AF284811
LOCUS       AF284811                 861 bp    DNA     linear   PLN 08-MAY-2001
DEFINITION  Momordica charantia MAP30I gene, complete cds.
ACCESSION   AF284811
VERSION     AF284811.1  GI:11225517
KEYWORDS    .
SOURCE      Momordica charantia (balsam pear)
  ORGANISM  Momordica charantia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Quanhong,Y., Rihe,P. and Aisheng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2000) Agrobiotech Research Center, Shanghai
            Academy of Agricultural Sciences, Beidi Road 2901#, Shanghai
            201106, China
FEATURES             Location/Qualifiers
     source          1. .861
                     /organism="Momordica charantia"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3673"
                     /country="China: Shanghai"
     CDS             1. .861
                     /codon_start=1
                     /product="MAP30I"
                     /protein_id="AAG33028.1"
                     /db_xref="GI:11225518"
                     /translation="MVKCLLLSFLIIAIFIGVPTAKGDVNFDLSTATAKTYTKFIEDF
                     RATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETISVAIDVTNVYVVAYRTRDV
                     SYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIRENIDLGLPALSSAITTL
                     FYYNAQSAPSALLVLIQTTAEAARFKYIERHVAKYVATNFKPNLAIISLENQWSALSK
                     QIFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSDVVKGNIKLLLNSRASTADENFITT
                     MTLLGESVVN"
ORIGIN

Alignment Scores:
Pred. No.:              4.31e-14       Length:        861
```

```
Score:                 215.50        Matches:       51
Percent Similarity:    59.9%         Conservative:  34
Best Local Similarity: 35.9%         Mismatches:    50
Query Match:           28.1%         Indels:        7
DB:                    15            Gaps:          3

US-10-758-902-9 (1-149) x AF284811 (1-861)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||         |||      |||      ||||||:::|||
Db         73 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 132

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              |||      :::|||:::         ||||||
Db        133 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 192

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::::::::|||:::   :::   :::|||:::
Db        193 TCGGACTCCAGACGTTTCATACTCCTCAATCTCACAAGTTATGCATATGAAACCATCTCG 252

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||:::||||||||||||   |||:::               :::
Db        253 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCCTATCGCACC-----------CGC 300

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        301 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 360

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        361 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 417

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||::::::::::::|||||:::      |||      :::|||
Db        418 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 477

Qy        142 IleTrp 143
              ::::::
Db        478 TTGTTT 483

RESULT 27
S79450
LOCUS       S79450                   919 bp    DNA     linear   PLN 04-MAY-2000
DEFINITION  Map30=anti-HIV protein/anti-tumor protein [Momordica
            charantia=bitter melons, leaves, Genomic, 919 nt].
ACCESSION   S79450
VERSION     S79450.1  GI:1110596
KEYWORDS    .
SOURCE      Momordica charantia (balsam pear)
  ORGANISM  Momordica charantia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   Lee-Huang,S., Huang,P.L., Chen,H.C., Huang,P.L., Bourinbaiar,A.,
            Huang,H.I. and Kung,H.F.
  TITLE     Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter
            melon
  JOURNAL   Gene 161 (2), 151-156 (1995)
   PUBMED   7665070
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 170698] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .919
                     /organism="Momordica charantia"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3673"
                     /tissue_type="leaves"
     gene            12. .872
                     /gene="Map30"
                     /note="MAP30"
     CDS             12. .872
                     /gene="Map30"
                     /note="anti-HIV protein/anti-tumor protein; conceptual
                     translation presented here differs from translation in
                     publication; mismatches(14[T->Y],165[I->T])"
                     /codon_start=1
                     /product="MAP30"
                     /protein_id="AAB35194.2"
                     /db_xref="GI:7706789"
                     /translation="MVKCLLLSFLIIAIFIGVPTAKGDVNFDLSTATAKTYTKFIEDF
                     RATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETISVAIDVTNVYVVAYRTRDV
                     SYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIRENIDLGLPALSSAITTL
                     FYYNAQSAPSALLVLIQTTAEAARFKYTERHVAKYVATNFKPNLAIISLENQWSALSK
                     QIFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSDVVKGNIKLLLNSRASTADENFITT
                     MTLLGESVVN"
ORIGIN

Alignment Scores:
Pred. No.:             4.64e-14      Length:        919
Score:                 215.50        Matches:       51
Percent Similarity:    59.9%         Conservative:  34
Best Local Similarity: 35.9%         Mismatches:    50
Query Match:           28.1%         Indels:        7
DB:                    15            Gaps:          3

US-10-758-902-9 (1-149) x S79450 (1-919)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||         |||      |||      ||||||:::|||
Db         84 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 143

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              |||      :::|||:::         ||||||
Db        144 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTGCTGTATTCCACTATT 203

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::::::::|||:::   :::   :::|||:::
Db        204 TCCGACTCCAGACGTTTCATACTCCTCAATCTCACAAGTTATGCATATGAAACCATCTCG 263

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||:::||||||||||||   |||:::               :::
Db        264 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCCTATCGCACC-----------CGC 311

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        312 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 371

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        372 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTCCAAACTGCTGCA 428

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||::::::::::::|||||:::      |||      :::|||
Db        429 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 488

Qy        142 IleTrp 143
              ::::::
Db        489 TTGTTT 494

RESULT 28
E03954
LOCUS       E03954                   762 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA encoding recombinant Mirabilis Antiviral Protein (MAP).
ACCESSION   E03954
VERSION     E03954.1  GI:2172165
KEYWORDS    JP 1992295499-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Habuka,N., Miyano,M., Matsumoto,T. and Noma,M.
  TITLE     ANTIVIRAL PROTEIN
  JOURNAL   Patent: JP 1992295499-A 1 20-OCT-1992;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial gene
```

```
           OC   Artificial sequence; Genes.
           PN   JP 1992295499-A/1
           PD   20-OCT-1992
           PF   22-MAR-1991 JP 1991083456
           PI   HABUKA NORIYUKI, MIYANO MASASHI, MATSUMOTO TAKASHI, PI   NOMA
           MASAKATA
           PC   C07K13/00,A61K37/02,C12N1/21,C12N15/29//C12P21/02,(C12N1/21,
           PC   C12R1:19),
           PC   (C12P21/02,C12R1:19);
           CC   strandedness: Double;
           CC   topology: Linear;
           CC   hypothetical: Yes;
           CC   anti-sense: No;
           CC   *source: clone=pSH7;
           FH   Key             Location/Qualifiers
           FH
           FT   mat_peptide     1. .750
           FT                   /product='recombinant Mirabilis Antiviral  FT
                          Protein'
           FT                   /note='recombinant MAP'
           FT   3'UTR           754. .762.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-13        Length:         762
Score:                  211.50          Matches:        53
Percent Similarity:     55.2%           Conservative:   27
Best Local Similarity:  36.6%           Mismatches:     56
Query Match:            27.5%           Indels:         9
DB:                     6               Gaps:           4

US-10-758-902-9 (1-149) x E03954 (1-762)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||                  |||   :::||||||   ::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 84

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||      |||                      |||:::|||   |||:::
Db         85 GTCGCAGACAAAACCGAA------------CAGTCGACCATCCAGAAAATCTCTAAAACC 132

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                 :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||||:::   |||:::||||||:::||||||   |||       :::   |||
Db        193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              ||||||   |||          |||                  :::      |||||||||
Db        253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||       |||
Db        313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                  :::   |||||||||       ||||||:::::::::||||||   ||||||
Db        373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429

Qy        141 AlaIleTrpGlyLys 145
                 |||:::||||||
Db        430 AACATTTATGGCAAA 444

RESULT 29
AF259548
LOCUS       AF259548               1932 bp    mRNA    linear   PLN 29-SEP-2000
DEFINITION  Cinnamomum camphora type II ribosome-inactivating protein
            cinnamomin mRNA, partial cds.
ACCESSION   AF259548
VERSION     AF259548.2  GI:10337766
KEYWORDS    .
SOURCE      Cinnamomum camphora (camphor tree)
  ORGANISM  Cinnamomum camphora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
            Cinnamomum.
REFERENCE   1  (bases 1 to 1932)
  AUTHORS   Xie,L., Liu,W.-Y. and Wang,E.-D.
  TITLE     Molecular cloning of cinnamomin A-, B-chain and the expression,
            purification, characterization and mutagenesis of the A-Chain
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1932)
  AUTHORS   Xie,L., Liu,W.-Y. and Wang,E.-D.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2000) Shanghai Institute of Biochemistry, Chinese
            Academy of Sciences, 320 Yue-yang Road, Shanghai 200031, China
REFERENCE   3  (bases 1 to 1932)
  AUTHORS   Xie,L., Liu,W.-Y. and Wang,E.-D.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-SEP-2000) Shanghai Institute of Biochemistry, Chinese
            Academy of Sciences, 320 Yue-yang Road, Shanghai 200031, China
  REMARK    Sequence update by submitter
COMMENT     On Sep 29, 2000 this sequence version replaced gi:7739713.
FEATURES             Location/Qualifiers
     source          1. .1932
                     /organism="Cinnamomum camphora"
                     /mol_type="mRNA"
                     /db_xref="taxon:13429"
     CDS             <1. .1650
                     /function="inactivates ribosomes and inhibits protein
                     synthesis"
                     /codon_start=1
                     /product="type II ribosome-inactivating protein
                     cinnamomin"
                     /protein_id="AAF68978.2"
                     /db_xref="GI:10337767"
                     /translation="YQTVTPTTKKATKTSYTQFIEALRAQLASGEEPHGIPVMRERST
                     VPDSKRFILVELSNWAADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPDPAIENLLP
                     DTKRYTFPPSGSYTDLEGVAGERREEILLGMDPLENAISALWISNLNQQRALARSLIV
                     VIQMVAEAVRFRFIEYRVRGSISRAEMFRPDPAMLSLENKWSALSNAVQQSNQGGVFS
                     SPVELRSISNKPVYVGSVSDRVISGLAIMLFICRSTDRASSDQFIDHMLMIRPILVDV
                     AEVATDADNDDTCADPEPTVRISGRNGLCVDVRDGKYNNGNPIQLWPCKQNSDVNQLW
                     TLRRDGAIRSNGKCLTTNGYSAGDYVMIYDCRTPVTAASIWQFWANGTIINPQSALVL
                     SAESGNPRTTLTVQANIYASRQGWLAGNNTEPFVTSIVGFNDLCMQANGDAMWVEECE
                     SSKAEQKWALYPDGSIRPHQDPGPAACPLLDNHPQGSIIISSCSPGSEGRRWVFMND
                     GTVLNLKNGLVMDVKGSNPSLHQIIIWPATGKPNHEWLPLL"
ORIGIN

Alignment Scores:
Pred. No.:              2.17e-11        Length:         1932
Score:                  194.50          Matches:        53
Percent Similarity:     52.0%           Conservative:   24
Best Local Similarity:  35.8%           Mismatches:     62
Query Match:            25.3%           Indels:         9
DB:                     15              Gaps:           5

US-10-758-902-9 (1-149) x AF259548 (1-1932)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIle 18
              |||   ||||||:::|||          :::|||   :::       |||       ||||||
Db          1 TACCAGACCGTGACCTTCACTACTAAAAAGGCCACCAAGACCAGCTACACACAGTTCATA 60

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeu 38
              :::   ||||||   :::||||||   |||                  :::||||||
Db         61 GAGGCTCTGCGAGCTCAATTGGCAAGTGGAGAAGAGCCGCATGGAATACCAGTGATGCGT 120

Qy         39 Gln------ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThr---Thr 55
              :::      |||:::   |||   ||||||||||:::||||||:::::::::
Db        121 GAGCGATCAACAGTGCCAGATTCCAAGCGGTTTATTTTGGTGGAACTCTCAAATTGGGCA 180
```

```
Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               :::          |||   :::|||:::||||||||||:::   |||||||||   |||:::
Db         181 GCAGATTCCCCCGTCACTTTGGCAGTAGATGTCACCAATGCTTATGTGGTGGCTTATCGG 240

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
                        |||                  :::          |||       |||
Db         241 ---------ACTGGAAGTCAGTCTTTCTTCTTACGTGAAGATAATCCTGACCCTGCAATT 291

Qy          96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
               |||   |||       |||   |||   |||       |||   |||||||||
Db         292 GAAAATCTTCTCCCAGAT---ACAAAGCGATATACATTTCCATTCTCCGGCAGCTATACA 348

Qy         116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
               |||          |||          |||:::::::::   ||||||:::     |||
Db         349 GACCTTGAAGGAGTCGCAGGTGAGCGTAGAGAGGAGATCCTGCTAGGAATGGACCCACTT 408

Qy         136 GluPheSerIleGluAlaIleTrp 143
               |||   :::|||   |||:::|||
Db         409 GAAAACGCCATCTCGGCCCTTTGG 432

RESULT 30
AY039803
LOCUS       AY039803                2010 bp    DNA     linear   PLN 14-MAR-2002
DEFINITION  Cinnamomum camphora type 2 ribosome-inactivating protein cinnamomin
            III precursor, gene, complete cds.
ACCESSION   AY039803
VERSION     AY039803.1  GI:15081587
KEYWORDS    .
SOURCE      Cinnamomum camphora (camphor tree)
  ORGANISM  Cinnamomum camphora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
            Cinnamomum.
REFERENCE   1  (bases 1 to 2010)
  AUTHORS   Yang,Q., Liu,R.S., Gong,Z.Z. and Liu,W.Y.
  TITLE     Studies of three genes encoding Cinnamomin (a type II RIP) isolated
            from the seeds of camphor tree and their expression patterns
  JOURNAL   Gene 284 (1-2), 215-223 (2002)
   PUBMED   11891062
REFERENCE   2  (bases 1 to 2010)
  AUTHORS   Yang,Q., Gong,Z.Z. and Liu,W.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-2001) Institute of Biochemistry and Cell Biology,
            Shanghai Institutes for Biological Sciences, Chinese Academy of
            Sciences, 320 Yue-Yang Road, Shanghai 200031, China
FEATURES             Location/Qualifiers
     source          1. .2010
                     /organism="Cinnamomum camphora"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:13429"
     mRNA            <16. .>1758
                     /product="type 2 ribosome-inactivating protein cinnamomin
                     III precursor"
     CDS             16. .1758
                     /note="type 2 RIP"
                     /codon_start=1
                     /product="type 2 ribosome-inactivating protein cinnamomin
                     III precursor"
                     /protein_id="AAK82460.1"
                     /db_xref="GI:15081588"
                     /translation="MSPQGILHLPYLQLLILLPSSPFMVVEPHTLNYQTVTFTTKNAT
                     KTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWAADSPVTLAVD
                     VTNAYVVAYRTGSQSPFLREDNPDPAIENLLPDTKRYTFPPFSGSYTDLERVAGERREE
                     ILLGMDPLENAISALWISNLNQQRALARSLIVVIQMVAEAVRFRFIEYRVRESITRAE
                     MFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGSVSDRVISGL
                     AIMLFICRSTDRASSDQFIDHLLMIRPILADVADVATDADNDDTCADPEPTVRISGRN
                     GLCVDVRDGKYNNGNPIQLWPCKQNSDVNQLWTLRRDGTIRSNGKCLTTNGYSAGDYV
                     MIYDCRTPVTAASIWQFWANGTIINPQSALVLSAESGNPRTTLTVQADIYASRQGWLA
                     GNNTEPFVTSIVGFNDLCMQANGDAMWVVECESSKAEQKWALYPDGSIRPHQDRDRCL
                     TSTDNHSQGSIIIISSCSPGSEGQRWVFMNDGTILNLKNGLVMDVKGSDPSLHQIIIW
                     PATGKPNQKWLPLL"
     sig_peptide     16. .111
                     /note="type 2 RIP"
     mat_peptide     112. .1755
                     /product="type 2 ribosome-inactivating protein cinnamomin
                     III"
                     /note="type 2 RIP"
     misc_feature    112. .924
                     /note="Region: A chain"
     misc_feature    925. .966
                     /note="Region: linker peptide"
     misc_feature    967. .1755
                     /note="Region: B chain"
ORIGIN

Alignment Scores:
Pred. No.:              2.92e-11      Length:          2010
Score:                  193.50        Matches:         53
Percent Similarity:     51.4%         Conservative:    23
Best Local Similarity:  35.8%         Mismatches:      63
Query Match:            25.2%         Indels:          9
DB:                     15            Gaps:            5

US-10-758-902-9 (1-149) x AY039803 (1-2010)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIle 18
               |||   ||||||:::|||          |||   :::      |||      ||||||
Db         112 TATCAAACGGTGACGTTTACCACCAAAAATGCCACCAAGACCAGCTACACACAGTTCATA 171

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeu 38
               :::   ||||||   :::||||||   |||                :::|||||
Db         172 GAGGCTCTGCGAGCTCAATTGGCAAGTGGAGAAGAACCGCATGGAATACCAGTGATGCGT 231

Qy          39 Gln------ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThr---Thr 55
               :::      |||:::   |||   |||||||||:::||||||:::::::::
Db         232 GAGCGATCAACAGTGCCAGATTCCAAGCGGTTTATTTTGGTGGAACTCTCAAATTGGGCA 291

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               :::          |||   :::|||:::||||||||||:::   |||||||||   |||:::
Db         292 GCAGATTCCCCCGTCACTTTGGCAGTAGATGTCACCAATGCTTATGTGGTGGCTTATCGG 351

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
                        |||                  :::          |||       |||
Db         352 ---------ACTGGAAGTCAGTCTTTCTTCTTACGTGAAGATAATCCTGACCCTGCAATT 402

Qy          96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
               |||   |||       |||   |||   |||       |||   |||||||||
Db         403 GAAAATCTTCTCCCAGAT---ACAAAGCGATATACATTTCCATTCTCCGGCAGCTATACA 459

Qy         116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
               |||          |||          |||:::::::::   ||||||:::     |||
Db         460 GACCTTGAAAGAGTCGCAGGTGAGCGTAGAGAGGAGATCCTGCTAGGAATGGACCCACTT 519

Qy         136 GluPheSerIleGluAlaIleTrp 143
               |||   :::|||   |||:::|||
Db         520 GAAAACGCCATCTCGGCCCTTTGG 543

RESULT 31
AY039801
LOCUS       AY039801                2024 bp    DNA     linear   PLN 14-MAR-2002
DEFINITION  Cinnamomum camphora type 2 ribosome-inactivating protein cinnamomin
            I precursor, gene, complete cds.
ACCESSION   AY039801
VERSION     AY039801.1  GI:15081583
KEYWORDS    .
SOURCE      Cinnamomum camphora (camphor tree)
  ORGANISM  Cinnamomum camphora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
            Cinnamomum.
REFERENCE   1  (bases 1 to 2024)
  AUTHORS   Yang,Q., Liu,R.S., Gong,Z.Z. and Liu,W.Y.
  TITLE     Studies of three genes encoding Cinnamomin (a type II RIP) isolated
            from the seeds of camphor tree and their expression patterns
  JOURNAL   Gene 284 (1-2), 215-223 (2002)
```

```
   PUBMED   11891062
REFERENCE   2  (bases 1 to 2024)
  AUTHORS   Yang,Q., Gong,Z.Z. and Liu,W.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-2001) Institute of Biochemistry and Cell Biology,
            Shanghai Institutes for Biological Sciences, Chinese Academy of
            Sciences, 320 Yue-Yang Road, Shanghai 200031, China
FEATURES             Location/Qualifiers
     source          1. .2024
                     /organism="Cinnamomum camphora"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:13429"
     mRNA            <16. .>1761
                     /product="type 2 ribosome-inactivating protein cinnamomin
                     I precursor"
     CDS             16. .1761
                     /note="type 2 RIP"
                     /codon_start=1
                     /product="type 2 ribosome-inactivating protein cinnamomin
                     I precursor"
                     /protein_id="AAK82458.1"
                     /db_xref="GI:15081584"
                     /translation="MSPQGILHLPYLQLLILLPSSPFMVVEPHTINYQTVTFTTKNAT
                     KTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWAADSPVTLAVD
                     VTNAYVVAYRTGSQSFFLREDNPDPAIENLLPDTKRYTFPFSGSYTDLEGVAGERREE
                     ILLGMDPLENAISALWISNLNQQRALARSLIVVIQMVAEAVRFRFIEYRVRGSISRAE
                     MFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGSVSDRVISGL
                     AIMLFICRSTDRASSDQFIDHMLMIRPILVDVAEVATDADNDDTCADPEPTVRISGRN
                     GLCVDVRDGKYNNGNPIQLWPCKQNSDVNQLWTLRRDGAIRSNGKCLTTNGYSAGDYV
                     MIYDCRTPVTAASIWQFWANGTIINPQSALVLSAESGNPRTTLTVQANIYASRQGWLA
                     GNNTEPFVTSIVGFNDLCMQANGDAMWVEECESSKAEQKWALYPDGSIRPHQDPGPAA
                     CPLLDNHPQGSIIIISSCSPGSEGRRWVFMNDGTVLNLKNGLVMDVKGSNPSLHQIII
                     WPATGKPNHEWLPLL"
     sig_peptide     16. .111
                     /note="type 2 RIP"
     mat_peptide     112. .1758
                     /product="type 2 ribosome-inactivating protein cinnamomin
                     I"
                     /note="type 2 RIP"
     misc_feature    112. .924
                     /note="Region: A chain"
     misc_feature    925. .966
                     /note="Region: linker peptide"
     misc_feature    967. .1758
                     /note="Region: B chain"
ORIGIN

Alignment Scores:
Pred. No.:              2.95e-11        Length:         2024
Score:                  193.50          Matches:        53
Percent Similarity:     51.4%           Conservative:   23
Best Local Similarity:  35.8%           Mismatches:     63
Query Match:            25.2%           Indels:         9
DB:                     15              Gaps:           5

US-10-758-902-9 (1-149) x AY039801 (1-2024)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIle 18
              |||   ||||||:::|||              |||   :::      |||      ||||||
Db        112 TATCAAACGGTGACGTTTACCACCAAAAATGCCACCAAGACCAGCTACACACAGTTCATA 171

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeu 38
              :::   ||||||   :::||||||   |||              :::||||||
Db        172 GAGGCTCTGCGAGCTCAATTGGCAAGTGGAGAAGAGCCGCATGGAATACCAGTGATGCGT 231

Qy         39 Gln------ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThr---Thr 55
              :::      |||:::   |||   |||||||||:::||||||:::::::::
Db        232 GAGCGATCAACAGTGCCAGATTCCAAGCGGTTTATTTTGGTGGAACTCTCAAATTGGGCA 291

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::      |||   :::|||:::|||||||||:::   |||||||||   |||:::
Db        292 GCAGATTCCCCCGTCACTTTGGCAGTAGATGTCACCAATGCTTATGTGGTGGCTTATCGG 351

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
                         |||                              :::      |||      |||
Db        352 ---------ACTGGAAGTCAGTCTTTCTTCTTACGTGAAGATAATCCTGACCCTGCAATT 402

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
                 |||   |||       |||   |||   |||       |||   |||||||||
Db        403 GAAAATCTTCTCCCAGAT---ACAAAGCGATATACATTTCCATTCTCCGGCAGCTATACA 459

Qy        116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
                 |||       |||       |||:::::::::   ||||||:::      |||
Db        460 GACCTTGAAGGAGTCGCAGGTGAGCGTAGAGAGGAGATCCTGCTAGGAATGGACCCACTT 519

Qy        136 GluPheSerIleGluAlaIleTrp 143
                 |||   :::|||   |||:::|||
Db        520 GAAAACGCCATCTCGGCCCTTTGG 543

RESULT 32
AY039802
LOCUS       AY039802               2020 bp    DNA     linear   PLN 14-MAR-2002
DEFINITION  Cinnamomum camphora type 2 ribosome-inactivating protein cinnamomin
            II precursor, gene, complete cds.
ACCESSION   AY039802
VERSION     AY039802.1  GI:15081585
KEYWORDS    .
SOURCE      Cinnamomum camphora (camphor tree)
  ORGANISM  Cinnamomum camphora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
            Cinnamomum.
REFERENCE   1  (bases 1 to 2020)
  AUTHORS   Yang,Q., Liu,R.S., Gong,Z.Z. and Liu,W.Y.
  TITLE     Studies of three genes encoding Cinnamomin (a type II RIP) isolated
            from the seeds of camphor tree and their expression patterns
  JOURNAL   Gene 284 (1-2), 215-223 (2002)
   PUBMED   11891062
REFERENCE   2  (bases 1 to 2020)
  AUTHORS   Yang,Q., Gong,Z.Z. and Liu,W.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-2001) Institute of Biochemistry and Cell Biology,
            Shanghai Institutes for Biological Sciences, Chinese Academy of
            Sciences, 320 Yue-Yang Road, Shanghai 200031, China
FEATURES             Location/Qualifiers
     source          1. .2020
                     /organism="Cinnamomum camphora"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:13429"
     mRNA            <16. .>1758
                     /product="type 2 ribosome-inactivating protein cinnamomin
                     II precursor"
     CDS             16. .1758
                     /note="type 2 RIP"
                     /codon_start=1
                     /product="type 2 ribosome-inactivating protein cinnamomin
                     II precursor"
                     /protein_id="AAK82459.1"
                     /db_xref="GI:15081586"
                     /translation="MSPQGILHLPYLQLLILLPSSPFMVVEPHTINYQTVTFTTKNAT
                     KTSYTQFIEALRAQLASGEEPHGIPVMRDGSTVPDSKRFILVELSNWAADSPVALAVD
                     VTNAYVVAYRTGSQSFFLREDNPDPAIENLLPDTKRYTFPFSGSYTDLERVAGELREE
                     ILLGMDPLENAISALWTSNLNQQRALARSLIVVIQMVAEAVRFRFIEYRVRESITRAE
                     MFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVELRSISNKPVYVGSVSDRVISGL
                     AIMLFICRSSDRTSSDQFIDHLLMIRPILVDVADVATDADNDDTCADPEPTVRISGRN
                     GLCVDVRDGKYNNGNPIQLWPCKQNSDVNQLWTLRRDGTIRSNGKCLTTNGYSAGDYV
                     MIYDCRTPVTAASIWQFWANGTIINPQSALVLSAESGNPRTTLTVQANIYASRQGWLA
                     GNNTEPFVTSIVGFNDLCMQANGDAMWVVECESSKAEQKWALYPDGSIRPHQDRDRCL
                     TSTDNHSQGSIIIISSCSPGSEGQRWVFMNDGTILNLKNGLVMDVKGSNPSLHQIIIW
                     PATGKPNQQWLPLL"
     sig_peptide     16. .111
                     /note="type 2 RIP"
     mat_peptide     112. .1755
                     /product="type 2 ribosome-inactivating protein cinnamomin
                     II"
                     /note="type 2 RIP"
```

```
     misc_feature    112. .924
                     /note="Region: A chain"
     misc_feature    925. .966
                     /note="Region: linker peptide"
     misc_feature    967. .1755
                     /note="Region: B chain"
ORIGIN

Alignment Scores:
Pred. No.:              4.87e-11        Length:         2020
Score:                  191.50          Matches:        54
Percent Similarity:     49.7%           Conservative:   22
Best Local Similarity:  35.3%           Mismatches:     68
Query Match:            24.9%           Indels:         9
DB:                     15              Gaps:           5

US-10-758-902-9 (1-149) x AY039802 (1-2020)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIle 18
              |||  ||||||:::|||            |||  :::      |||      ||||||
Db        112 TATCAAACGGTGACGTTTACCACCAAAAATGCCACCAAGACCAGCTACACACAGTTCATA 171

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeu 38
              :::   ||||||   :::||||||  |||               :::||||||
Db        172 GAGGCTCTGCGAGCTCAATTGGCAAGTGGAGAAGAGCCGCATGGAATACCAGTGATGCGT 231

Qy         39 ------GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThr---Thr 55
                    |||:::   |||   |||||||||:::||||||:::::::::
Db        232 GACGGATCAACAGTGCCAGATTCCAAGCGGTTTATTTTGGTGGAACTCTCAAATTGGGCA 291

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::          |||   :::|||:::|||||||||:::   |||||||||   |||:::
Db        292 GCAGATTCCCCCGTCGCTTTGGCAGTAGATGTCACCAATGCTTATGTGGTGGCTTATCGG 351

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
                    |||                  :::      |||      |||
Db        352 ---------ACTGGAAGTCAGTCTTTCTTCTTACGTGAAGATAATCCTGACCCTGCAATT 402

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
                 |||   |||      |||   |||   |||      |||   |||||||||
Db        403 GAAAATCTTCTCCCAGAT---ACAAAGCGATATACATTTCCATTCTCCGGCAGCTATACA 459

Qy        116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
               |||          |||          |||:::::::::   ||||||:::      |||
Db        460 GACCTTGAAAGAGTCGCAGGTGAGCTTAGAGAGGAGATCCTGCTAGGAATGGACCCACTT 519

Qy        136 GluPheSerIleGluAlaIleTrpGlyLysThrGlnAsn 148
              |||   :::|||   |||:::|||          |||
Db        520 GAAAACGCCATCTCGGCCCTTTGGACCAGCAACTTAAAT 558

RESULT 33
AF409135
LOCUS       AF409135               1692 bp    mRNA    linear   PLN 16-SEP-2001
DEFINITION  Sambucus nigra ribosome-inactivating protein (AVl) mRNA, complete
            cds.
ACCESSION   AF409135
VERSION     AF409135.1  GI:15625502
KEYWORDS    .
SOURCE      Sambucus nigra (European elder)
  ORGANISM  Sambucus nigra
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
REFERENCE   1  (bases 1 to 1692)
  AUTHORS   Van Damme,E.J.M.
  TITLE     Characterization and cloning of lectins and ribosome-inactivating
            proteins from Sambucus nigra leaves
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1692)
  AUTHORS   Van Damme,E.J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-AUG-2001) Lab. Phytopathology and Plant Protection,
            K.U.Leuven, Willem de Croylaan 42, Leuven, B 3001, Belgium
FEATURES             Location/Qualifiers
     source          1. .1692
                     /organism="Sambucus nigra"
                     /mol_type="mRNA"
                     /db_xref="taxon:4202"
                     /tissue_type="leaf"
     gene            1. .1692
                     /gene="AVl"
     CDS             1. .1692
                     /gene="AVl"
                     /note="SNA-Vl"
                     /codon_start=1
                     /product="ribosome-inactivating protein"
                     /protein_id="AAL04123.1"
                     /db_xref="GI:15625503"
                     /translation="MRVIAAAMLYFYIVVLAICSVGIQGIDYPSVSFNLDGAKSATYR
                     DFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNYNGNTVTLAVDVTNLY
                     VVAPSGNANSYFFKDATEVQKSNLFVGTKQNTLSFTGNYDNLETAANTRRESIELGPS
                     PLDGAITSLYHGDSVARSLLVVIQMVSEAARFRYIEQEVRRSLQQATSFTPNALMLSM
                     ENNWSSMSLEIQQAGNNVSPFFGTVQLLNYDHTHRLVDNFEELYKITGIAILLFRCSS
                     PSNDNAIRMPLDLAGGDNKYNDGETCTLRTSFTRNIVGRDGLCVDVRNGYDTDGTPLQ
                     LWPCGTQRNQRWTFDSDDTIRSMGKCMTANGLNNGSNIVIFNCSTAAENAIKWEVPID
                     GSIINPSSGLVMTAPRAASRTILLLEDNIYAASQGWTVTNNVKPIVASIVGYKEMCLQ
                     SNGENNGVWMEDCEATSLQQQWALYGDRTIRVNSTRGLCVTTNGYNSKDLIIILKCQG
                     LPSQRWFFNSDGAIVNPKSRHVMDVRASNVSLREIIIFPATGNPNQQWVTQVLPS"
ORIGIN

Alignment Scores:
Pred. No.:              4.51e-11        Length:         1692
Score:                  191.00          Matches:        54
Percent Similarity:     54.1%           Conservative:   26
Best Local Similarity:  36.5%           Mismatches:     58
Query Match:            24.9%           Indels:         10
DB:                     15              Gaps:           5

US-10-758-902-9 (1-149) x AF409135 (1-1692)

Qy          1 TyrAsnThrValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIle 18
              |||   :::|||||||||||||||        ::::::      |||      |||:::
Db         82 TATCCCTCCGTCTCCTTCAACTTGGATGGAGCCAAGTCGGCTACATACAGGGACTTCCTC 141

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThr---ProValCysGlnLeuProValThr 37
                 :::||||||      :::|||   ||||||      |||      |||||||||
Db        142 AGCAACCTGCGAAAAACAGTGGCAACTGGCACCTATGAAGTAAACGGTTTACCAGTACTG 201

Qy         38 LeuGln------ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::         :::              ||||||||||||||   :::|||
Db        202 AGGCGCGAAAGTGAAGTACAGGTCAAGAGTCGGTTCGTTCTCGTCCCTCTCACCAATTAC 261

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::      ||||||   :::|||:::||||||||:::::|||||||||   :::
Db        262 AATGGAAACACCGTCACGTTGGCAGTAGATGTGACCAACCTTTACGTGGTGGCTTTT--- 318

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
                        |||          :::   |||                        |||
Db        319 ---------AGTGGAAATGCAAACTCCTACTTTTTCAAGGACGCTACGGAAGTTCAAAAG 369

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
              |||   ||||||   |||   |||   :::   ||||||:::|||   |||:::|||
Db        370 AGTAATTTATTCGTTGGC---ACCAAGCAAAATACGTTATCCTTCACGGGTAATTATGAC 426

Qy        116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
                 |||      ||||||          |||:::   :::|||||||||         |||
Db        427 AACCTTGAGACTGCGGCGAATACTAGGAGGGAGTCTATCGAACTGGGACCCAGTCCGCTA 486

Qy        136 GluPheSerIleGluAlaIleTrp 143
              :::   :::|||   :::::::::
Db        487 GATGGAGCCATTACAAGTTTGTAT 510

RESULT 34
SNU41299
LOCUS       SNU41299               1879 bp    mRNA    linear   PLN 31-DEC-1996
DEFINITION  Sambucus nigra ribosome inactivating protein precursor mRNA,
```

```
            complete cds.
ACCESSION   U41299
VERSION     U41299.1  GI:1754980
KEYWORDS    .
SOURCE      Sambucus nigra (European elder)
  ORGANISM  Sambucus nigra
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
REFERENCE   1  (bases 1 to 1879)
  AUTHORS   Van Damme E.J.,Peumans,W.
  TITLE     Characterization and molecular cloning of nigrin b (SNAV), a
            GalNAc-specific type 2 ribosome inactivating protein from the bark
            of elderberry (Sambucus nigra)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1879)
  AUTHORS   Van Damme,E.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-1995) Els J. Van Damme, Lab Phytopathology and
            Plant Protection, Catholic University of Leuven, Willem De Croylaan
            42, Leuven Heverlee, Brabant 3001, Belgium
FEATURES             Location/Qualifiers
     source          1. .1879
                     /organism="Sambucus nigra"
                     /mol_type="mRNA"
                     /db_xref="taxon:4202"
                     /clone="LECNIGb"
                     /tissue_type="bark"
     5'UTR           <1. .5
     CDS             6. .1697
                     /codon_start=1
                     /evidence=experimental
                     /product="ribosome inactivating protein precursor"
                     /protein_id="AAB39475.1"
                     /db_xref="GI:1754981"
                     /translation="MRVVAAAMLYFYIVVLAICSVGIQGIDYPSVSFNLDGAKSATYR
                     DFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNYNGNTVTLAVDVTNLY
                     VVAFSGNANSYFFKDATEVQKSNLFVGTKQNTLSFTGNYDNLETAANTRRESIELGPS
                     PLDGAITSLYHGDSVARSLLVVIQMVSEAARFRYIEQEVRRSLQQATSFTPNALMLSM
                     ENNWSSMSLEIQQAGNNVSPFFGTVQLLNYDHTHRLVDNFEELYKITGIAILLFRCSS
                     PSNDNAIRMPLDLAGEDNKYNDGETCTLRTSFTRNIVGRDGLCVDVRNGYDTDGTPLQ
                     LWPCGTQRNQRWTFDSDDTIRSMGKCMTANGLNNGSNIVIFNCSTAAENAIKWEVPID
                     GSIINPSSGLVMTAPRAASRTILLLEDNIYAASQGWTVTNNVKPIVASIVGYKEMCLQ
                     SNGENNGVWMEDCEATSLQQQWALYGDRTIRVNSTRGLCVTTNGYNSKDLIIILKCQG
                     LPSQRWFFNSDGAIVNPKSRHVMDVRASNVSLREIIIFPATGNPNQQWVTQVLPS"
     sig_peptide     6. .80
     mat_peptide     81. .896
                     /product="ribosome inactivating protein, A chain"
     mat_peptide     897. .1694
                     /product="Ribosome inactivating protein, B chain"
     3'UTR           1698. .1879
     polyA_signal    1833. .1838
ORIGIN

Alignment Scores:
Pred. No.:              5.09e-11        Length:         1879
Score:                  191.00          Matches:        54
Percent Similarity:     54.1%           Conservative:   26
Best Local Similarity:  36.5%           Mismatches:     58
Query Match:            24.9%           Indels:         10
DB:                     15              Gaps:           5

US-10-758-902-9 (1-149) x SNU41299 (1-1879)

Qy          1 TyrAsnThrValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIle 18
              |||   :::|||||||||||||||        ::::::      |||       |||:::
Db         87 TATCCCTCCGTCTCCTTCAACTTGGATGGAGCCAAGTCGGCTACATACAGGGACTTCCTC 146

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThr---ProValCysGlnLeuProValThr 37
                 :::|||||      :::|||   ||||||      |||       |||||||||
Db        147 AGCAACCTGCGAAAAACAGTGGCAACTGGCACCTATGAAGTAAACGGTTTACCAGTACTG 206

Qy         38 LeuGln------ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::         :::             ||||||||||||||   :::|||
Db        207 AGGCGCGAAAGTGAAGTACAGGTCAAGAGTCGGTTCGTTCTCGTCCCTCTCACCAATTAC 266

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
                 :::      ||||||   :::|||:::|||||||||:::::|||||||||   :::
Db        267 AATGGAAACACCGTCACGTTGGCAGTAGATGTGACCAACCTTTACGTGGTGGCTTTT--- 323

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
                        |||         :::   |||                     |||
Db        324 ---------AGTGGAAATGCAAACTCCTACTTTTTCAAGGACGCTACGGAAGTTCAAAAG 374

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
              |||   ||||||   |||   |||   :::   ||||||:::|||   |||:::|||
Db        375 AGTAATTTATTCGTTGGC---ACCAAGCAAAATACGTTATCCTTCACGGGTAATTATGAC 431

Qy        116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
                |||       ||||||          |||:::   :::|||||||||          |||
Db        432 AACCTTGAGACTGCGGCGAATACTAGGAGGGAGTCTATCGAACTGGGACCCAGTCCGCTA 491

Qy        136 GluPheSerIleGluAlaIleTrp 143
                 :::   :::|||   ::::::::
Db        492 GATGGAGCCATTACAAGTTTGTAT 515

RESULT 35
AF249280
LOCUS       AF249280               1906 bp    mRNA    linear   PLN 14-DEC-2002
DEFINITION  Sambucus nigra type 2 ribosome-inactivating protein Nigrin 1
            precursor, mRNA, complete cds.
ACCESSION   AF249280
VERSION     AF249280.1  GI:26793995
KEYWORDS    .
SOURCE      Sambucus nigra (European elder)
  ORGANISM  Sambucus nigra
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
REFERENCE   1  (bases 1 to 1906)
  AUTHORS   Girbes,T., Arias,F.J. and Antolin,P.
  TITLE     Characterization and molecular cloning of Nigrin 1, a type two
            ribosome-inactivating protein from leaves of elder (Sambucus nigra)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1906)
  AUTHORS   Girbes,T., Arias,F.J. and Antolin,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2000) Biochemistry, University of Valladolid,
            Faculty of Sciences, Dr. Mergelina s/n, Valladolid 47005, Spain
FEATURES             Location/Qualifiers
     source          1. .1906
                     /organism="Sambucus nigra"
                     /mol_type="mRNA"
                     /db_xref="taxon:4202"
                     /tissue_type="leaf"
     CDS             22. .1713
                     /EC_number="3.2.2.22"
                     /codon_start=1
                     /product="type 2 ribosome-inactivating protein Nigrin 1
                     precursor"
                     /protein_id="AAN86130.1"
                     /db_xref="GI:26793996"
                     /translation="MRVVAAAMLYFYIVVLAICSVGIQGIDYPSVSFNLDGAKSATYR
                     DFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNYNGNTVTLAVDVTNLY
                     VVAFSGNANSYFFKDATEVQKSNLFVGTKQNTLSFTGNYDNLETAANTRRESIELGPS
                     PLDGAITSLYHGDSVARSLLVVIQMVSEAARFRYIEQEVRRSLQQATSFTPNASMLSM
                     ENNWSSMSLEIQQAGNNVSPFSGTVQLLNYDHTHRLVDNFEELYKITGIAILLFRCSS
                     PSNDNAIRMPLDLAGEDNKYNDGETCTLRTSFTRNIVGRDGLCVDVRNGYDTDGTPLQ
                     LWPCGTQRNQRWTFNTDDTIRSMGKCMTANGLNNGSNIVIFNCSTAVENAIKWEVPID
                     GSIINPSSGRVVTAPSAASRTILLLEDNIYAASQGWTVTNNVKPIVASIVGYKEMCLQ
                     SNGENNGVWMEDCEATSLQQQWALYGDRTIRVNSTRGLCVTTNGYNSKDLIIILKCQG
                     LPSQRWFFNSDGAIVNPKSRLVMDVRASNVSLREIIIFPATGNPNQQWVTQVLPS"
ORIGIN

Alignment Scores:
Pred. No.:              5.17e-11        Length:         1906
```

```
Score:                 191.00        Matches:       54
Percent Similarity:    54.1%         Conservative:  26
Best Local Similarity: 36.5%         Mismatches:    58
Query Match:           24.9%         Indels:        10
DB:                    15            Gaps:          5

US-10-758-902-9 (1-149) x AF249280 (1-1906)

Qy          1 TyrAsnThrValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIle 18
              |||   :::|||||||||||||||||        ::::::     |||      |||:::
Db        103 TATCCCTCCGTCTCCTTCAACTTGGATGGAGCCAAGTCGGCTACATACAGGGACTTCCTC 162

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThr---ProValCysGlnLeuProValThr 37
              :::||||||      :::|||   ||||||      |||      |||||||||
Db        163 AGCAACCTGCGAAAAACAGTGGCAACTGGCACCTATGAAGTAAACGGTTTACCAGTGCTG 222

Qy         38 LeuGln------ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThr 55
              :::         :::             ||||||||||||||   :::|||
Db        223 AGGCGCGAAAGTGAAGTACAGGTCAAGAGTCGGTTCGTTCTCGTCCCTCTCACCAATTAC 282

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::      ||||||   :::|||:::|||||||||:::::::|||||||||   :::
Db        283 AATGGAAACACCGTCACGTTGGCAGTAGATGTGACCAACCTTTACGTGGTGGCTTTT--- 339

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
                 ||      |||          :::   |||                  |||
Db        340 ---------AGTGGAAATGCAAACTCCTACTTTTTCAAGGACGCTACGGAAGTTCAAAAG 390

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
              |||   ||||||   |||   |||   :::   ||||||:::|||   |||:::|||
Db        391 AGTAATTTATTCGTTGGC---ACCAAGCAAAATACGTTATCCTTCACGGGTAATTATGAC 447

Qy        116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
              |||      ||||||         |||:::   :::|||||||||         |||
Db        448 AACCTTGAGACTGCGGCGAATACTAGGAGGGAGTCTATCGAACTGGGACCCAGTCCGCTA 507

Qy        136 GluPheSerIleGluAlaIleTrp 143
              :::   :::|||   :::::::::
Db        508 GATGGAGCCATTACAAGTTTGTAT 531

RESULT 36
I34238
LOCUS       I34238                  962 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 14 from patent US 5597569.
ACCESSION   I34238
VERSION     I34238.1  GI:1825029
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 962)
  AUTHORS   Siegall,C.B., Gawlak,S.L. and Marquardt,H.
  TITLE     Bryodin 2 a ribosome-inactivating protein isolated from the plant
            Bryonia dioica
  JOURNAL   Patent: US 5597569-A 14 28-JAN-1997;
FEATURES             Location/Qualifiers
     source          1. .962
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:             2.69e-11      Length:        962
Score:                 190.50        Matches:       50
Percent Similarity:    57.8%         Conservative:  24
Best Local Similarity: 39.1%         Mismatches:    47
Query Match:           24.8%         Indels:        7
DB:                    6             Gaps:          4

US-10-758-902-9 (1-149) x I34238 (1-962)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro---ValCys 32
              |||   |||||||||::::::||||||   :::|||      |||||||||   |||

Db        133 TACAAAACTTTTATAAGGAATCTGCGCACCAAACTCACGGTTGGAACTCCAAGGGTGTAC 192

Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
              :::||||||                  |||      ||||||   ||||||   :::
Db        193 GATATACCTGTCCTGAGAAACGCAGCAGCCGGGCTCGCGCGCTTTCAATTAGTTACCCTC 252

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
              |||      :::   ::::::|||   ||||||:::||||||   :::|||||||||||
Db        253 ACAAATTACAATGGCGAATCTGTCACTGTGGCTTTAGATGTAGTGAACGTGTACGTTGTT 312

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
                 |||:::                  :::   |||   ||||||            |||
Db        313 GCATATCGA-----------GCTGGAAACACTGCTTACTTTCTCGCAGATGCATCAACA 360

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||   |||:::   |||   |||   |||   :::   |||
Db        361 GAAGCCAACAATGTGTTGTTTGCAGGCATC---AATCATGTAAGACTTCCTTATGGAGGG 417

Qy        113 SerTyrGlnLysLeuValAsnAlaAla---LysValAspArgLysAspLeuGluLeuGly 131
              :::|||      |||      ||||||   ::::::   |||:::::::::|||||||||
Db        418 AATTACGATGGCCTTGAGACAGCTGCAGGCAGAATTTCGAGGGAAAATATTGAACTTGGA 477

Qy        132 ValTyrLysLeuGluPheSerIle 139
                    ::::::      :::|||
Db        478 TTTTCCGAAATAAGTAGTGCCATT 501

RESULT 37
AY148091
LOCUS       AY148091                1129 bp    mRNA    linear   PLN 23-DEC-2002
DEFINITION  Mirabilis expansa ribosome-inactivating protein ME1 mRNA, complete
            cds.
ACCESSION   AY148091
VERSION     AY148091.1  GI:25136300
KEYWORDS    .
SOURCE      Mirabilis expansa
  ORGANISM  Mirabilis expansa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Mirabilis.
REFERENCE   1  (bases 1 to 1129)
  AUTHORS   Vepachedu,R.S., Bais,H.P. and Vivanco,J.M.
  TITLE     Cloning, characterization and induction of ME1, a type I
            ribosome-inactivating protein from Mirabilis expansa
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1129)
  AUTHORS   Vepachedu,R.S., Bais,H.P. and Vivanco,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-SEP-2002) Horticulture & LA, Colorado State
            University, 217 Shepardson Bldg., Fort Collins, CO 80523, USA
FEATURES             Location/Qualifiers
     source          1. .1129
                     /organism="Mirabilis expansa"
                     /mol_type="mRNA"
                     /db_xref="taxon:213308"
     CDS             31. .984
                     /note="type I ribosome-inactivating protein"
                     /codon_start=1
                     /product="ribosome-inactivating protein ME1"
                     /protein_id="AAN65450.1"
                     /db_xref="GI:25136301"
                     /translation="METMRLLFLLLTIWTTVVGSTWAQQPGTDQTLLAPPTLATLDLT
                     AAANYPPFITNMRNVLSEKDKNGKDVLLCTMKKISTTVPSPRYAYVDIKASATQTVTL
                     AIDRTNTYVLGYRDIFGGTDRAAFFKDVYDDAKDLFPDAKGKNRIKLSYGSQYTTLGD
                     RTKVPLGIKSLRISITAIYGEAAGTDLDKNRREFFLLALQMVAEATRFKYISDKIPTE
                     RDYDTLKVDNHMIALENGWDLLSTAIYNAKSSTTKPTKCELLKTPVSLIWLGQNEWNF
                     NSVEEIAKVVGLLKAKGKKLSTNNDDDNNGDDCGSVVVASS"
ORIGIN

Alignment Scores:
Pred. No.:             3.23e-11      Length:        1129
Score:                 190.50        Matches:       52
Percent Similarity:    51.0%         Conservative:  24
Best Local Similarity: 34.9%         Mismatches:    58
```

```
Query Match:          24.8%      Indels:        15
DB:                   15         Gaps:          5

US-10-758-902-9 (1-149) x AY148091 (1-1129)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::   :::|||      |||       ||||||   ||||||   ::::::||||||
Db        148 ACCCTTGATCTCACGGCGGCCGCCAATTACCCTCCATTTATCACAAACATGCGAAATGTA 207

Qy         25 LeuAla-----------------LysGlyThrProValCysGlnLeuProValThrLeu 38
              |||:::                |||         :::|||   :::         :::
Db        208 TTGTCGGAAAAAGATAAGAATGGAAAAGATGTACTGCTATGTACCATGAAA---AAAATA 264

Qy         39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
                |||                 |||:::      |||||||||      ::::::   :::
Db        265 AGCACCACAGTCCCATCCCCGCGATACGCGTACGTAGACATTAAAGCCTCTGCAACACAA 324

Qy         59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
              ||||||   :::|||||||||   |||:::   ||||||:::||||||:::|||   :::
Db        325 ACGGTAACATTAGCAATAGATCGAACTAATACTTATGTGTTGGGTTATCGTGATATATTC 384

Qy         79 AspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeu 98
              |||   |||||||||   |||         |||         |||         |||
Db        385 GGTGGGACTGATCGTGCCGCCTTCTTTAAAGACGTGTACGATGATGCC---AAAGACCTT 441

Qy         99 PheProGlyVal------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||                ||||||:::   |||::::::         |||
Db        442 TTCCCAGATGCCAAGGGGAAAAATCGAATTAAATTGAGTTATGGCTCACAATATACTACC 501

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              |||                ||||||      :::   ||||||:::      |||
Db        502 TTA---------------GGAGATAGGACTAAAGTTCCATTAGGAATTAAAAGCTTAAGG 546

Qy        137 PheSerIleGluAlaIleTrpGlyLys 145
              ||||||   ||||||:::|||:::
Db        547 ATAAGCATAACTGCTATCTATGGGGAA 573

RESULT 38
AY082349
LOCUS       AY082349               1809 bp    DNA     linear   PLN 24-MAR-2003
DEFINITION  Trichosanthes kirilowii trichosanthin precursor (TCS) gene,
            complete cds.
ACCESSION   AY082349
VERSION     AY082349.2  GI:29165640
KEYWORDS    .
SOURCE      Trichosanthes kirilowii
  ORGANISM  Trichosanthes kirilowii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
REFERENCE   1  (bases 1 to 1809)
  AUTHORS   Yuan,H., Wang,L., Wang,Y., Liu,T., An,C. and Chen,Z.
  TITLE     Trichosanthes kirilowii trichosanthin precursor (TCS) gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1809)
  AUTHORS   Yuan,H., Wang,L., Wang,Y., Liu,T., An,C. and Chen,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-2002) National Laboratory of Protein Engineering
            and Plant Genetic Engineering, College of Life Sciences, Peking
            University, Beijing 100871, China
REFERENCE   3  (bases 1 to 1809)
  AUTHORS   Yuan,H., Wang,L., Wang,Y., Liu,T., An,C. and Chen,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-2003) National Laboratory of Protein Engineering
            and Plant Genetic Engineering, College of Life Sciences, Peking
            University, Beijing 100871, China
  REMARK    Sequence update by submitter
COMMENT     On Mar 24, 2003 this sequence version replaced gi:20977596.
FEATURES             Location/Qualifiers
     source          1. .1809
                     /organism="Trichosanthes kirilowii"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3677"
     gene            1. .1809
                     /gene="TCS"
     CDS             940. .1809
                     /gene="TCS"
                     /codon_start=1
                     /product="trichosanthin precursor"
                     /protein_id="AAO72728.1"
                     /db_xref="GI:29165641"
                     /translation="MIRFLVLSLLILTLFLTTPAVEGDVSFRLSGATSSSYGVFISNL
                     RKALPNERKLYDIPLLRSTLPGSQRYALIHLTNYADETISVAIDVTNVYIMGYRAGDT
                     SYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAIT
                     TLFYYNANSAASALMVLIQSTSEAARYKFIEQQIGKRVDKTFLPSLAIISLENSWSAL
                     SKQIQIASTNNGQFESPVVLINAQNQRVTITNVDAGVVTSNIALLLNRNNMAAMDDDV
                     PMTQSFGCGSYAI"
ORIGIN

Alignment Scores:
Pred. No.:            1.18e-10      Length:        1809
Score:                187.50        Matches:       45
Percent Similarity:   53.5%         Conservative:  31
Best Local Similarity: 31.7%        Mismatches:    61
Query Match:          24.4%         Indels:        5
DB:                   15            Gaps:          2

US-10-758-902-9 (1-149) x AY082349 (1-1809)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||            |||      ||||||   :::|||
Db       1012 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 1071

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||                ::      :::|||:::         |||:::
Db       1072 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCACTCTT 1131

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||      :::   :::|||:::
Db       1132 CCAGGTTCTCAACGCTACGCATTGATCCATCTGACAAATTACGCCGATGAAACCATTTCA 1191

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::           |||
Db       1192 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 1242

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                       |||   :::          |||   |||         :::|||
Db       1243 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 1302

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db       1303 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCA 1362

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::   ||||||:::      |||:::   :::|||
Db       1363 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCTGCTTTGGACAGTGCCATTACCACT 1422

Qy        142 IleTrp 143
              ::::::
Db       1423 TTGTTT 1428

RESULT 39
SEB400822
LOCUS       SEB400822              1892 bp    mRNA    linear   PLN 27-FEB-2001
DEFINITION  Sambucus ebulus mRNA for ribosome-inactivating protein precursor
            (ebul gene).
ACCESSION   AJ400822
VERSION     AJ400822.1  GI:13171072
KEYWORDS    ebul gene; ribosome-inactivating protein precursor.
SOURCE      Sambucus ebulus
  ORGANISM  Sambucus ebulus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
REFERENCE   1
  AUTHORS   Girbes,T., Iglesias,R., Perez,Y., Ferreras,J.M. and Citores,L.
```

```
  TITLE     Molecular cloning of ebulin 1
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1892)
  AUTHORS   Girbes,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2000) Girbes T., Bioquimica, Biologia Molecular y
            Fisiologia, Universidad de Valladolid, Dr. Mergelina s/n,
            Valladolid, 47005, SPAIN
FEATURES             Location/Qualifiers
     source          1. .1892
                     /organism="Sambucus ebulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:28503"
                     /tissue_type="leaves"
                     /country="Spain:Palencia"
     gene            1. .1892
                     /gene="ebul"
     5'UTR           1. .33
                     /gene="ebul"
     CDS             34. .1728
                     /gene="ebul"
                     /EC_number="3.2.2.22"
                     /function="unknown"
                     /codon_start=1
                     /product="ribosome-inactivating protein precursor"
                     /protein_id="CAC33178.1"
                     /db_xref="GI:13171073"
                     /db_xref="GOA:Q9AVR2"
                     /db_xref="UniProt/TrEMBL:Q9AVR2"
                     /translation="MRVVKAAMLYLHIVVLAIYSVGIQGIDYPSVSFNLAGAKSTTYR
                     DFLKNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLVRLTNYNGDTVTSAVDVTNLY
                     LVAFSANGNSYFFKDATELQKSNLFLGTTQHTLSFTGNYDNLETAAGTRRESIELGPN
                     PLDGAITSLWYDGGVARSLLVLIQMVPEAARFRYIEQEVRRSLQQLTSFTPNALMLSM
                     ENNWSSMSLEVQLSGDNVSPFSGTVQLQNYDHTPRLVDNFEELYKITGIAILLFRCVA
                     TKTTHNAIRMPHVLVGEDNKFNDGETCAIPAPFTRRIVGRDGLCVDVRNGYDTDGTPI
                     QLWPCGTQRNQQWTFYNDKTIRSMGKCMTANGLNSGSYIMITDCSTAAEDATKWEVLI
                     DGSIINPSSGLVMTAPSGASRTTLLLENNIHAASQGWTVSNDVQPIATLIVGYNEMCL
                     QANGENNNVWMEDCDVTSVQQQWALFDDRTIRVNNSRGLCVTSNGYVSKDLIVIRKCQ
                     GLATQRWFFNSDGSVVNLKSTRVMDVKESDVSLQEVIIFPATGNPNQQWRTQVPQI"
     sig_peptide     34. .108
                     /gene="ebul"
     mat_peptide     109. .927
                     /gene="ebul"
                     /product="ebulin 1 A-chain"
                     /EC_number="3.2.2.22"
     mat_peptide     928. .1725
                     /gene="ebul"
                     /product="ebulin 1 B-chain"
                     /EC_number="3.2.2.22"
     misc_feature    109. .1728
                     /gene="ebul"
                     /note="encodes transition peptide that is
                     post-translationally processed into mature peptides A an
                     B"
     3'UTR           1729. .1872
                     /gene="ebul"
     polyA_signal    1771. .1776
                     /gene="ebul"
     polyA_site      1872
                     /gene="ebul"
ORIGIN

Alignment Scores:
Pred. No.:              1.41e-10        Length:         1892
Score:                  187.00          Matches:        53
Percent Similarity:     52.7%           Conservative:   25
Best Local Similarity:  35.8%           Mismatches:     60
Query Match:            24.3%           Indels:         10
DB:                     15              Gaps:           5

US-10-758-902-9 (1-149) x SEB400822 (1-1892)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIle 18

                 |||   :::|||||||||||||||||      |||            |||      |||::: 
Db        115 TATCCCTCCGTCTCCTTCAATTTGGCGGGAGCCAAGTCGACTACATACAGGGACTTCTTA 174

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThr---ProValCysGlnLeuProValThr 37
              ::::::||||||:::   :::|||  ||||||     |||     |||||||||
Db        175 AAGAACCTGCGAGATAGGGTCGCAACTGGCACCTATGAAGTAAATGGTTTACCAGTGCTG 234

Qy         38 LeuGln------ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::         :::           ||||||||||||||   :::|||
Db        235 AGACGCGAAAGTGAAGTACAGGTCAAGAATCGGTTCGTTTTGGTCCGTCTCACCAATTAC 294

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::      ||||||      |||:::||||||||:::::::|||:::|||   :::
Db        295 AATGGAGACACCGTCACCTCGGCAGTAGATGTGACCAACCTTTACTTGGTGGCTTTT--- 351

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
                                     :::   |||                  :::
Db        352 ---------AGTGCAAATGGAAACTCCTACTTTTTCAAGGACGCTACGGAACTTCAAAAG 402

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
              |||   ||||||   |||   |||         ||||||:::|||   |||:::|||
Db        403 AGTAATTTATTCCTTGGCACCACGCAACAT---ACGTTATCCTTCACGGGAAACTATGAC 459

Qy        116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
                 |||      ||||||         |||:::   :::|||||||||         |||
Db        460 AACCTTGAGACTGCGGCAGGAACTAGGAGGGAGTCTATCGAACTGGGACCCAATCCCCTA 519

Qy        136 GluPheSerIleGluAlaIleTrp 143
              :::   :::|||   ::::::|||
Db        520 GATGGGGCCATTACTAGTTTGTGG 543

RESULT 40
AY669811
LOCUS       AY669811                741 bp    DNA     linear   PLN 10-AUG-2004
DEFINITION  Trichosanthes kirilowii trichosanthin precursor (TCS) gene, partial
            cds.
ACCESSION   AY669811
VERSION     AY669811.1  GI:50980408
KEYWORDS    .
SOURCE      Trichosanthes kirilowii
  ORGANISM  Trichosanthes kirilowii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   Mi,S.-L., Wang,Y., Li,Y.-Y., Chen,Z.-L. and An,C.-C.
  TITLE     Trichosanthes kirilowii trichosanthin (TCS) mature peptide gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 741)
  AUTHORS   Mi,S.-L., Wang,Y., Li,Y.-Y., Chen,Z.-L. and An,C.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-2004) College of Life Sciences, Peking
            University, No.5, Yiheyuan Road, Beijing, Beijing 100871, China
FEATURES             Location/Qualifiers
     source          1. .741
                     /organism="Trichosanthes kirilowii"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3677"
     gene            <1. .>741
                     /gene="TCS"
     mRNA            <1. .>741
                     /gene="TCS"
                     /product="trichosanthin precursor"
     CDS             <1. .>741
                     /gene="TCS"
                     /note="ribosome-inactivating protein; glycosidase"
                     /codon_start=1
                     /product="trichosanthin precursor"
                     /protein_id="AAT91090.1"
                     /db_xref="GI:50980409"
                     /translation="DVSFRLSGATSSSYGVFISNLRKALPNERRLYDIPLLRSTLQGS
                     QRYALIHLTNYADETISVAIDVTNVYIMGYRAGDTSYFFNEASATEAAKYVFKDAMRK
                     VTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTLFYYNANSAASALMVLIQSTSE
```

```
                     AARYKFIEQQIGKRADKTFLPSLAIISLENSWSALSKQIQIASTNNGQFETPVVLINA
                     QNQRVAITNVDAGVVTSNIALLLNRNNMA"
     mat_peptide     1. .741
                     /gene="TCS"
                     /product="trichosanthin"
ORIGIN

Alignment Scores:
Pred. No.:              5.47e-11        Length:         741
Score:                  186.50          Matches:        45
Percent Similarity:     53.5%           Conservative:   31
Best Local Similarity:  31.7%           Mismatches:     61
Query Match:            24.3%           Indels:         5
DB:                     15              Gaps:           2

US-10-758-902-9 (1-149) x AY669811 (1-741)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db          4 GTTAGCTTCCGGTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 63

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              :::      :::|||:::         |||:::
Db         64 AGAAAAGCTCTTCCAAATGAAAGGAGACTATACGATATCCCTCTGTTACGTTCCACTCTT 123

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        124 CAAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 183

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::|||||:::          |||
Db        184 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 234

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::          |||   |||          :::|||
Db        235 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 294

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::||||||||||   :::   |||:::|||:::::::|||      ||||||
Db        295 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 354

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                |||:::::::::   ||||||:::      |||:::   :::|||
Db        355 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 414

Qy        142 IleTrp 143
              ::::::
Db        415 TTGTTT 420


Search completed: February 20, 2006, 13:14:27
Job time : 6021.94 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2006, 23:33:13 ; Search time 735.011 Seconds
(without alignments)
1351.053 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160757_3660/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h
-USER=US10758902_@CGN_1_1_900_@runat_17022006_160757_3660 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	609	79.3	363	2	AAV81468	Aav81468 Ribosome-
2	221.5	28.8	756	2	AAQ05763	Aaq05763 Sequence
3	221.5	28.8	756	2	AAQ10568	Aaq10568 Mirabilis
4	220.5	28.7	913	2	AAQ42307	Aaq42307 Momordin
5	220.5	28.7	913	2	AAQ76184	Aaq76184 Type I ri
6	211.5	27.5	762	2	AAQ28570	Aaq28570 Synthetic
7	190.5	24.8	962	2	AAQ89874	Aaq89874 Bryodin-2
8	183.5	23.9	751	2	AAQ75305	Aaq75305 Trichosan
9	183.5	23.9	800	2	AAQ06346	Aaq06346 Synthetic
10	183.5	23.9	800	2	AAQ26500	Aaq26500 Trichosan
11	183.5	23.9	870	4	AAH41473	Aah41473 Trichosan
12	183.5	23.9	870	6	ABA95171	Aba95171 Native tr
13	183.5	23.9	870	14	AEC15951	Aec15951 Trichosan
14	183.5	23.9	886	2	AAQ65573	Aaq65573 Alpha-tri
15	183.5	23.9	886	2	AAT47094	Aat47094 Chinese c
16	183.5	23.9	886	2	AAT61376	Aat61376 Chinese c
17	183.5	23.9	886	2	AAX29143	Aax29143 Chinese c
18	183.5	23.9	886	2	AAX03385	Aax03385 DNA seque
19	183.5	23.9	886	3	AAA12393	Aaa12393 Chinese c
20	183.5	23.9	886	10	ADH44105	Adh44105 Chinese c
21	183.5	23.9	886	12	ADO43820	Ado43820 Chinese c
22	183.5	23.9	1227	2	AAQ06343	Aaq06343 Encodes T
23	183.5	23.9	1227	2	AAQ31826	Aaq31826 Recombina
24	183.5	23.9	1228	2	AAQ26499	Aaq26499 Trichosan
25	183.5	23.9	1380	13	ADW14401	Adw14401 Trichosan
26	182.5	23.8	885	2	AAQ37679	Aaq37679 Encodes c
27	182.5	23.8	1169	2	AAQ06350	Aaq06350 Alpha-Tri
28	182.5	23.8	1169	2	AAQ26504	Aaq26504 Ribosome
29	179.5	23.4	758	4	AAC60425	Aac60425 DNA encod
30	179.5	23.4	762	2	AAZ09107	Aaz09107 Mistletoe
31	179.5	23.4	762	2	AAZ09104	Aaz09104 Mistletoe
32	179.5	23.4	768	2	AAZ09105	Aaz09105 Mistletoe
33	179.5	23.4	768	2	AAZ09108	Aaz09108 Mistletoe
34	179.5	23.4	1094	2	AAT16208	Aat16208 Bryodin 1
35	179.5	23.4	1499	4	AAC60429	Aac60429 BD1-G28.5
36	176.5	23.0	756	2	AAV51343	Aav51343 Mistletoe
37	176.5	23.0	762	2	AAV51341	Aav51341 Mistletoe
38	176.5	23.0	774	2	AAT91660	Aat91660 Prepro mi
39	176.5	23.0	774	2	AAV74180	Aav74180 Mistletoe
40	176.5	23.0	855	9	ACC85526	Acc85526 Mistletoe
41	176.5	23.0	1596	2	AAZ09106	Aaz09106 Mistletoe
42	176.5	23.0	1596	2	AAZ09103	Aaz09103 Mistletoe
43	176.5	23.0	1923	2	AAT91659	Aat91659 Prepro mi
44	176.5	23.0	1923	2	AAV74182	Aav74182 Mistletoe
45	176.5	23.0	1958	9	ACC85528	Acc85528 Mistletoe
46	174.5	22.7	1656	6	ABL56947	Abl56947 Galactose
47	174.5	22.7	1873	11	ADM64632	Adm64632 Viscum al
48	171.5	22.3	762	4	AAC85473	Aac85473 A-chain g
49	171	22.3	686	2	AAQ06347	Aaq06347 Trichosan
50	170.5	22.2	1185	2	AAQ06351	Aaq06351 Alpha-Tri
51	170.5	22.2	1185	2	AAQ26505	Aaq26505 Ribosome
52	170	22.1	686	2	AAQ26501	Aaq26501 Ribosome
53	169	22.0	600	1	AAN80190	Aan80190 DNA encod
54	169	22.0	848	4	AAS02363	Aas02363 Castor be
55	169	22.0	1050	1	AAN50380	Aan50380 Ricin-A s
56	169	22.0	1050	1	AAN70152	Aan70152 Ricin A g
57	169	22.0	1050	1	AAN70519	Aan70519 Sequence
58	169	22.0	1050	1	AAN91281	Aan91281 Cloning i
59	169	22.0	1140	2	AAQ27876	Aaq27876 Ricin A g
60	169	22.0	1731	4	AAI64138	Aai64138 Castor be
61	169	22.0	1731	4	AAI64139	Aai64139 Castor be
62	169	22.0	1805	4	AAI64145	Aai64145 Modified
63	169	22.0	1807	5	AAI79901	Aai79901 Mutant pr
64	169	22.0	1810	5	AAI79884	Aai79884 Mutant pr
65	169	22.0	1813	5	AAI79929	Aai79929 Mutant pr
66	169	22.0	1819	5	AAI79925	Aai79925 Mutant pr
67	169	22.0	1822	5	AAI79892	Aai79892 Mutant pr
68	169	22.0	1822	5	AAI79888	Aai79888 Mutant pr
69	169	22.0	1825	5	AAI79921	Aai79921 Mutant pr
70	169	22.0	1828	5	AAI79909	Aai79909 Mutant pr
71	169	22.0	1831	5	AAI79905	Aai79905 Mutant pr
72	169	22.0	1831	5	AAI79880	Aai79880 Mutant pr
73	169	22.0	1834	5	AAI79876	Aai79876 Mutant pr
74	169	22.0	1837	5	AAH77622	Aah77622 Mutant pr
75	169	22.0	1843	5	AAI79937	Aai79937 Mutant pr
76	169	22.0	1849	5	AAI79933	Aai79933 Mutant pr
77	169	22.0	1855	5	AAI79872	Aai79872 Mutant pr

78	169	22.0	1855	5	AAI79897	Aai79897 Mutant pr
79	169	22.0	1855	5	AAI79913	Aai79913 Mutant pr
80	169	22.0	1855	5	AAI79917	Aai79917 Mutant pr
81	169	22.0	1922	1	AAN70525	Aan70525 Sequence
82	169	22.0	1923	1	AAN91039	Aan91039 DNA seque
83	169	22.0	1946	1	AAN70526	Aan70526 Sequence
84	169	22.0	1979	2	AAQ85386	Aaq85386 Anti-cata
85	169	22.0	2344	2	AAT91638	Aat91638 Castorbea
86	169	22.0	2344	2	AAZ30663	Aaz30663 Castor be
87	169	22.0	2344	3	AAZ90019	Aaz90019 Ricinus c
88	169	22.0	3077	1	AAN90068	Aan90068 Ricin D g
89	168.5	21.9	762	4	AAC85472	Aac85472 A-chain g
90	168.5	21.9	852	2	AAZ23155	Aaz23155 A. viridi
91	168.5	21.9	1019	3	ABL50968	Abl50968 Virus inf
92	168.5	21.9	1047	3	ABL50893	Abl50893 Amaranthu
93	168	21.9	807	2	AAQ46085	Aaq46085 Sequence
94	168	21.9	1050	2	AAQ05786	Aaq05786 Ricin A e
95	168	21.9	7306	8	ABZ77370	Abz77370 Nucleotid
96	168	21.9	8155	8	ABZ77369	Abz77369 Nucleotid
97	167	21.7	1698	4	AAI64137	Aai64137 Castor be
98	167	21.7	1855	2	AAT97913	Aat97913 Plasmid p
99	167	21.7	1855	2	AAT97919	Aat97919 Plasmid p
100	167	21.7	1855	2	AAT97910	Aat97910 Plasmid p

ALIGNMENTS

RESULT 1
AAV81468
ID AAV81468 standard; DNA; 363 BP.
XX
AC AAV81468;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE Ribosome-inactivating protein, coding sequence fragment.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; ss.
XX
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX
PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 24; 39pp; English.
XX
CC This sequence represents a fragment of the DNA encoding the ribosome-
CC inactivating protein (RIP) of the invention. The RIP is designated
CC bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,
CC where the amino-terminal end exhibits 50 % homology with the sequence
CC shown in AAW67752. The proteins and conjugates form compositions in
CC treating various human diseases or conditions, including cancer, graft-
CC versus-host disease, organ transplant rejection, type I diabetes,
CC multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC viral agents in plants and mammals. Compositions containing the
CC polynucleotide encoding bouganin are useful in gene therapy. Bouganin
CC possesses low non-specific toxicity, which makes it very suitable for use
CC as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 363 BP; 110 A; 68 C; 85 G; 100 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.64e-69	Length:	363
Score:	609.00	Matches:	120
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	79.3%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-9 (1-149) x AAV81468 (1-363)

```
Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361
```

RESULT 2
AAQ05763
ID AAQ05763 standard; DNA; 756 BP.
XX
AC AAQ05763;
XX
DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 04-JAN-1991 (first entry)
XX
DE Sequence encoding Mirabilis antiviral protein (MAP).
XX
KW E.coli expression vector; ds.
XX
OS Unidentified.
XX
PN JP02186988-A.
XX
PD 23-JUL-1990.
XX
PF 18-APR-1988; 88JP-00093494.
XX
PR 14-APR-1988; 88JP-00090166.
XX
PA (NISB) JAPAN TOBACCO & SALT PUBLIC.
XX
DR WPI; 1990-265444/35.
DR P-PSDB; AAR06542.
XX
PT Anti:viral protein prepn. - by culturing E. coli transformant and protein
PT produced is sepd. and purified.

XX
PS Claim 2; Fig 2; 14pp; Japanese.
XX
CC Sequence may be used to transform E.coli expression system to obtain
CC product. Recombinant plasmid used is pKK233-3. (Updated on 10-MAR-2003 to
CC add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 756 BP; 219 A; 195 C; 148 G; 194 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.24e-18	Length:	756
Score:	221.50	Matches:	54
Percent Similarity:	55.9%	Conservative:	27
Best Local Similarity:	37.2%	Mismatches:	55
Query Match:	28.8%	Indels:	9
DB:	2	Gaps:	4

US-10-758-902-9 (1-149) x AAQ05763 (1-756)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||                 |||   :::||||||   :::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 84

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||       |||       |||           |||:::|||   |||:::
Db         85 GTCGCAGACAAAACCGAACAGTGT-----------ACCATCCAGAAAATCTCTAAAACC 132

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                 :::|||:::     :::|||:::     :::|||   :::   :::   :::
Db        133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||||:::   |||:::||||||:::||||||   |||       :::   |||
Db        193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              ||||||   |||       |||                :::       |||||||||
Db        253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||       |||
Db        313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                 :::   |||||||||       ||||||:::::::::||||||   ||||||
Db        373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429

Qy        141 AlaIleTrpGlyLys 145
                |||:::||||||
Db        430 AACATTTATGGCAAA 444
```

RESULT 3
AAQ10568
ID AAQ10568 standard; DNA; 756 BP.
XX
AC AAQ10568;
XX
DT 26-APR-1991 (first entry)
XX
DE Mirabilis antiviral protein gene.
XX
KW Mirabilis antiviral protein; MAP; Omp A signal sequence; ds.
XX
OS Mirabilis jalapa.
XX
PN EP414134-A.
XX
PD 27-FEB-1991.
XX
PF 16-AUG-1990; 90EP-00115718.
XX
PR 17-AUG-1989; 89JP-00210767.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
PI Habuka N, Akiyama K, Tsuge H, Matsumoto T, Noma M;
XX
DR WPI; 1991-059386/09.
XX
PT Gene encoding Mirabilis Antiviral Protein and OmPa signal peptide - for
PT mass-prodn. of extracellular map.
XX
PS Claim 1; Page 8; 15pp; English.
XX
CC This Mirabilis antiviral protein (MAP) gene is contained in a rec-
CC ombinant plasmid, flanked on its 5' side by an OmpA signal peptide-
CC encoding sequence to ensure its extracellular secretion. The plasmid is
CC used to transform E.coli host cells in the large-scale prodn. of MAP. See
CC also AAQ10569
XX
SQ Sequence 756 BP; 219 A; 195 C; 148 G; 194 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.24e-18	Length:	756
Score:	221.50	Matches:	54
Percent Similarity:	55.9%	Conservative:	27
Best Local Similarity:	37.2%	Mismatches:	55
Query Match:	28.8%	Indels:	9
DB:	2	Gaps:	4

US-10-758-902-9 (1-149) x AAQ10568 (1-756)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||                 |||   :::||||||   :::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 84

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||       |||       |||           |||:::|||   |||:::
Db         85 GTCGCAGACAAAACCGAACAGTGT-----------ACCATCCAGAAAATCTCTAAAACC 132

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                 :::|||:::     :::|||:::     :::|||   :::   :::   :::
Db        133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||||:::   |||:::||||||:::||||||   |||       :::   |||
Db        193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              ||||||   |||       |||                :::       |||||||||
Db        253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||       |||
Db        313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                 :::   |||||||||       ||||||:::::::::||||||   ||||||
Db        373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429

Qy        141 AlaIleTrpGlyLys 145
                |||:::||||||
Db        430 AACATTTATGGCAAA 444
```

RESULT 4
AAQ42307
ID AAQ42307 standard; cDNA; 913 BP.
XX
AC AAQ42307;
XX
DT 25-MAR-2003 (revised)
DT 13-SEP-1993 (first entry)
XX
DE Momordin II coding sequence.
XX
KW Type I Ribosome Inactivating Protein; RIP; immunoconjugate;

```
KW   autoimmune disease; cell killing; toxin; polymerase chain reaction; ss.
XX
OS   Momordica balsamina.
XX
PN   WO9309130-A1.
XX
PD   13-MAY-1993.
XX
PF   04-NOV-1992;   92WO-US009487.
XX
PR   04-NOV-1991;   91US-00787567.
PR   19-JUN-1992;   92US-00901707.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Berhard SL,  Better MD,  Carroll SF,  Lane JA,  Lei SP;
XX
DR   WPI; 1993-167617/20.
XX
PT   Analogues of type I ribosome inactivating protein - useful as cytotoxic
PT   agents, immuno toxins for treating auto immune diseases, cancer, graft
PT   versus host disease and selective cell killing in=vivo.
XX
PS   Example 14; Page 88; 163pp; English.
XX
CC   Two partially degenerate primers (AAQ42302 and AAQ42303) were synthesised
CC   based on the amino acid sequence of the first 27 amino acids of momordin
CC   II (Experimentia, 36: 524-527 (1991)). The resulting 81bp PCR product
CC   amplified from M.balsamina cDNA was cloned in pUC18 and one of the
CC   candidate clones (pMO110) which was sequenced was identified as encoding
CC   the N-terminal 27 amino acids of momordin II. A hybridisation probe
CC   (AAQ42304) was designed for screening the momordin II cDNA library based
CC   on the sequence of pMO110. The full-length Momordin II coding sequence
CC   was isolated i.e. AAQ42307. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 913 BP; 274 A; 206 C; 159 G; 274 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.14e-18      Length:         913
Score:                  220.50        Matches:        52
Percent Similarity:     59.9%         Conservative:   33
Best Local Similarity:  36.6%         Mismatches:     50
Query Match:            28.7%         Indels:         7
DB:                     2             Gaps:           3

US-10-758-902-9 (1-149) x AAQ42307 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||              |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::    |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                       |||::::::::::::||||||:::      |||  .    :::|||
```

```
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
                 ::::::
Db        487 TTGTTT 492

RESULT 5
AAQ76184
ID   AAQ76184 standard; cDNA; 913 BP.
XX
AC   AAQ76184;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   28-JUL-1995  (first entry)
XX
DE   Type I ribosome-inactivating protein mormordin II cDNA.
XX
KW   Type I ribosome-inactivating proteins; mormordin II; RIPs;
KW   cytotoxic therapeutic agents; autoimmune disease; cancer;
KW   graft-versus-host disease; MOMOII; ss.
XX
OS   Momordica balsamina.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     79. .720
FT                   /*tag=  a
FT                   /transl_except= pos:661. .720
FT                   /note= "corresponding amino acids 195. .263 of AAR63905"
XX
PN   WO9426910-A1.
XX
PD   24-NOV-1994.
XX
PF   12-MAY-1994;   94WO-US005348.
XX
PR   12-MAY-1993;   93US-00064691.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Better MD,  Carroll SF,  Studnicka GM;
XX
DR   WPI; 1995-006804/01.
DR   P-PSDB; AAR63905.
XX
PT   Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT   are suitable for use as components of cytotoxic therapeutic agents.
XX
PS   Example 25; Page 156-157; 221pp; English.
XX
CC   AAQ76184 encodes AAR63905 the type I ribosome-inactivating protein (RIP)
CC   momordin II, one of the nine RIPs described in AAR63903-R63911. RIPs are
CC   key components of cytotoxic therapeutic agents (CTAs), which include gene
CC   fusion products and immunoconjugates. CTAs may be used to selectively
CC   eliminate any cell type to which a RIP component is targetted, by the
CC   specific binding capacity of the second component of the agent. They can
CC   be used in the treatment of diseases where the elimination of a
CC   particular cell type is desired, such as autoimmune disease, cancer and
CC   graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 913 BP; 274 A; 205 C; 160 G; 274 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.14e-18      Length:         913
Score:                  220.50        Matches:        52
Percent Similarity:     59.9%         Conservative:   33
Best Local Similarity:  36.6%         Mismatches:     50
Query Match:            28.7%         Indels:         7
DB:                     2             Gaps:           3

US-10-758-902-9 (1-149) x AAQ76184 (1-913)
```

```
Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||          |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              |||      :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::               :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
              |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::::|||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492
```

```
RESULT 6
AAQ28570
ID   AAQ28570 standard; DNA; 762 BP.
XX
AC   AAQ28570;
XX
DT   25-MAR-2003  (revised)
DT   18-FEB-1993  (first entry)
XX
DE   Synthetic gene encoding MAP.
XX
KW   Mirabilis antiviral protein; ribosome inactivating protein; toxic;
KW   immunotoxin; analogue; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .753
FT                   /*tag=  a
FT   misc_feature    1. .76
FT                   /*tag=  b
FT                   /note= "synthetic oligomer 1"
FT   misc_feature    77. .172
FT                   /*tag=  c
FT                   /note= "synthetic oligomer 2"
FT   misc_feature    173. .303
FT                   /*tag=  d
FT                   /note= "synthetic oligomer 3"
FT   misc_feature    303. .396
FT                   /*tag=  e
FT                   /note= "synthetic oligomer 4"
FT   misc_feature    397. .508
FT                   /*tag=  f
FT                   /note= "synthetic oligomer 5"
FT   misc_feature    509. .614
FT                   /*tag=  g
FT                   /note= "synthetic oligomer 6"
FT   misc_feature    615. .678
FT                   /*tag=  h
FT                   /note= "synthetic oligomer 7"
FT   misc_feature    679. .756
FT                   /*tag=  i
FT                   /note= "synthetic oligomer 8"
XX
PN   EP504919-A2.
XX
PD   23-SEP-1992.
XX
PF   20-MAR-1992;   92EP-00104879.
XX
PR   22-MAR-1991;   91JP-00083456.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
PI   Habuka N,  Miyano M,  Matsumoto T,  Noma M;
XX
DR   WPI; 1992-317828/39.
DR   P-PSDB; AAR27241.
XX
PT   Protein isolated from Mirabilis Jalapa - is Mirabilis antiviral protein
PT   variant, acts as an immuno-toxin in treating viral infections.
XX
PS   Claim 2; Fig 1; 35pp; English.
XX
CC   The synthetic MAP gene was constructed from eight synthetic oligomer
CC   blocks which were synthesised based on sequences obtd. from a MAP protein
CC   isolated from Mirabilis jalapa. The two Cys codons were replaced with Ser
CC   codons. The gene was then ligated into an E. coli expression vector with
CC   appropriate control sequences and the OmpA signal for secretion of the
CC   MAP protein. MAP is a ribosome inactivating protein and is toxic. This
CC   toxicity can be used to develop immunotoxins having high selectivity by
CC   linking the protein to various antibodies. The native protein however has
CC   only 1/30 th of the toxicity of the ricin A chain. The protein encoded by
CC   the synthetic gene shown is designated MAP-H and has a disulphide bond
CC   removed. This results in an analogue with greater protein synthesis
CC   inhibitory activity and hence greater toxicity than native MAP. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 762 BP; 222 A; 198 C; 147 G; 195 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              2.44e-17        Length:         762
Score:                  211.50          Matches:        53
Percent Similarity:     55.2%           Conservative:   27
Best Local Similarity:  36.6%           Mismatches:     56
Query Match:            27.5%           Indels:         9
DB:                     2               Gaps:           4

US-10-758-902-9 (1-149) x AAQ28570 (1-762)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||              |||   :::||||||   ::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 84

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||      |||                     |||:::|||   |||:::
Db         85 GTCGCAGACAAAACCGAA-----------CAGTCGACCATCCAGAAAATCTCTAAAACC 132

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                 :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||||:::   |||:::||||||:::||||||   |||      :::   |||
Db        193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              ||||||   |||          |||                :::      |||||||||
Db        253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||      |||
Db        313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372
```

```
Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                  :::   ||||||||      ||||||:::::::::||||||   ||||||
Db        373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429

Qy        141 AlaIleTrpGlyLys 145
                ||||::||||||
Db        430 AACATTTATGGCAAA 444

RESULT 7
AAQ89874
ID   AAQ89874 standard; cDNA; 962 BP.
XX
AC   AAQ89874;
XX
DT   21-OCT-2004  (revised)
DT   25-MAR-2003  (revised)
DT   31-JAN-1997  (first entry)
XX
DE   Bryodin-2 cDNA.
XX
KW   Ribosome inactivating protein; cell death; proliferation; tumour; cancer;
KW   virus; malaria; trypanosomiasis; inflammation; autoimmune; disease;
KW   purging; bone marrow; ss.
XX
OS   Bryonia dioica.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             28. .876
FT                   /*tag=  b
FT                   /product= "Bryodin-2"
FT   sig_peptide     28. .90
FT                   /*tag=  a
FT   mat_peptide     91. .873
FT                   /*tag=  c
XX
PN   WO9511977-A2.
XX
PD   04-MAY-1995.
XX
PF   25-OCT-1994;   94WO-US012382.
XX
PR   25-OCT-1993;   93US-00141891.
PR   20-OCT-1994;   94US-00324301.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Siegall CB,  Gawlak SL,  Marquardt H;
XX
DR   WPI; 1995-178870/23.
DR   P-PSDB; AAR74217.
XX
PT   New ribosome inactivating protein bryodin-2 and related conjugates - for
PT   killing target cells, e.g. in treatment of cancer, also related nucleic
PT   acid, vectors and transformed cells.
XX
PS   Claim 21; Page 54-55; 81pp; English.
XX
CC   The sequence encodes the ribosome inactivating protein termed bryodin-2,
CC   isolated from Bryonia dioica. Conjugates of the protein with a ligand may
CC   be used to kill target cells (i.e. those to which the ligand component
CC   binds specifically) or to inhibit proliferation of tumour cells. Typical
CC   applications include the treatment of cancer, viral infections, malaria,
CC   trypanosomiasis, inflammatory or autoimmune diseases, including in vitro
CC   purging of e.g. bone marrow. (Updated on 25-MAR-2003 to correct PN
CC   field.)
CC
CC   Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
SQ   Sequence 962 BP; 274 A; 198 C; 212 G; 278 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.71e-14       Length:        962
Score:                  190.50         Matches:       50
Percent Similarity:     57.8%          Conservative:  24
Best Local Similarity:  39.1%          Mismatches:    47
Query Match:            24.8%          Indels:        7
DB:                     2              Gaps:          4

US-10-758-902-9 (1-149) x AAQ89874 (1-962)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro---ValCys 32
              |||   |||||||||:::::||||||   :::|||      |||||||||   |||
Db        133 TACAAAACTTTTATAAGGAATCTGCGCACCAAACTCACGGTTGGAACTCCAAGGGTGTAC 192

Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
                 :::||||||              |||          ||||||   ||||||   :::
Db        193 GATATACCTGTCCTGAGAAACGCAGCAGCCGGGCTCGCGCGCTTTCAATTAGTTACCCTC 252

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
              |||      :::   ::::::|||   ||||||:::|||||||   :::|||||||||||||
Db        253 ACAAATTACAATGGCGAATCTGTCACTGTGGCTTTAGATGTAGTGAACGTGTACGTTGTT 312

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
              |||:::                ::::   |||   ||||||                |||
Db        313 GCATATCGA------------GCTGGAAACACTGCTTACTTTCTCGCAGATGCATCAACA 360

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||   |||:::   |||   |||   |||   :::   |||
Db        361 GAAGCCAACAATGTGTTGTTTGCAGGCATC---AATCATGTAAGACTTCCTTATGGAGGG 417

Qy        113 SerTyrGlnLysLeuValAsnAlaAla---LysValAspArgLysAspLeuGluLeuGly 131
              :::|||      |||      ||||||   ::::::   |||:::::::::|||||||||
Db        418 AATTACGATGGCCTTGAGACAGCTGCAGGCAGAATTTCGAGGGAAAATATTGAACTTGGA 477

Qy        132 ValTyrLysLeuGluPheSerIle 139
                    ::::::      :::|||
Db        478 TTTTCCGAAATAAGTAGTGCCATT 501

RESULT 8
AAQ75305
ID   AAQ75305 standard; DNA; 751 BP.
XX
AC   AAQ75305;
XX
DT   25-MAR-2003  (revised)
DT   26-JUL-1995  (first entry)
XX
DE   Trichosanthin antiviral protein DNA.
XX
KW   Antiviral agent; trichosanthin; HIV; hepatitis virus; ds.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     6. .746
FT                   /*tag=  a
XX
PN   WO9426898-A1.
XX
PD   24-NOV-1994.
XX
PF   17-MAY-1994;   94WO-CN000037.
XX
PR   19-MAY-1993;   93CN-00112436.
XX
PA   (SHAN-) SHANGHAI INST ORGANIC CHEM.
XX
PI   Chen H,  Xia Y,  Jiang K,  Bao J;
XX
DR   WPI; 1995-006794/01.
DR   P-PSDB; AAR67359.
XX
PT   New genetically engineered gene for trichosanthin protein - expressed in
PT   E.coli, used to produce the protein for use as antiviral agent against
PT   HIV and hepatitis virus.
```

```
XX
PS   Claim 1; Fig 1; 37pp; Chinese.
XX
CC   AAQ75305 encodes AAR67359 an antiviral protein isolated from the roots of
CC   Trichosanthes kirilowii. The trichosanthin antiviral protein is useful
CC   for controlling viral infections such as HIV and hepatitis. (Updated on
CC   25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 751 BP; 196 A; 212 C; 155 G; 188 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.8e-14       Length:        751
Score:                  183.50        Matches:       44
Percent Similarity:     53.5%         Conservative:  32
Best Local Similarity:  31.0%         Mismatches:    61
Query Match:            23.9%         Indels:        5
DB:                     2             Gaps:          2

US-10-758-902-9 (1-149) x AAQ75305 (1-751)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db          9 GTCAGCTTCCGTCTGTCTGGTGCAACGAGCTCTTCATATGGCGTTTTCATCTCTAACCTG 68

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||           :::      :::|||:::         ::::::
Db         69 CGTAAGGCCCTTCCGAACGAACGTAAACTGTACGACATCCCCCTGCTGAGATCTTCTCTC 128

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        129 CCCGGATCCCAGCGCTATGCATTGATCCATCTGACCAACTACGCTGATGAAACCATTTCT 188

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||::::::||||||:::           |||
Db        189 GTGGCTATCGATGTAACTAACGTATACATCATGGGATATCGC---------GCTGGCGAC 239

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                 |||   :::         |||   |||         :::|||
Db        240 ACTTCCTACTTTTTCAACGAAGCGTCTGCCACAGAGGCTGCAAAATACGTATTCAAAGAC 299

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 :::||||||||||   :::   |||:::|||:::::::|||      ||||||
Db        300 GCTATGCGTAAGGTTACCCTGCCGTACTCTGGCAACTACGAACGTCTGCAGACCGCAGCC 359

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                |||:::::::::   ||||||:::      |||:::   :::|||
Db        360 GGCAAAATCCGTGAAAACATTCCCCTTGGTCTCCCAGCTCTAGACAGCGCTATCACCACG 419

Qy        142 IleTrp 143
              ::::::
Db        420 CTGTTT 425

RESULT 9
AAQ06346
ID   AAQ06346 standard; DNA; 800 BP.
XX
AC   AAQ06346;
XX
DT   06-FEB-1991  (first entry)
XX
DE   Synthetic Trichosanthin gene.
XX
KW   trichosanthin (TCS); Human Immunodeficiency Virus; inhibition; ss.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             38. .787
FT                   /*tag= a
FT                   /product= "mature alpha-TCS"
XX
PN   WO9012097-A.
XX
PD   18-OCT-1990.
XX
PF   04-APR-1989;   89US-00333184.
XX
PR   04-APR-1989;   89US-00333184.
XX
PA   (GENE-) GENELABS INC.
XX
PI   Piatek M,  Chow T,  Fry K;
XX
DR   WPI; 1990-334847/44.
DR   P-PSDB; AAR07518.
XX
PT   Recombinant tri:chosanthin protein - with selective inhibitory effect on
PT   viral expression in HIV infected T-cells or monocyte-macrophase.
XX
PS   Example; Fig 11; 102pp; English.
XX
CC   Synthetic gene containing unique restriction sites spaced 20 to 90 bp
CC   apart. Introduction of mutantions is facilitated by cassette replacement.
CC   The effect of mutations on inhibitory action can be investigated. For
CC   example, a double mutant containing the amino acid substitutions Glu(160)
CC   to Asp and Arg(163) to Lys was found to be almost 3 logs less active at
CC   inhibiting in vitro translation in rabbit reticulocyte lysate. See also
CC   AAQ06343-5 and AAQ06347-Q06351
XX
SQ   Sequence 800 BP; 207 A; 208 C; 182 G; 203 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.07e-13      Length:        800
Score:                  183.50        Matches:       44
Percent Similarity:     53.5%         Conservative:  32
Best Local Similarity:  31.0%         Mismatches:    61
Query Match:            23.9%         Indels:        5
DB:                     2             Gaps:          2

US-10-758-902-9 (1-149) x AAQ06346 (1-800)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db         44 GTTTCTTTTCGTCTTTCCGGTGCAACCTCTTCATCTTATGGTGTATTTATTTCTAACCTG 103

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||           :::      :::|||:::         ::::::
Db        104 CGTAAAGCTTTGCCGAACGAACGCAAACTGTATGACATCCCGCTGTTGCGTAGCTCCCTG 163

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        164 CCGGGCAGCCAGCGTTATGCATTAATTCATCTGACGAATTACGCCGATGAAACTATCTCC 223

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||::::::||||||:::           |||
Db        224 GTGGCAATCGATGTTACCAATGTCTACATTATGGGCTATCGC---------GCCGGTGAC 274

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::         |||   |||         :::|||
Db        275 ACTAGTTATTTCTTTAATGAGGCTAGCGCGACTGAAGCCGCTAAATACGTATTCAAGGAT 334

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 :::||||||||||   :::   |||:::|||:::::::|||      ||||||
Db        335 GCGATGCGTAAAGTGACCCTGCCATACAGCGGCAACTATGAACGTCTGCAGACGGCAGCC 394

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                |||:::::::::   ||||||:::      |||:::   :::|||
Db        395 GGTAAGATCCGTGAGAACATTCCGCTTGGCTTACCAGCTCTAGACTCCGCGATCACGACT 454

Qy        142 IleTrp 143
              ::::::
Db        455 CTCTTC 460

RESULT 10
AAQ26500
ID   AAQ26500 standard; DNA; 800 BP.
```

```
XX
AC   AAQ26500;
XX
DT   25-MAR-2003  (revised)
DT   13-JAN-1993  (first entry)
XX
DE   Trichosanthin synthetic gene.
XX
KW   TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient;
KW   ribosome inactivating protein; RIP; HIV-infected human T cells;
KW   human immunodeficiency virus; Trichosanthes kirilowii; ss.
XX
OS   Synthetic.
XX
PN   US5128460-A.
XX
PD   07-JUL-1992.
XX
PF   04-APR-1990;   90US-00504775.
XX
PR   04-APR-1989;   89US-00333184.
PR   07-SEP-1989;   89US-00404326.
XX
PA   (GENE-) GENELABS INC.
XX
PI   Piatak M,  Chow TP,  Fry K;
XX
DR   WPI; 1992-249485/30.
DR   P-PSDB; AAR25573.
XX
PT   Nucleic acid encoding trichosanthin protein - which can be used to
PT   inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV
PT   expression.
XX
PS   Example 6; Fig 11; 53pp; English.
XX
CC   A synthetic alpha-trichosanthin gene was constructed to facilitate
CC   mutational analysis of alpha-TCS in experiments to investigate structure-
CC   function relationships. The synthetic gene contains unique restriction
CC   sites spaced 20-90bp apart. The translation product of the synthetic gene
CC   corresponds to the mature alpha-TCS. Variants of the protein can be
CC   generated by mutagenesis of the synthetic gene. The variants can then be
CC   screened for changes in ribosome inhibitory and/or HIV-1 inhibitory
CC   activities. See AAQ26499-Q26505. (Updated on 25-MAR-2003 to correct PF
CC   field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 800 BP; 207 A; 208 C; 182 G; 203 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.07e-13        Length:         800
Score:                  183.50          Matches:        44
Percent Similarity:     53.5%           Conservative:   32
Best Local Similarity:  31.0%           Mismatches:     61
Query Match:            23.9%           Indels:         5
DB:                     2               Gaps:           2

US-10-758-902-9 (1-149) x AAQ26500 (1-800)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||            |||      ||||||   :::|||
Db         44 GTTTCTTTTCGTCTTTCCGGTGCAACCTCTTCATCTTATGGTGTATTTATTTCTAACCTG 103

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               :::      :::|||:::         ::::::
Db        104 CGTAAAGCTTTGCCGAACGAACGCAAACTGTATGACATCCCGCTGTTGCGTAGCTCCCTG 163

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        164 CCGGGCAGCCAGCGTTATGCATTAATTCATCTGACGAATTACGCCGATGAAACTATCTCC 223

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||:::||||||:::::||||||:::            |||
Db        224 GTGGCAATCGATGTTACCAATGTCTACATTATGGGCTATCGC---------GCCGGTGAC 274

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
                     |||   :::         |||   |||         :::|||
Db        275 ACTAGTTATTTCTTTAATGAGGCTAGCGCGACTGAAGCCGCTAAATACGTATTCAAGGAT 334

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db        335 GCGATGCGTAAAGTGACCCTGCCATACAGCGGCAACTATGAACGTCTGCAGACGGCAGCC 394

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::      |||:::   :::|||
Db        395 GGTAAGATCCGTGAGAACATTCCGCTTGGCTTACCAGCTCTAGACTCCGCGATCACGACT 454

Qy        142 IleTrp 143
                 ::::::
Db        455 CTCTTC 460

RESULT 11
AAH41473
ID   AAH41473 standard; DNA; 870 BP.
XX
AC   AAH41473;
XX
DT   23-AUG-2001  (first entry)
XX
DE   Trichosanthes kirilowii trichosanthin (TCS) nucleotide sequence.
XX
KW   Trichosanthes kirilowii; trichosanthin; TCS; mutagenesis; mutation; MTCS;
KW   mutant of trichosanthin; Mongolian snake-gourd; bioactivity; selectivity;
KW   cancer; virus; HIV; metaphase induced labour; ds.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .870
FT                   /*tag=  a
FT                   /product= "trichosanthin (TCS)"
FT                   /transl_except= (pos:688. .690,aa:Gly)
XX
PN   CN1283630-A.
XX
PD   14-FEB-2001.
XX
PF   02-AUG-2000; 2000CN-00119553.
XX
PR   02-AUG-2000; 2000CN-00119553.
XX
PA   (SHAN-) SHANGHAI INST CYTOBIOLOGY CHINESE ACAD.
XX
PI   Ke Y,  Nie H;
XX
DR   WPI; 2001-291745/31.
DR   P-PSDB; AAB99329.
XX
PT   Trichosanthin mutant and its preparing process.
XX
PS   Disclosure; Page 2 (disclosure); 15pp; Chinese.
XX
CC   The present invention describes a trichosanthin mutant which is prepared
CC   through the mutational deformation of the trichosanthin gene and using an
CC   expression system. The trichosanthin gene is isolated from Trichosanthes
CC   kirilowii (Mongolian snake-gourd). The trichosanthin mutant has several
CC   advantages including high bioactivity, high selectivity to target, and
CC   strong kill action to cancer cells, virus and HIV. It can also be used
CC   for metaphase induced labour. The present sequence represents the
CC   nucleotide sequence of wild type trichosanthin which is given in the
CC   exemplification of the present invention
XX
SQ   Sequence 870 BP; 248 A; 193 C; 176 G; 253 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.19e-13        Length:         870
Score:                  183.50          Matches:        44
```

```
Percent Similarity:     53.5%          Conservative:  32
Best Local Similarity:  31.0%          Mismatches:    61
Query Match:            23.9%          Indels:        5
DB:                     4              Gaps:          2

US-10-758-902-9 (1-149) x AAH41473 (1-870)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||             |||      ||||||   :::|||
Db         73 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 132

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               :::      :::|||:::         ::::::
Db        133 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCAGTCTT 192

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::   :::|||     :::   :::|||:::
Db        193 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 252

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::           |||
Db        253 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 303

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::      |||   |||       :::|||
Db        304 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 363

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db        364 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCA 423

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::   ||||||:::      |||:::   :::|||
Db        424 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCTGCTTTGGACAGTGCCATTACCACT 483

Qy        142 IleTrp 143
                 ::::::
Db        484 TTGTTT 489

RESULT 12
ABA95171
ID   ABA95171 standard; cDNA; 870 BP.
XX
AC   ABA95171;
XX
DT   20-MAY-2002  (first entry)
XX
DE   Native trichosanthin (TCS) encoding cDNA.
XX
KW   Trichosanthin; TCS; mutant; MTCS; therapeutic; cytostatic; antitumour;
KW   anti-human immunodeficiency virus; virucide; immunostimulant; gene;
KW   ectopic pregnancy; ss.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .870
FT                   /*tag=  a
FT                   /transl_except= (pos: 16. .18, aa: Val)
FT                   /transl_except= (pos: 523. .525, aa: Met)
FT                   /transl_except= (pos: 865. .867, aa: Leu)
FT                   /product= "TCS"
FT   sig_peptide     1. .69
FT                   /*tag=  b
FT   mat_peptide     70. .867
FT                   /*tag=  c
XX
PN   WO200212537-A2.
XX
PD   14-FEB-2002.
XX
PF   18-JUL-2001; 2001WO-CN001178.
XX
PR   02-AUG-2000; 2000CN-00119553.
PR   18-JAN-2001; 2001CN-00103102.
XX
PA   (BEIJ-) BEIJING STM BIOTECH LTD.
PA   (KEYY/) KE Y.
PA   (NIEH/) NIE H.
XX
PI   Ke Y,  Nie H;
XX
DR   WPI; 2002-227165/28.
DR   P-PSDB; ABB07660.
XX
PT   Mutant trichosanthin protein of low antigenicity useful for treating
PT   tumor e.g. leukemia, comprises a sequence of native trichosanthin with
PT   modification of at least one amino acid residue in three specific
PT   regions.
XX
PS   Example 1; Fig 1; 42pp; English.
XX
CC   The invention relates to a mutant trichosanthin (MTCS) protein of low
CC   antigenicity comprising a sequence of native TCS with the modification of
CC   at least one amino acid residue in three regions which is 174-180, 203-
CC   227 and 230-244 and substantially retaining the biological activities of
CC   the native TCS. The MTCS protein, its fragment or derivative is useful as
CC   an therapeutic agent; or for preparing a medicament for treating viral
CC   disease e.g. acquired immunodeficiency syndrome (AIDS), tumour e.g.
CC   leukemia, for inducing abortion and/or treating ectopic pregnancy. The
CC   present sequence represents the native TCS encoding cDNA
XX
SQ   Sequence 870 BP; 249 A; 192 C; 176 G; 253 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.19e-13       Length:        870
Score:                  183.50         Matches:       44
Percent Similarity:     53.5%          Conservative:  32
Best Local Similarity:  31.0%          Mismatches:    61
Query Match:            23.9%          Indels:        5
DB:                     6              Gaps:          2

US-10-758-902-9 (1-149) x ABA95171 (1-870)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||             |||      ||||||   :::|||
Db         73 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 132

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               :::      :::|||:::         ::::::
Db        133 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCAGTCTT 192

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::   :::|||     :::   :::|||:::
Db        193 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 252

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::           |||
Db        253 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 303

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::      |||   |||       :::|||
Db        304 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 363

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db        364 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCA 423

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::   ||||||:::      |||:::   :::|||
Db        424 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCTGCTTTGGACAGTGCCATTACCACT 483

Qy        142 IleTrp 143
                 ::::::
Db        484 TTGTTT 489
```

```
RESULT 13
AEC15951
ID   AEC15951 standard; DNA; 870 BP.
XX
AC   AEC15951;
XX
DT   20-OCT-2005  (first entry)
XX
DE   Trichosanthin mutant associated DNA.
XX
KW   trichosanthin; cancer; neoplasm; cytostatic;
KW   acquired immune deficiency syndrome; anti-hiv; immune disorder; ds; gene.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .870
FT                   /*tag=  a
XX
PN   CN1580264-A.
XX
PD   16-FEB-2005.
XX
PF   18-MAY-2004; 2004CN-00042402.
XX
PR   18-MAY-2004; 2004CN-00042402.
XX
PA   (XIAN-) XIANGTIANMU BIOLOGICAL SCI TECHNOLOGY CO.
XX
PI   Ke Y,  Nie H,  Ke X;
XX
DR   WPI; 2005-372979/39.
DR   P-PSDB; AEC15952.
XX
PT   New highly soluble expressed trichosanthin mutant for curing tumor,
PT   acquired immunodeficiency syndrome, gravidity outside of womb and
PT   inducing labor in midpregnancy.
XX
PS   Disclosure; Fig 1; 20pp; Chinese.
XX
CC   The invention relates to a trichosanthin mutant with capability of high
CC   dissolubility. The drug in this method can cure tumor, acquired
CC   immunodeficiency syndrome (AIDS), gravidity outside of womb and induction
CC   of labor in midpregnancy, is highly active and low mammalian toxicity.
CC   The present sequence represents a trichosanthin mutant associated DNA.
XX
SQ   Sequence 870 BP; 249 A; 192 C; 176 G; 253 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.19e-13       Length:          870
Score:                  183.50         Matches:         44
Percent Similarity:     53.5%          Conservative:    32
Best Local Similarity:  31.0%          Mismatches:      61
Query Match:            23.9%          Indels:          5
DB:                     14             Gaps:            2

US-10-758-902-9 (1-149) x AEC15951 (1-870)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||            |||      ||||||   :::||| 
Db         73 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 132

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               :::      :::|||:::         ::::::
Db        133 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCAGTCTT 192

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::   :::|||       :::   :::|||:::
Db        193 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 252

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::            |||
Db        253 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 303

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
                     |||   :::          |||   |||          :::|||
Db        304 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 363

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||:::::::|||       ||||||
Db        364 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCA 423

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::       |||:::   :::|||
Db        424 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCTGCTTTGGACAGTGCCATTACCACT 483

Qy        142 IleTrp 143
                 ::::::
Db        484 TTGTTT 489

RESULT 14
AAQ65573
ID   AAQ65573 standard; DNA; 886 BP.
XX
AC   AAQ65573;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   11-JAN-1995  (first entry)
XX
DE   Alpha-trichosanthin coding sequence.
XX
KW   Virus; recombination; plant virus; alpha trichosanthin; phenotype;
KW   alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus;
KW   rice necrosis virus tobamovirus; gene expression; chinese cucumber; ss.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             8. .877
FT                   /*tag=  a
FT                   /product= "Alpha-trichosanthin."
XX
PN   US5316931-A.
XX
PD   31-MAY-1994.
XX
PF   31-JUL-1992;   92US-00923692.
XX
PR   26-FEB-1988;   88US-00160766.
PR   26-FEB-1988;   88US-00160771.
PR   15-JUL-1988;   88US-00219279.
PR   17-FEB-1989;   89US-00310881.
PR   05-MAY-1989;   89US-00347637.
PR   08-JUN-1989;   89US-00363138.
PR   22-OCT-1990;   90US-00600244.
PR   16-JAN-1991;   91US-00641617.
PR   26-JUL-1991;   91US-00737899.
PR   01-AUG-1991;   91US-00739143.
XX
PA   (BIOS-) BIOSOURCE GENETICS CORP.
XX
PI   Garger SJ,  Turpen AM,  Grill LK,  Granthan GL,  Dawson WO,  Donson J;
PI   Turpen TH;
XX
DR   WPI; 1994-176269/21.
DR   P-PSDB; AAR55129.
XX
PT   New recombinant plant viral nucleic acid - capable of systemic infection
PT   and stable expression of non-native nucleic acid in plant host.
XX
PS   Example 4; Col 45-48; 44pp; English.
XX
CC   The alpha-trichosanthin gene may be inserted into a recombinant plant
CC   virus which can then be used to infect plants for the production of non-
CC   native products (in this case alpha- trichosanthin). Other genes which
```

```
CC   may be inserted into the virus are those which control a phenotypic
CC   trait, such as male sterility, or sequences encoding anti-sense RNA which
CC   can be useful to prevent the expression of undesired phenotypic traits.
CC   The recombinant virus is derived from a plus sense, single stranded virus
CC   selected from tobamovirus, brome mosic virus, rice necrosis virus or a
CC   gemini virus. (Updated on 25-MAR-2003 to correct PF field.) (Updated on
CC   27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 886 BP; 250 A; 199 C; 181 G; 256 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-13       Length:         886
Score:                  183.50         Matches:        44
Percent Similarity:     53.5%          Conservative:   32
Best Local Similarity:  31.0%          Mismatches:     61
Query Match:            23.9%          Indels:         5
DB:                     2              Gaps:           2

US-10-758-902-9 (1-149) x AAQ65573 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||          |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||           :::      :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::          |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::          |||   |||          :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||:::::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496

RESULT 15
AAT47094
ID   AAT47094 standard; DNA; 886 BP.
XX
AC   AAT47094;
XX
DT   17-OCT-2003  (revised)
DT   26-APR-1997  (first entry)
XX
DE   Chinese cucumber alpha-trichosanthin gene.
XX
KW   Recombinant viral nucleic acid; RNA virus; vector; tobacco mosaic virus;
KW   TMV; Chinese cucumber; alpha-trichosanthin;
KW   ribosome inactivating protein; antiviral; virucide; transgenic plant; ss.
XX
OS   Trichosanthes kirilowii; Maximowicz.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .7
FT                   /*tag=  a
FT                   /function= "XhoI linker"
FT   CDS             8. .877
FT                   /*tag=  b
FT   misc_feature    881. .886
FT                   /*tag=  c
FT                   /function= "XhoI linker"
XX
PN   WO9640867-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009299.
XX
PR   07-JUN-1995;   95US-00483502.
XX
PA   (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX
PI   Donson J,  Dawson WO,  Grantham GL,  Turpen TH,  Turpen AM;
PI   Garger SJ,  Grill LK;
XX
DR   WPI; 1997-065181/06.
DR   P-PSDB; AAW10468.
XX
PT   Recombinant viral nucleic acid producing, e.g. male sterility in plants -
PT   comprises nucleic acid whose transcription is controlled by another
PT   sequence.
XX
PS   Example 4; Page 124-125; 149pp; English.
XX
CC   A DNA sequence (AAT47094) codes for Chinese cucumber alpha- trichosanthin
CC   (AAW10468), a ribosome inactivating protein of potential use in the
CC   treatment of HIV infection. Expression vector pBCG152 was constructed in
CC   which the alpha-trichosanthin coding sequence was placed under control of
CC   the promoter of the tobacco mosaic virus-U1 coat protein gene, which had
CC   been deleted. The viral nucleic acid was capable of self-replication,
CC   encapsidation and systemic spread in infected Nicotiana benthamiana
CC   plants, and directed the high-level expression of biologically active
CC   alpha- trichosanthin in plant tissues. (Updated on 17-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 886 BP; 250 A; 199 C; 181 G; 256 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-13       Length:         886
Score:                  183.50         Matches:        44
Percent Similarity:     53.5%          Conservative:   32
Best Local Similarity:  31.0%          Mismatches:     61
Query Match:            23.9%          Indels:         5
DB:                     2              Gaps:           2

US-10-758-902-9 (1-149) x AAT47094 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||          |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||           :::      :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::          |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::          |||   |||          :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||:::::::|||      ||||||
```

```
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                ::::::
Db        491 TTGTTT 496
```

RESULT 16
AAT61376
ID AAT61376 standard; DNA; 886 BP.
XX
AC AAT61376;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-APR-1997 (first entry)
XX
DE Chinese cucumber alpha-trichosanthin cDNA with XhoI linkers.
XX
KW Recombinant virus; alpha-haemoglobin; human; chinese cucumber;
KW alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin;
KW subgenomic promoter; coat protein; ss.
XX
OS Cucumis sp.
XX
FH Key   Location/Qualifiers
FT CDS   8. .877
FT   /*tag= a
FT   /product= "Chinese cucmber alpha-trichosanthin"
XX
PN US5589367-A.
XX
PD 31-DEC-1996.
XX
PF 19-JAN-1994; 94US-00184237.
XX
PR 26-FEB-1988; 88US-00160766.
PR 26-FEB-1988; 88US-00160771.
PR 15-JUL-1988; 88US-00219279.
PR 17-FEB-1989; 89US-00310881.
PR 05-MAY-1989; 89US-00347637.
PR 08-JUN-1989; 89US-00363138.
PR 22-OCT-1990; 90US-00600244.
PR 16-JAN-1991; 91US-00641617.
PR 26-JUL-1991; 91US-00737899.
PR 01-AUG-1991; 91US-00739143.
PR 31-JUL-1992; 92US-00923692.
XX
PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX
PI Garger SJ, Turpen AM, Grill LK, Granthan GL, Donson J, Dawson WO;
PI Turpen TH;
XX
DR WPI; 1997-076845/07.
DR P-PSDB; AAW11870.
XX
PT Recombinant viral DNA for altering plant phenotype or protein prodn -
PT contains non-native sub-genomic promoter for expression of heterologous
PT protein and native promoter for expression of coat protein.
XX
PS Example 4; Col 45-46; 42pp; English.
XX
CC The sequences given in AAT61374-77 encode heterologous proteins which
CC were used in the recombinant viruses of the invention. The viruses are
CC recombinant plant viruses which comprise a native plant virus subgenomic
CC promoter, at least one non-native plant virus subgenomic promoter, and a
CC sequence encoding a plant virus coat protein. These heterologous
CC sequences are preferably under the control of the native promoter
CC sequence. By using a plant virus existing cells can be altered with a new
CC coding sequences without involving germ cell. The recombinant viruses are
CC stable and can cause systemic infection, with stable
CC expression/transcription in plants that are hosts for the non-native part
CC of the vector. These sequences are preferably integrated in plant viruses
CC having either the O-coat protein or the U1-coat protein gene. (Updated on
CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 886 BP; 250 A; 199 C; 181 G; 256 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.22e-13	Length:	886
Score:	183.50	Matches:	44
Percent Similarity:	53.5%	Conservative:	32
Best Local Similarity:	31.0%	Mismatches:	61
Query Match:	23.9%	Indels:	5
DB:	2	Gaps:	2

US-10-758-902-9 (1-149) x AAT61376 (1-886)

```
Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||     |||           |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               :::      :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                     :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::          |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProProGly 101
                     |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                     :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                ::::::
Db        491 TTGTTT 496
```

RESULT 17
AAX29143
ID AAX29143 standard; DNA; 886 BP.
XX
AC AAX29143;
XX
DT 20-MAR-2003 (revised)
DT 04-JUN-1999 (first entry)
XX
DE Chinese cucumber alpha-trichosanthin encoding DNA.
XX
KW Recombinant; plant virus; coat protein; systemic infection;
KW transcription; therapeutic; chinese cucumber; alpha-trichosanthin; ss.
XX
OS Cucumis sp.
XX
PN US5889190-A.
XX
PD 30-MAR-1999.
XX
PF 07-JUN-1995; 95US-00480432.
XX

```
PR   26-FEB-1988;   88US-00160766.
PR   26-FEB-1988;   88US-00160771.
PR   15-JUL-1988;   88US-00219279.
PR   17-FEB-1989;   89US-00310881.
PR   05-MAY-1989;   89US-00347637.
PR   08-JUN-1989;   89US-00363138.
PR   22-OCT-1990;   90US-00600244.
PR   16-JAN-1991;   91US-00641617.
PR   26-JUL-1991;   91US-00737899.
PR   01-AUG-1991;   91US-00739143.
PR   31-JUL-1992;   92US-00923692.
PR   19-JAN-1994;   94US-00184237.
XX
PA   (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX
PI   Garger SJ,  Turpen AM,  Grill LK,  Grantham GL,  Donson J,  Dawson WO;
PI   Turpen TH;
XX
DR   WPI; 1999-243290/20.
DR   P-PSDB; AAY01374.
XX
PT   Recombinant plant viral nucleic acid derived from a plus sense, single
PT   stranded RNA plant virus - useful for the transcription of products in a
PT   host.
XX
PS   Example 4; Col 43-46; 46pp; English.
XX
CC   The invention relates to a recombinant plant viral nucleic acid derived
CC   from a plus sense, single stranded RNA plant virus. The recombinant plant
CC   viral nucleic acid comprises: (a) a first plant viral subgenomic promoter
CC   that is native to the plus sense, single stranded RNA plant virus and
CC   operably joined to a first nucleic acid expression sequence; and (b) a
CC   second plant viral subgenomic promoter that is non-native and is operably
CC   joined to a second nucleic acid expression sequence; where, (i) (a) and
CC   (b) are incapable of recombination with one another, (ii) either the
CC   first or the second nucleic acid expression sequence is a plant viral
CC   coat protein coding sequence. The recombinant plant viral nucleic acid
CC   allows the transcription of products in a host, such as therapeutic and
CC   other useful polypeptides or proteins e.g. enzymes, complex biomolecules
CC   and ribozymes. It also gives the option of applying the coding sequence
CC   to the desired organism, tissue, organ or cell, is stable for the foreign
CC   coding sequences and is capable of systemic infection in the plant host.
CC   The transformation and regeneration of target organisms become
CC   unnecessary. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence 886 BP; 250 A; 199 C; 181 G; 256 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-13      Length:          886
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     2             Gaps:            2

US-10-758-902-9 (1-149) x AAX29143 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||       ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||             :::      :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||       :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::::||||||:::           |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                          |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::|||||||||   :::   |||:::|||:::::::|||       ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::   ||||||:::       |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                 ::::::
Db        491 TTGTTT 496

RESULT 18
AAX03385
ID   AAX03385 standard; DNA; 886 BP.
XX
AC   AAX03385;
XX
DT   27-AUG-2003  (revised)
DT   01-APR-1999  (first entry)
XX
DE   DNA sequence encoding chinese cucumber alpha-trichosanthin.
XX
KW   Chinese cucumber; alpha-trichosanthin; plant virus;
KW   RNA plant virus promoter; systemic infection; foreign gene expression;
KW   AIDS therapeutic drug; ss.
XX
OS   Momordica cochinchinensis.
XX
FH   Key             Location/Qualifiers
FT   CDS             8. .877
FT                   /*tag=  a
FT                   /product= "alpha-trichosanthin"
XX
PN   US5866785-A.
XX
PD   02-FEB-1999.
XX
PF   07-JUN-1995;   95US-00482920.
XX
PR   26-FEB-1988;   88US-00160766.
PR   26-FEB-1988;   88US-00160771.
PR   15-JUL-1988;   88US-00219279.
PR   17-FEB-1989;   89US-00310881.
PR   05-MAY-1989;   89US-00347637.
PR   08-JUN-1989;   89US-00363138.
PR   22-OCT-1990;   90US-00600244.
PR   16-JAN-1991;   91US-00641617.
PR   26-JUL-1991;   91US-00737899.
PR   01-AUG-1991;   91US-00739143.
PR   31-JUL-1992;   92US-00923692.
PR   19-JAN-1994;   94US-00184237.
XX
PA   (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX
PI   Garger SJ,  Turpen AM,  Grill LK,  Granthan GL,  Donson J,  Dawson WO;
PI   Turpen TH;
XX
DR   WPI; 1999-142035/12.
DR   P-PSDB; AAW84292.
XX
PT   Recombinant plant viral vector - that is capable of systemic infection in
PT   host plant and stable production of heterologous DNA useful for producing
PT   therapeutic proteins for treating e.g. AIDS.
XX
PS   Example 4; Col 43-46; 45pp; English.
XX
CC   The present sequence encodes chinese cucumber alpha-trichosanthin. The
CC   nucleic acid sequence can be expressed in the plant viral constructs of
```

```
CC   the invention. The specification describes a recombinant plant viral
CC   nucleic acid derived from a positive (+)-sense RNA plant virus comprising
CC   a native (+)-sense RNA plant virus promoter that is linked to an
CC   expression sequence and a heterologous (+)-sense RNA plant virus promoter
CC   that is linked to an expression sequence. The promoters are incapable of
CC   recombination with each other, and one of the expression sequences
CC   encodes a plant viral coat protein while the other is optionally a
CC   heterologous coding sequence. The plant viral nucleic acid is capable of
CC   systemic infection in a host plant. The viral construct is useful for the
CC   introduction and expression of non-viral foreign genes in plants and the
CC   production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-
CC   2003 to correct OS field.)
XX
SQ   Sequence 886 BP; 250 A; 199 C; 181 G; 256 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-13       Length:         886
Score:                  183.50         Matches:        44
Percent Similarity:     53.5%          Conservative:   32
Best Local Similarity:  31.0%          Mismatches:     61
Query Match:            23.9%          Indels:         5
DB:                     2              Gaps:           2

US-10-758-902-9 (1-149) x AAX03385 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              :::      :::|||:::        ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||::::::||||||:::          |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||::::::|||       ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496

RESULT 19
AAA12393
ID   AAA12393 standard; DNA; 886 BP.
XX
AC   AAA12393;
XX
DT   06-AUG-2003  (revised)
DT   24-AUG-2000  (first entry)
XX
DE   Chinese cucumber alpha-trichosanthin DNA.
XX
KW   Animal RNA virus; viral coat protein; plant; male sterility; interleukin;
KW   EPO; erythropoietin; CSF; colony stimulating factor; Factor VIII; hGH;
KW   human growth hormone; melanin; insulin; vaccine;
KW   stereo specific catalysis; alpha-trichosanthin; ss.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             8. .877
FT                   /*tag=  a
FT                   /product= "Alpha-trichosanthin"
XX
PN   US6054566-A.
XX
PD   25-APR-2000.
XX
PF   07-JUN-1995;   95US-00484341.
XX
PR   26-FEB-1988;   88US-00160766.
PR   26-FEB-1988;   88US-00160771.
PR   15-JUL-1988;   88US-00219279.
PR   17-FEB-1989;   89US-00310881.
PR   05-MAY-1989;   89US-00347637.
PR   08-JUN-1989;   89US-00363138.
PR   22-OCT-1990;   90US-00600244.
PR   16-JAN-1991;   91US-00641617.
PR   26-JUL-1991;   91US-00737899.
PR   01-AUG-1991;   91US-00739143.
PR   31-JUL-1992;   92US-00923692.
XX
PA   (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX
PI   Garger SJ,  Grill LK,  Turpen TH,  Granthan GL,  Dawson WO;
PI   Turpen AM,  Donson J;
XX
DR   WPI; 2000-338510/29.
DR   P-PSDB; AAY87791.
XX
PT   Recombinant non-retroviral nucleic acid for producing proteins such as
PT   interleukins, melanin and vaccines, comprises subgenomic promoters linked
PT   to sequences coding for viral coat protein and heterologous proteins.
XX
PS   Example 4; Col 57-60; 51pp; English.
XX
CC   This invention describes a novel recombinant viral nucleic acid (I) from
CC   a non-retroviral (+) sense, single stranded animal RNA virus comprising a
CC   nucleic acid sequence coding for a viral coat protein regulated by a
CC   native subgenomic promoter and other two heterologous nucleic acid
CC   sequences regulated by two other subgenomic promoters. (I) is useful for
CC   expressing foreign genes e.g. genes inducing male sterility in plants.
CC   (I) is also useful for producing proteins such as interleukins, EPO
CC   (erythropoietin), CSF (colony stimulating factor), Factor VIII, hGH
CC   (human growth hormone), melanin, insulin, vaccines etc., and enzymes that
CC   are useful for stereo specific catalysis of organic compounds. (I) is
CC   stable and transcribed systemically. The dual subgenomic promoter system
CC   reduces the frequency of recombination thus reducing regeneration of the
CC   wild type virus. This sequence encodes a chinese cucumber alpha-
CC   trichosanthin protein which is described in the method of the invention.
CC   (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 886 BP; 250 A; 199 C; 181 G; 256 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-13       Length:         886
Score:                  183.50         Matches:        44
Percent Similarity:     53.5%          Conservative:   32
Best Local Similarity:  31.0%          Mismatches:     61
Query Match:            23.9%          Indels:         5
DB:                     3              Gaps:           2

US-10-758-902-9 (1-149) x AAA12393 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              :::      :::|||:::        ::::::
```

```
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::  :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::|||||:::           |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                     |||   :::         |||   |||          :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496
```

```
RESULT 20
ADH44105
ID   ADH44105 standard; cDNA; 886 BP.
XX
AC   ADH44105;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Chinese cucumber alpha-trichosanthin cDNA.
XX
KW   RVNA; cis-acting replication; RNA plant virus; capped RNA molecule;
KW   coat gene; movement protein gene; subgenomic promoter;
KW   herbicide resistance; extreme temperature resistance; drought;
KW   osmotic stress; pests resistance; male sterility; female sterility;
KW   yield; collagenase cleavage site; Chinese cucumber; ss;
KW   alpha-trichosanthin; gene; plant.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             8. .877
FT                   /*tag=  b
FT                   /product= "Alpha-trichosanthin"
FT   mat_peptide     8. .76
FT                   /*tag=  a
FT   mat_peptide     77. .874
FT                   /*tag=  c
FT                   /note= "Mature Alpha-trichosanthin"
XX
PN   US2003150019-A1.
XX
PD   07-AUG-2003.
XX
PF   24-OCT-2002; 2002US-00280679.
XX
PR   26-FEB-1988;   88US-00160766.
PR   26-FEB-1988;   88US-00160771.
PR   15-JUL-1988;   88US-00219279.
PR   22-OCT-1990;   90US-00600244.
PR   16-JAN-1991;   91US-00641617.
PR   26-JUL-1991;   91US-00737899.
PR   01-AUG-1991;   91US-00739143.
PR   31-JUL-1992;   92US-00923692.
PR   07-JUN-1995;   95US-00484341.
PR   24-APR-2000; 2000US-00557941.
XX
PA   (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI   Turpen TH,  Turpen AM,  Garger SJ,  Grill LK,  Donson J,  Dawson WO;
PI   Granthan GL;
XX
DR   WPI; 2003-897624/82.
DR   P-PSDB; ADH44106.
XX
PT   New recombinant viral RNA molecules, useful in modifying a plant host
PT   cell, genotypically or phenotypically, e.g. male sterility or improved
PT   resistance to pests or diseases, or for producing pharmaceuticals,
PT   hormones or antibodies.
XX
PS   Example 4; SEQ ID NO 3; 50pp; English.
XX
CC   The invention relates to an RNA molecule (RVNA) comprising a cis-acting
CC   replication element from a positive strand RNA plant virus capable of
CC   replication in a plant cell and comprising an exogenous RNA segment
CC   capable of expressing its function in a host cell. The exogenous RNA
CC   segment is located in a region of the RNA molecule able to tolerate the
CC   segment without disrupting RNA replication in the absence of a trans-
CC   acting replication element in the host cell. Also included are a capped
CC   RNA molecule capable of infecting a host plant cell (where the capped RNA
CC   molecule: (a) comprises a cis-acting replication element derived from a
CC   positive strand RNA plant virus, has no extraneous non-viral sequences
CC   between the cap site and the 5' terminus of the viral sequence, and
CC   further comprises an exogenous RNA segment capable of expressing its
CC   function in a host cell in a region of the capped RNA molecule able to
CC   tolerate the segment without disrupting RNA replication of the capped RNA
CC   molecule in the absence of a trans-acting replication element in the host
CC   cell; or (b) has no extraneous non-viral sequences between the cap site
CC   and the 5' terminus of the viral sequence, and where the capped RNA
CC   molecule comprises the entire genome of the positive strand RNA virus,
CC   such as luteovirus, potexvirus, potyvirus, tombusvirus, tymovirus and
CC   tobamovirus, carmovirus, or sobemovirus, and an exogenous RNA segment
CC   capable of expressing its function in a host cell, where the exogenous
CC   RNA segment inserted into the genome of the positive strand RNA virus at
CC   a gene site consisting of a coat gene site, a movement protein gene site,
CC   or another gene site under the control of a subgenomic promoter, which is
CC   one of at least two subgenomic promoters present in the virus), a DNA
CC   transcription vector comprising cDNA having one strand complementary to
CC   the (capped) RNA molecule cited above and methods of modifying a host
CC   cell, genotypically or phenotypically (comprising introducing into the
CC   cell the (capped) RNA molecule cited above, where the exogenous RNA
CC   segment confers a detectable trait in the host cell which modifies the
CC   host cell). The cis-acting replication element is derived from a
CC   monopartite plant virus, tobamovirus, or tobacco mosaic virus. The
CC   (capped) RNA molecules and DNA transcription vectors are useful in
CC   modifying a host cell, genotypically or phenotypically, e.g. improved
CC   tolerance to herbicides, extremes of heat or cold, drought or osmotic
CC   stress, improved resistance to pests or diseases, male or female
CC   sterility, or improved yield. The RNA molecules are also useful for
CC   transcription or expression of foreign genes in the host to produce the
CC   desired product, such as pharmaceuticals, hormones, antibiotics,
CC   pigments, or antibodies. The present sequence is the Chinese cucumber
CC   alpha-trichosanthin cDNA, which was used as the exogenous RNA in an RVNA
CC   of the invention.
XX
SQ   Sequence 886 BP; 250 A; 199 C; 181 G; 256 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              1.22e-13      Length:          886
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     10            Gaps:            2

US-10-758-902-9 (1-149) x ADH44105 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||     |||          |||     ||||||  :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139
```

```
Qy          22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
               |||   ;  |||                 :::      :::|||:::         ::::::
Db         140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy          42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                     :::|||:::   |||:::   :::|||      :::   :::|||:::
Db         200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy          62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
               ||||||||||||||||||:::||||||:::::||||||:::             |||
Db         260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy          82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                     |||   :::         |||   |||         :::|||
Db         311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy         102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                     :::||||||||||   :::   |||:::|||:::::|||      ||||||
Db         371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                     |||:::::::::   ||||||:::      |||:::   :::|||
Db         431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy         142 IleTrp 143
               ::::::
Db         491 TTGTTT 496

RESULT 21
ADO43820
ID   ADO43820 standard; DNA; 886 BP.
XX
AC   ADO43820;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Chinese cucumber alpha-trichosanthin DNA.
XX
KW   recombinant viral nucleic acid; animal virus; subgenomic promoter;
KW   viral coat protein; IL-1; IL-2; IL-3; IL-4; IL-5; IL-6; IL-7; IL-8; IL-9;
KW   IL-10; IL-11; IL-12; EPO; G-CSF; GM-CSF; M-CSF; Factor VIII; Factor IX;
KW   tissue plasminogen activator; human growth hormone; neuro-polypeptide;
KW   melanin; lipase; hormone; pharmaceutical; antibiotic; vaccine; insulin;
KW   chinese cucumber; alpha-trichosanthin; gene; ds.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             8. .877
FT                   /*tag=  a
FT                   /product= "Chinese cucumber alpha-trichosanthin"
XX
PN   US2004049025-A1.
XX
PD   11-MAR-2004.
XX
PF   24-OCT-2002; 2002US-00280725.
XX
PR   26-FEB-1988;   88US-00160766.
PR   26-FEB-1988;   88US-00160771.
PR   15-JUL-1988;   88US-00219279.
PR   17-FEB-1989;   89US-00310881.
PR   05-MAY-1989;   89US-00347637.
PR   08-JUN-1989;   89US-00363138.
PR   22-OCT-1990;   90US-00600244.
PR   16-JAN-1991;   91US-00641617.
PR   26-JUL-1991;   91US-00737899.
PR   01-AUG-1991;   91US-00739143.
PR   31-JUL-1992;   92US-00923692.
PR   07-JUN-1995;   95US-00484341.
PR   24-APR-2000; 2000US-00557941.
XX
PA   (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI   Donson J,  Dawson WO,  Grantham GL,  Turpen TH,  Turpen AM;
PI   Garger SJ,  Grill LK;
XX
DR   WPI; 2004-238515/22.
DR   P-PSDB; ADO43821.
XX
PT   New recombinant viral nucleic acid derived from an animal virus having a
PT   native subgenomic promoter, useful in production of products such as
PT   interleukins, enzymes, and hormones.
XX
PS   Example 4; SEQ ID NO 3; 49pp; English.
XX
CC   The invention describes a recombinant viral nucleic acid derived from an
CC   animal virus possessing a native subgenomic promoter. The recombinant
CC   viral nucleic acid comprises: a first viral sub genomic promoter; a first
CC   nucleic acid sequence that codes for a viral coat protein whose
CC   transcription is regulated by the first viral subgenomic promoter; a
CC   second viral sub genomic promoter; and a second nucleic acid sequence
CC   whose transcription is regulated by the second viral sub genomic
CC   promoter, where the first and second viral subgenomic promoters possess
CC   different nucleic acid sequences relative to each other, and the second
CC   nucleic acid sequence is upstream to the first nucleic acid sequence.
CC   Also described are: a non-human host animal infected by a viral vector
CC   comprising the recombinant viral nucleic acid; and a process for
CC   transcribing a nucleic acid sequence in a non-human host animal. The
CC   recombinant viral nucleic acid is useful in sustained systemic
CC   transcription of nucleotide sequences within host cells and in producing
CC   gene products, e.g. IL-1-12, EPO, G-CSF, GM-CSF, M-CSF, Factor VIII,
CC   Factor IX, tissue plasminogen activator, human growth hormone, receptors,
CC   receptor antagonists, antibodies, neuro-polypeptides, melanin, lipase,
CC   hormones, pharmaceuticals, antibiotics, vaccines and insulin within a
CC   host animal. This sequence encodes chinese cucumber alpha-trichosanthin
CC   that can be incorporated into the recombinant viral protein of the
CC   invention.
XX
SQ   Sequence 886 BP; 250 A; 199 C; 181 G; 256 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-13      Length:         886
Score:                  183.50        Matches:        44
Percent Similarity:     53.5%         Conservative:   32
Best Local Similarity:  31.0%         Mismatches:     61
Query Match:            23.9%         Indels:         5
DB:                     12            Gaps:           2

US-10-758-902-9 (1-149) x ADO43820 (1-886)

Qy           4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
               |||||||||   |||       |||             |||       ||||||   :::|||
Db          80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy          22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
               |||       |||                 :::      :::|||:::         ::::::
Db         140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy          42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                     :::|||:::   |||:::   :::|||      :::   :::|||:::
Db         200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy          62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
               ||||||||||||||||||:::||||||:::::||||||:::             |||
Db         260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy          82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                     |||   :::         |||   |||         :::|||
Db         311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy         102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                     :::||||||||||   :::   |||:::|||:::::|||      ||||||
Db         371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
```

```
                    |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496

RESULT 22
AAQ06343
ID   AAQ06343 standard; DNA; 1227 BP.
XX
AC   AAQ06343;
XX
DT   06-FEB-1991  (first entry)
XX
DE   Encodes Trichosanthin from Trichosanthes kirilowii.
XX
KW   trichosanthin (TCS); Human Immunodeficiency Virus; inhibition; ss.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             340. .1209
FT                   /*tag=  a
FT   mat_peptide     409. .1209
FT                   /*tag=  b
FT                   /product= "TCS"
XX
PN   WO9012097-A.
XX
PD   18-OCT-1990.
XX
PF   04-APR-1989;   89US-00333184.
XX
PR   04-APR-1989;   89US-00333184.
XX
PA   (GENE-) GENELABS INC.
XX
PI   Piatek M,  Chow T,  Fry K;
XX
DR   WPI; 1990-334847/44.
DR   P-PSDB; AAR07514.
XX
PT   Recombinant tri:chosanthin protein - with selective inhibitory effect on
PT   viral expression in HIV infected T-cells or monocyte-macrophase.
XX
PS   Claim 2; Page 59; 102pp; English.
XX
CC   Genomic DNA was isolated from T.kirilowii leaves from Korea and a library
CC   was constructed. Clone pQ21D was identified as likely to contain a TCS-
CC   encoding sequence in its 4kb insert. The deduced amino acid sequence is
CC   identical to that of TCS purified from Cantonese T.kirilowii roots,
CC   except for 2 conservative substitu- tions. The isolated coding sequence
CC   can be used to produce TCS in pure form for use as a therapeutic agent.
CC   See also AAQ06344-Q06351
XX
SQ   Sequence 1227 BP; 402 A; 250 C; 223 G; 352 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.9e-13       Length:         1227
Score:                  183.50        Matches:        44
Percent Similarity:     53.5%         Conservative:   32
Best Local Similarity:  31.0%         Mismatches:     61
Query Match:            23.9%         Indels:         5
DB:                     2             Gaps:           2

US-10-758-902-9 (1-149) x AAQ06343 (1-1227)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db        412 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 471

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
                 |||       |||                 :::      :::|||:::         ::::::
Db        472 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 531

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||       :::   :::|||:::
Db        532 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 591

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::              |||
Db        592 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 642

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
                        |||   :::         |||   |||         :::|||
Db        643 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 702

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::|||||||||   :::   |||:::|||:::::|||      ||||||
Db        703 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 762

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||::::::::::   ||||||:::      |||:::   :::|||
Db        763 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 822

Qy        142 IleTrp 143
              ::::::
Db        823 TTGTTT 828

RESULT 23
AAQ31826
ID   AAQ31826 standard; DNA; 1227 BP.
XX
AC   AAQ31826;
XX
DT   25-MAR-2003  (revised)
DT   16-APR-1993  (first entry)
XX
DE   Recombinant TCS sequence (pQ21D).
XX
KW   TCS; alpha-trichosanthin; Radix-trichosanthin; primer; inhibition;
KW   viral expression; HIV; T-cell; macrophage; ss.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             340. .1209
FT                   /*tag=  a
FT                   /label= TCS
FT   sig_peptide     342. .410
FT                   /*tag=  b
FT                   /note= "putative N-terminal extension of the mature TCS"
FT   mat_peptide     411. .1151
FT                   /*tag=  c
FT                   /note= "Claim 3; page 36"
FT   misc_RNA        1152. .1208
FT                   /*tag=  d
FT                   /note= "putative C-terminal extension of the mature TCS"
XX
PN   US5166056-A.
XX
PD   24-NOV-1992.
XX
PF   09-DEC-1991;   91US-00804293.
XX
PR   04-APR-1989;   89US-00333184.
PR   07-SEP-1989;   89US-00404326.
XX
PA   (GENE-) GENELABS INC.
XX
PI   Piatak M,  Chow TP;
XX
DR   WPI; 1992-414954/50.
DR   P-PSDB; AAR29272.
XX
```

```
PT   Recombinant Trichosanthin protein prodn. in E. coli - for use in the
PT   selective inhibition of viral expression in HIV infected cells.
XX
PS   Disclosure; Fig 4; 37pp; English.
XX
CC   The TCS coding sequence was amplified using the primers of AAQ31828-30.
CC   The amplified prod. has the sequence of AAQ31827, which was used as a
CC   probe. One isolate, pQ21D, comprises the sequence of AAQ31826. The
CC   recombinant TCS sequence may be used in the recombinant prodn. of TCS.
CC   TCS can be used for the selective inhibition of viral expression in HIV-
CC   infected human T-cells or macrophages. (Updated on 25-MAR-2003 to correct
CC   PF field.)
XX
SQ   Sequence 1227 BP; 402 A; 250 C; 223 G; 352 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.9e-13       Length:         1227
Score:                  183.50        Matches:        44
Percent Similarity:     53.5%         Conservative:   32
Best Local Similarity:  31.0%         Mismatches:     61
Query Match:            23.9%         Indels:         5
DB:                     2             Gaps:           2

US-10-758-902-9 (1-149) x AAQ31826 (1-1227)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||             |||      ||||||   :::|||
Db        412 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 471

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||          :::     :::|||:::       ::::::
Db        472 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 531

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        532 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 591

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::          |||
Db        592 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 642

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::         |||   |||         :::|||
Db        643 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 702

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||::::::|||       ||||||
Db        703 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 762

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                 |||:::::::::   ||||||:::     |||:::   :::|||
Db        763 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 822

Qy        142 IleTrp 143
              ::::::
Db        823 TTGTTT 828

RESULT 24
AAQ26499
ID   AAQ26499 standard; DNA; 1228 BP.
XX
AC   AAQ26499;
XX
DT   25-MAR-2003  (revised)
DT   13-JAN-1993  (first entry)
XX
DE   Trichosanthin coding sequence from T.kirilowii.
XX
KW   TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient;
KW   ribosome inactivating protein; RIP; HIV-infected human T cells;
KW   human immunodeficiency virus; ss.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             341. .1210
FT                   /*tag=  a
FT   mat_peptide     410. .1150
FT                   /*tag=  b
FT                   /product= "trichosanthin"
XX
PN   US5128460-A.
XX
PD   07-JUL-1992.
XX
PF   04-APR-1990;   90US-00504775.
XX
PR   04-APR-1989;   89US-00333184.
PR   07-SEP-1989;   89US-00404326.
XX
PA   (GENE-) GENELABS INC.
XX
PI   Piatak M,  Chow TP,  Fry K;
XX
DR   WPI; 1992-249485/30.
DR   P-PSDB; AAR25572.
XX
PT   Nucleic acid encoding trichosanthin protein - which can be used to
PT   inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV
PT   expression.
XX
PS   Claim 1; Col 3; 53pp; English.
XX
CC   Trichosanthin protein was isolated from T.kirilowii root tuber and
CC   sequenced. The amino acid sequence was used to design sets of degenerate
CC   primers (see AAQ26506-8) for PCR amplification of the TCS coding
CC   sequence. The amplified product was used as a probe to isolate TCS coding
CC   sequence from T.kirilowii genomic libraries. One clone (pQ21D) contained
CC   a 4kb insert. The amino acid sequence deduced from the pQ21D insert
CC   differed from the purified TCS sequence at amino acids 211 and 224. The
CC   substitutions at each position were conservative and are postulated to
CC   indicate minor variations between strains; the purified TCS was obtained
CC   from the Canton region of China and the genomic DNA was obtained from
CC   T.kirilowii leaves from Korea. The claimed nucleic acid encodes at least
CC   the mature TCS and may further include the regions coding for the N- and
CC   C-terminal amino acid extensions or encodes TCS fused to a ligand peptide
CC   which confers cell-surface recognition properties on the fused protein.
CC   See also AAQ26500-Q26505. (Updated on 25-MAR-2003 to correct PF field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1228 BP; 403 A; 250 C; 223 G; 352 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.9e-13       Length:         1228
Score:                  183.50        Matches:        44
Percent Similarity:     53.5%         Conservative:   32
Best Local Similarity:  31.0%         Mismatches:     61
Query Match:            23.9%         Indels:         5
DB:                     2             Gaps:           2

US-10-758-902-9 (1-149) x AAQ26499 (1-1228)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||             |||      ||||||   :::|||
Db        413 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 472

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||          :::     :::|||:::       ::::::
Db        473 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 532

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        533 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 592

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::          |||
```

```
Db        593 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 643

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
                  |||   :::          |||   |||         :::|||
Db        644 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 703

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 :::|||||||||   :::   |||:::|||:::::::|||      ||||||
Db        704 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 763

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                |||:::::::::   ||||||:::      |||:::   :::|||
Db        764 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 823

Qy        142 IleTrp 143
                ::::::
Db        824 TTGTTT 829

RESULT 25
ADW14401
ID   ADW14401 standard; DNA; 1380 BP.
XX
AC   ADW14401;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Trichosanthin suicide gene ENH-TCS SEQ ID NO:1.
XX
KW   ds; gene; ENH-TCS; trichosanthin; apoptosis.
XX
OS   Trichosanthes kirilowii.
XX
PN   CN1504571-A.
XX
PD   16-JUN-2004.
XX
PF   28-NOV-2002; 2002CN-00150905.
XX
PR   28-NOV-2002; 2002CN-00150905.
XX
PA   (SHAN-) SHANGHAI INST BIOLOGICAL SCI.
XX
PI   Nie H,  Ke Y,  Zhu L;
XX
DR   WPI; 2004-678256/67.
XX
PT   New Trichosanthin suicide gene ENH-TCS, recombinant carrier and
PT   application.
XX
PS   Claim 1; SEQ ID NO 1; 17pp; Chinese.
XX
CC   The invention relates to a Trichosanthin suicide gene ENH-TCS, whose
CC   nucleic acid sequence is provided in the specification (ADW14401).
XX
SQ   Sequence 1380 BP; 413 A; 294 C; 257 G; 416 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:            2.22e-13       Length:          1380
Score:                183.50         Matches:         44
Percent Similarity:   53.5%          Conservative:    32
Best Local Similarity: 31.0%         Mismatches:      61
Query Match:          23.9%          Indels:          5
DB:                   13             Gaps:            2

US-10-758-902-9 (1-149) x ADW14401 (1-1380)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||          |||      ||||||   :::|||
Db        626 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 685

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||             :::      :::|||:::         ::::::
Db        686 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCAGTCTT 745

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        746 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 805

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||::|||||::::::|||||:::                ||||
Db        806 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 856

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
                         |||   :::          |||   |||         :::|||
Db        857 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 916

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::|||||||||   :::   |||:::|||:::::::|||      ||||||
Db        917 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCA 976

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                   |||:::::::::   ||||||:::      |||:::   :::|||
Db        977 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCTGCTTTGGACAGTGCCATTACCACT 1036

Qy        142 IleTrp 143
                ::::::
Db       1037 TTGTTT 1042

RESULT 26
AAQ37679
ID   AAQ37679 standard; DNA; 885 BP.
XX
AC   AAQ37679;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   17-JUN-1993  (first entry)
XX
DE   Encodes chinese cucumber alpha-tricosanthin.
XX
KW   Recombinant products; commercial production; fermentation; biosynthesis;
KW   natural products; recombinant proteins; product expression;
KW   protein expression; expressed proteins.
XX
OS   Cucurbitaceae.
XX
PN   WO9303161-A1.
XX
PD   18-FEB-1993.
XX
PF   31-JUL-1992;   92WO-US006359.
XX
PR   01-AUG-1991;   91US-00739143.
XX
PA   (DONS/) DONSON J.
PA   (DAWS/) DAWSON W O.
PA   (GRAN/) GRANTHAM G L.
PA   (TURP/) TURPEN T H.
PA   (TURP/) TURPEN A M.
PA   (GARG/) GARGER S J.
PA   (GRIL/) GRILLE L K.
XX
PI   Donson J,  Dawson WO,  Grantham GL,  Turpen TH,  Turpen AM;
PI   Garger SJ,  Grille LK;
XX
DR   WPI; 1993-076518/09.
DR   P-PSDB; AAR32986.
XX
PT   Recombinant plant viral nucleic acids - used to express a prod., e.g.
PT   antibody or IL-1 in a plant.
XX
PS   Example 4; Page 96; 30pp; English.
XX
CC   This sequence encodes chinese cucumber alpha-tricosanthin. It is inserted
CC   into a recombinant plant viral nucleic acid which is then used to express
CC   a recombinant product (in this case alpha- tricosanthin) in a plant. The
```

```
CC   plant viral sequence may be from tobacco mosaic, cucumber green mottle,
CC   cowpea mosaic, brome mosaic, broad bean mottle, rice necrosis,
CC   geminiviruses, tomato golden mosaic, Cassava latent and maize streak
CC   viruses. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR
CC   -2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 885 BP; 248 A; 199 C; 182 G; 251 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.:              1.64e-13       Length:         885
Score:                  182.50         Matches:        44
Percent Similarity:     52.8%          Conservative:   31
Best Local Similarity:  31.0%          Mismatches:     62
Query Match:            23.8%          Indels:         5
DB:                     2              Gaps:           2

US-10-758-902-9 (1-149) x AAQ37679 (1-885)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||            |||      ||||||   :::|||
Db         79 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 138

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||             :::     :::|||:::         ::::::
Db        139 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 198

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        199 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 258

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::             |||
Db        259 GTGGCCATAGACGTAACGAACGTCTATATCATGGGATATCGC---------GCTGGCGAT 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::       |||   |||       :::|||
Db        310 ACATCCTATTTTTTCAACGAGGCTTCNGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 :::||||||||||   :::   |||:::|||::::::|||      ||||||
Db        370 GCTATGCGAAAAGTNACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 429

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                 |||:::::::::   ||||||:::      |||:::      |||
Db        430 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGGNATTACCACT 489

Qy        142 IleTrp 143
              ::::::
Db        490 TTGTTT 495

RESULT 27
AAQ06350
ID   AAQ06350 standard; DNA; 1169 BP.
XX
AC   AAQ06350;
XX
DT   06-FEB-1991  (first entry)
XX
DE   Alpha-Trichosanthin encoding insert sequence from clone 3.
XX
KW   trichosanthin (TCS); Human Immunodeficiency Virus; inhibition; ss.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             132. .950
FT                   /*tag=  a
FT                   /product= "pre-pro-alpha-TCS"
FT   sig_peptide     132. .200
FT                   /*tag=  b
FT   mat_peptide     201. .947
FT                   /*tag=  c
FT                   /product= "alpha-TCS"
XX
PN   WO9012097-A.
XX
PD   18-OCT-1990.
XX
PF   04-APR-1989;   89US-00333184.
XX
PR   04-APR-1989;   89US-00333184.
XX
PA   (GENE-) GENELABS INC.
XX
PI   Piatek M,  Chow T,  Fry K;
XX
DR   WPI; 1990-334847/44.
DR   P-PSDB; AAR07522.
XX
PT   Recombinant tri:chosanthin protein - with selective inhibitory effect on
PT   viral expression in HIV infected T-cells or monocyte-macrophase.
XX
PS   Example; Fig 19; 102pp; English.
XX
CC   pQ30E was used as a probe to identify clones containing sequences coding
CC   for TCS in a T.kirilowii genomic library. Five clones were eventually
CC   isolated and sequenced, including clone 3. They were found to have
CC   homology to the alpha-TCS coding sequence. See also AAQ06343-9 and
CC   AAQ06351
XX
SQ   Sequence 1169 BP; 387 A; 229 C; 209 G; 344 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.39e-13       Length:         1169
Score:                  182.50         Matches:        45
Percent Similarity:     53.1%          Conservative:   32
Best Local Similarity:  31.0%          Mismatches:     61
Query Match:            23.8%          Indels:         7
DB:                     2              Gaps:           3

US-10-758-902-9 (1-149) x AAQ06350 (1-1169)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              |||   :::   |||::::::      |||            |||      ||||||
Db        201 AATGATATCATCTTCAGTATGGCGAGTGCTGATTCCAGATCCTATAGGAAGTTCATAACA 260

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGln 39
                 ||||||:::   |||   |||          |||   ::::::|||:::   |||
Db        261 TCGCTGAGGAGCGTTCTCCCAAAAGATGGAGAAGTGTTCAAGATACCTCTATTGCTTGCC 320

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
              :::   :::      :::|||:::   |||:::   ::::::         :::||||||
Db        321 AGTTCTTCAGGCTCCAGACGCTACAAACTAATGCAACTCTCAAATTATGAGGAGAAAACC 380

Qy         60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp 79
              :::   ||||||||||||||||||:::||||||:::::||||||
Db        381 ATCACGGTGGCCATAGACGTAACAAACGTTTATATTATGGGATATCTT------------ 428

Qy         80 GlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---Leu 98
                        :::   |||   ::::::                      ||||||   :::
Db        429 GTCAATACAACGTCCTACTTTTTCAATGAGCCTGATGCTGCTACAGCTTCTAAATTTGTA 488

Qy         99 PheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuVal 118
              |||                  |||||||||   :::   |||:::|||:::||||||
Db        489 TTCACAAATGCTCAGAAGAGTGTTACACTTCCATATTCTGGCAACTACGAAAAGCTTCAA 548

Qy        119 AsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSer 138
                ||||||        |||:::   :::   ||||||:::      |||      :::
Db        549 ACTGCTGCAGACAAAAAGAGAGAGAAAATTCCACTTGGACTCCCAGCATTGAGCAGTGCC 608

Qy        139 IleGluAlaIleTrp 143
              |||      ::::::
Db        609 ATTTCCACCTTGTAT 623

RESULT 28
AAQ26504
```

```
ID   AAQ26504 standard; DNA; 1169 BP.
XX
AC   AAQ26504;
XX
DT   25-MAR-2003  (revised)
DT   13-JAN-1993  (first entry)
XX
DE   Ribosome inactivating protein-coding clone pQ3.
XX
KW   TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient; RIP;
KW   multi-gene family; Maxim; HIV-infected human T cells;
KW   human immunodeficiency virus; probe; ss.
XX
OS   Trichosanthes kirilowii.
XX
FH   Key             Location/Qualifiers
FT   CDS             132. .950
FT                   /*tag= a
FT                   /product= "RIP_like_protein"
XX
PN   US5128460-A.
XX
PD   07-JUL-1992.
XX
PF   04-APR-1990;   90US-00504775.
XX
PR   04-APR-1989;   89US-00333184.
PR   07-SEP-1989;   89US-00404326.
XX
PA   (GENE-) GENELABS INC.
XX
PI   Piatak M,  Chow TP,  Fry K;
XX
DR   WPI; 1992-249485/30.
DR   P-PSDB; AAR25577.
XX
PT   Nucleic acid encoding trichosanthin protein - which can be used to
PT   inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV
PT   expression.
XX
PS   Example 7; Fig 19; 53pp; English.
XX
CC   The clone pQ30E, containing a 0.6kb insert, which was isolated from a
CC   T.kirilowii library (see AAQ26501), was used as a probe to isolate
CC   additional sequences homologous to alpha-TCS, i.e. other members of the
CC   RIP multi-gene family. Four unique cloned inserts were identified and
CC   designated pQ2, pQ3, pQ12 and pQ24. Each insert encoded a putative full
CC   length RIP protein. See AAQ26499-Q26508. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1169 BP; 387 A; 229 C; 209 G; 344 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.39e-13       Length:         1169
Score:                  182.50         Matches:        45
Percent Similarity:     53.1%          Conservative:   32
Best Local Similarity:  31.0%          Mismatches:     61
Query Match:            23.8%          Indels:         7
DB:                     2              Gaps:           3

US-10-758-902-9 (1-149) x AAQ26504 (1-1169)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              |||   :::   |||::::::      |||             |||      ||||||
Db        201 AATGATATCATCTTCAGTATGGCGAGTGCTGATTCCAGATCCTATAGGAAGTTCATAACA 260

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGln 39
                ||||||:::   |||   |||       |||   ::::::|||:::   |||
Db        261 TCGCTGAGGAGCGTTCTCCCAAAAGATGGAGAAGTGTTCAAGATACCTCTATTGCTTGCC 320

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
              :::   :::     :::|||:::   |||:::   ::::::         :::||||||
Db        321 AGTTCTTCAGGCTCCAGACGCTACAAACTAATGCAACTCTCAAATTATGAGGAGAAAACC 380

Qy         60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp 79
              :::   ||||||||||||||||||:::||||||:::::::||||||
Db        381 ATCACGGTGGCCATAGACGTAACAAACGTTTATATTATGGGATATCTT------------ 428

Qy         80 GlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---Leu 98
                        :::   |||   ::::::                    ||||||   :::
Db        429 GTCAATACAACGTCCTACTTTTTCAATGAGCCTGATGCTGCTACAGCTTCTAAATTTGTA 488

Qy         99 PheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuVal 118
              |||                  |||||||||   :::   |||:::|||:::||||||
Db        489 TTCACAAATGCTCAGAAGAGTGTTACACTTCCATATTCTGGCAACTACGAAAAGCTTCAA 548

Qy        119 AsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSer 138
                ||||||          |||:::   :::   ||||||:::       |||      :::
Db        549 ACTGCTGCAGACAAAAAGAGAGAGAAAATTCCACTTGGACTCCCAGCATTGAGCAGTGCC 608

Qy        139 IleGluAlaIleTrp 143
              |||       ::::::
Db        609 ATTTCCACCTTGTAT 623

RESULT 29
AAC60425
ID   AAC60425 standard; DNA; 758 BP.
XX
AC   AAC60425;
XX
DT   06-AUG-2003  (revised)
DT   19-FEB-2001  (first entry)
XX
DE   DNA encoding residues 1-247 of plant toxin BD1.
XX
KW   Plant toxin; cancer; high yield; ds.
XX
OS   Bryonia dioica.
XX
PN   US6140075-A.
XX
PD   31-OCT-2000.
XX
PF   29-JUL-1997;   97US-00902486.
XX
PR   25-JUL-1994;   94US-00279772.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Miller MJ,  Russell DR,  Fuller JT;
XX
DR   WPI; 2001-040301/05.
DR   P-PSDB; AAB36824.
XX
PT   Obtaining protein toxins from tobacco cells useful as therapeutic agent,
PT   by transforming a cell suspension with a DNA construct comprising a
PT   signal sequence for the secretion of the proteins.
XX
PS   Example; Col 13-16; 19pp; English.
XX
CC   The present invention relates to obtaining secretable plant protein
CC   toxins from plant cells. The invention is useful for obtaining
CC   commercially useful and higher quantities of plant protein toxins. These
CC   proteins may be used as a therapeutic agent or cytotoxin directed against
CC   specific cancer cells by covalently linking the toxin to an antibody that
CC   recognizes a particular antigenic determinant associated with the cancer
CC   cell. The new method allows production of relatively large quantities of
CC   polypeptide toxins in a heterologous expression system, where the
CC   specific yield and concentration of the desired protein are markedly
CC   higher than those reporter in previous methods. (Updated on 06-AUG-2003
CC   to correct OS field.)
XX
SQ   Sequence 758 BP; 240 A; 160 C; 145 G; 213 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.26e-13       Length:         758
```

```
Score:                 179.50        Matches:       44
Percent Similarity:    54.5%         Conservative:  34
Best Local Similarity: 30.8%         Mismatches:    58
Query Match:           23.4%         Indels:        7
DB:                    4             Gaps:          3

US-10-758-902-9 (1-149) x AAC60425 (1-758)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||     |||          |||       ||||||::::::|||
Db          9 GTGAGCTTTCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 68

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||     |||               |||      :::|||:::         :::|||
Db         69 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 128

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::       |||:::   |||:::  :::|||      :::   :::|||:::
Db        129 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 188

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||:::::||||||
Db        189 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 236

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||   :::   |||   ::::::                 :::|||   :::|||
Db        237 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 296

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                  :::|||||||||   :::   |||:::|||::::::|||      |||
Db        297 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 356

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||         |||:::::::::   ||||||:::     |||:::   :::|||
Db        357 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 416

Qy        141 AlaIleTrp 143
                :::::
Db        417 ACTTTGTAT 425

RESULT 30
AAZ09107
ID   AAZ09107 standard; DNA; 762 BP.
XX
AC   AAZ09107;
XX
DT   18-OCT-1999  (first entry)
XX
DE   Mistletoe lectin A1 (variant) DNA fragment.
XX
KW   Mistletoe; lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
KW   ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW   lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW   cancer; cytotoxicity; antigen; isoform; lectin A1; ds.
XX
OS   Viscum album.
XX
PN   DE19804210-A1.
XX
PD   12-AUG-1999.
XX
PF   03-FEB-1998;   98DE-01004210.
XX
PR   03-FEB-1998;   98DE-01004210.
XX
PA   (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
PI   Morris P,  Stiefel T,  Welters P,  Voelter W;
XX
DR   WPI; 1999-445335/38.
DR   P-PSDB; AAY25983.
XX
PT   Preparation of mistletoe lectins in heterologous systems, particularly
PT   for use as anticancer agents and immunostimulants.
XX
PS   Claim 19; Fig 5A; 78pp; German.
XX
CC   This invention describes a novel mistletoe lectin (I) and its fragments
CC   which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC   of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC   ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-
CC   producing macrophages, so stimulate immunity. (I) and its fragments are
CC   used to treat uncontrolled cell growth (particularly cancers) and if they
CC   lack cytotoxicity, to increase the strength of the immune response,
CC   particularly to a co-administered antigen (tumour-associated, bacterial
CC   or viral). The method allows production of mistletoe lectin, and its
CC   individual chains, in many different isoforms and on a large scale, at
CC   any time of the year. Recombinant products are free from toxins present
CC   in natural mistletoe extracts. This sequence encodes a fragment of a
CC   mistletoe lectin A1 protein variant
XX
SQ   Sequence 762 BP; 192 A; 141 C; 163 G; 266 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             3.28e-13      Length:        762
Score:                 179.50        Matches:       50
Percent Similarity:    57.1%         Conservative:  26
Best Local Similarity: 37.6%         Mismatches:    48
Query Match:           23.4%         Indels:        9
DB:                    2             Gaps:          4

US-10-758-902-9 (1-149) x AAZ09107 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::       |||:::         ::::::|||   :::||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   :::|||      |||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTGTTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||       |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||       |||          |||          |||       :::
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||       |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 31
AAZ09104
ID   AAZ09104 standard; DNA; 762 BP.
XX
AC   AAZ09104;
XX
DT   18-OCT-1999  (first entry)
XX
DE   Mistletoe lectin A1 DNA fragment.
XX
KW   Mistletoe; lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
KW   ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW   lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW   cancer; cytotoxicity; antigen; isoform; lectin A1; ds.
XX
```

```
OS   Viscum album.
XX
PN   DE19804210-A1.
XX
PD   12-AUG-1999.
XX
PF   03-FEB-1998;   98DE-01004210.
XX
PR   03-FEB-1998;   98DE-01004210.
XX
PA   (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
PI   Morris P,  Stiefel T,  Welters P,  Voelter W;
XX
DR   WPI; 1999-445335/38.
DR   P-PSDB; AAY25980.
XX
PT   Preparation of mistletoe lectins in heterologous systems, particularly
PT   for use as anticancer agents and immunostimulants.
XX
PS   Claim 15; Fig 2A; 78pp; German.
XX
CC   This invention describes a novel mistletoe lectin (I) and its fragments
CC   which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC   of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC   ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-
CC   producing macrophages, so stimulate immunity. (I) and its fragments are
CC   used to treat uncontrolled cell growth (particularly cancers) and if they
CC   lack cytotoxicity, to increase the strength of the immune response,
CC   particularly to a co-administered antigen (tumour-associated, bacterial
CC   or viral). The method allows production of mistletoe lectin, and its
CC   individual chains, in many different isoforms and on a large scale, at
CC   any time of the year. Recombinant products are free from toxins present
CC   in natural mistletoe extracts. This sequence encodes a fragment of the
CC   mistletoe lectin A1 protein
XX
SQ   Sequence 762 BP; 171 A; 230 C; 183 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.28e-13      Length:          762
Score:                    179.50        Matches:         50
Percent Similarity:       57.1%         Conservative:    26
Best Local Similarity:    37.6%         Mismatches:      48
Query Match:              23.4%         Indels:          9
DB:                       2             Gaps:            4

US-10-758-902-9 (1-149) x AAZ09104 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      |||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||:::::|||         :::   :::|||      |||||||||||||||:::
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGGTTACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||           |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
```

```
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 32
AAZ09105
ID   AAZ09105 standard; DNA; 768 BP.
XX
AC   AAZ09105;
XX
DT   18-OCT-1999  (first entry)
XX
DE   Mistletoe lectin A2 DNA fragment.
XX
KW   Mistletoe; lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
KW   ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW   lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW   cancer; cytotoxicity; antigen; isoform; lectin A2; ds.
XX
OS   Viscum album.
XX
PN   DE19804210-A1.
XX
PD   12-AUG-1999.
XX
PF   03-FEB-1998;   98DE-01004210.
XX
PR   03-FEB-1998;   98DE-01004210.
XX
PA   (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
PI   Morris P,  Stiefel T,  Welters P,  Voelter W;
XX
DR   WPI; 1999-445335/38.
DR   P-PSDB; AAY25981.
XX
PT   Preparation of mistletoe lectins in heterologous systems, particularly
PT   for use as anticancer agents and immunostimulants.
XX
PS   Claim 15; Fig 3A; 78pp; German.
XX
CC   This invention describes a novel mistletoe lectin (I) and its fragments
CC   which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC   of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC   ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-
CC   producing macrophages, so stimulate immunity. (I) and its fragments are
CC   used to treat uncontrolled cell growth (particularly cancers) and if they
CC   lack cytotoxicity, to increase the strength of the immune response,
CC   particularly to a co-administered antigen (tumour-associated, bacterial
CC   or viral). The method allows production of mistletoe lectin, and its
CC   individual chains, in many different isoforms and on a large scale, at
CC   any time of the year. Recombinant products are free from toxins present
CC   in natural mistletoe extracts. This sequence encodes a fragment of the
CC   mistletoe lectin A2 protein
XX
SQ   Sequence 768 BP; 175 A; 224 C; 182 G; 187 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.32e-13      Length:          768
Score:                    179.50        Matches:         49
Percent Similarity:       56.7%         Conservative:    27
Best Local Similarity:    36.6%         Mismatches:      49
Query Match:              23.4%         Indels:          9
DB:                       2             Gaps:            4

US-10-758-902-9 (1-149) x AAZ09105 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      |||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165
```

```
Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||:::;::|||          :::   ::::::          ||||||||||||||:::
Db        166 GTGGAGGTCACCAACCAGGGGCAGGACTCGATCACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||               |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThr---AsnArgValThrLeu 108
              |||       |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGCACCACCCGAGATAGATCCTCTCTC 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||       |||       |||       |||          :::
Db        334 CCATTCACTGGAAGCTACACCGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATC 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCTCTCGGTATAGAGCAACTCATTCAATCCGTCTCTGCGCTT 432

RESULT 33
AAZ09108
ID   AAZ09108 standard; DNA; 768 BP.
XX
AC   AAZ09108;
XX
DT   18-OCT-1999  (first entry)
XX
DE   Mistletoe lectin A2 (variant) DNA fragment.
XX
KW   Mistletoe; lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
KW   ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW   lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW   cancer; cytotoxicity; antigen; isoform; lectin A2; ds.
XX
OS   Viscum album.
XX
PN   DE19804210-A1.
XX
PD   12-AUG-1999.
XX
PF   03-FEB-1998;   98DE-01004210.
XX
PR   03-FEB-1998;   98DE-01004210.
XX
PA   (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
PI   Morris P,  Stiefel T,  Welters P,  Voelter W;
XX
DR   WPI; 1999-445335/38.
DR   P-PSDB; AAY25984.
XX
PT   Preparation of mistletoe lectins in heterologous systems, particularly
PT   for use as anticancer agents and immunostimulants.
XX
PS   Claim 19; Fig 6A; 78pp; German.
XX
CC   This invention describes a novel mistletoe lectin (I) and its fragments
CC   which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC   of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC   ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-
CC   producing macrophages, so stimulate immunity. (I) and its fragments are
CC   used to treat uncontrolled cell growth (particularly cancers) and if they
CC   lack cytotoxicity, to increase the strength of the immune response,
CC   particularly to a co-administered antigen (tumour-associated, bacterial
CC   or viral). The method allows production of mistletoe lectin, and its
CC   individual chains, in many different isoforms and on a large scale, at
CC   any time of the year. Recombinant products are free from toxins present
CC   in natural mistletoe extracts. This sequence encodes a fragment of a
CC   mistletoe lectin A2 protein variant
XX
SQ   Sequence 768 BP; 192 A; 138 C; 166 G; 272 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              3.32e-13      Length:          768
Score:                  179.50        Matches:         49
Percent Similarity:     56.7%         Conservative:    27
Best Local Similarity:  36.6%         Mismatches:      49
Query Match:            23.4%         Indels:          9
DB:                     2             Gaps:            4

US-10-758-902-9 (1-149) x AAZ09108 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||          :::   ::::::          ||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTATTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||               |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG------------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThr---AsnArgValThrLeu 108
              |||       |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGTACAACACGGGATAGAAGTTCTTTG 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||       |||       |||       |||          :::
Db        334 CCTTTTACTGGTTCTTATACAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATT 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCATTGGGAATTGAGCAGTTGATCCAGAGTGTTTCTGCTTTG 432

RESULT 34
AAT16208
ID   AAT16208 standard; cDNA; 1094 BP.
XX
AC   AAT16208;
XX
DT   10-JUL-1996  (first entry)
XX
DE   Bryodin 1 cDNA.
XX
KW   Bryodin 1; ribosome-inactivating protein; ligand; toxin; immunotoxin;
KW   cytotoxin; cancer; ss.
XX
OS   Bryonia dioica.
XX
FH   Key             Location/Qualifiers
FT   CDS             44. .916
FT                   /*tag=  a
FT   sig_peptide     44. .115
FT                   /*tag=  b
FT   mat_peptide     116. .913
FT                   /*tag=  c
FT   polyA_signal    999. .1004
FT                   /*tag=  d
FT   polyA_signal    1059. .1064
FT                   /*tag=  e
XX
PN   CA2148724-A.
XX
PD   18-NOV-1995.
XX
PF   05-MAY-1995;   95CA-02148724.
XX
PR   17-MAY-1994;   94US-00245754.
```

```
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Siegall CB;
XX
DR   WPI; 1996-077793/09.
DR   P-PSDB; AAR92481.
XX
PT   Oligo:nucleotide encoding ribosome-inactivating bryodin 1 from Bryonia
PT   dioica - inhibits protein synthesis in vitro and is useful as ligand or
PT   toxin conjugates or fusion proteins to selectively kill, e.g. cancer
PT   cells.
XX
PS   Claim 2; Page 27-28; 46pp; English.
XX
CC   A full-length cDNA (AAT16208) codes for bryodin 1 (AAR92481), a ribosome-
CC   inactivating protein. The cDNA was obtd. following PCR amplification of
CC   cDNA derived from Bryonia dioica leaf, 3'RACE and 5'RACE (see also
CC   AAT16209-16). The cDNA can be incorporated into a vector and used for
CC   large-scale prodn. of recombinant bryodin 1 in transformed host cells.
CC   Fusion proteins including bryodin 1 may also be produced for use e.g. as
CC   immunotoxins
XX
SQ   Sequence 1094 BP; 356 A; 213 C; 201 G; 324 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                5.33e-13      Length:          1094
Score:                    179.50        Matches:         44
Percent Similarity:       54.5%         Conservative:    34
Best Local Similarity:    30.8%         Mismatches:      58
Query Match:              23.4%         Indels:          7
DB:                       2             Gaps:            3

US-10-758-902-9 (1-149) x AAT16208 (1-1094)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||:::::|||
Db        116 GTTAGCTTCCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 175

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::         :::|||
Db        176 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 235

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::       |||:::   |||:::  :::|||      :::  :::|||:::
Db        236 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 295

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||:::::||||||
Db        296 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 343

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||   :::   |||   ::::::                  :::|||   :::|||
Db        344 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 403

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                  :::|||||||||   :::   |||:::|||:::::|||      |||
Db        404 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 463

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||         |||:::::::::   ||||||:::      |||:::   :::|||
Db        464 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 523

Qy        141 AlaIleTrp 143
                 ::::::
Db        524 ACTTTGTAT 532

RESULT 35
AAC60429
ID   AAC60429 standard; DNA; 1499 BP.
XX
AC   AAC60429;
XX
DT   06-AUG-2003  (revised)
DT   19-FEB-2001  (first entry)
XX
DE   BD1-G28.5 fusion gene.
XX
KW   Plant toxin; cancer; high yield; ds.
XX
OS   Bryonia dioica.
OS   Synthetic.
XX
PN   US6140075-A.
XX
PD   31-OCT-2000.
XX
PF   29-JUL-1997;   97US-00902486.
XX
PR   25-JUL-1994;   94US-00279772.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Miller MJ,  Russell DR,  Fuller JT;
XX
DR   WPI; 2001-040301/05.
DR   P-PSDB; AAB36828.
XX
PT   Obtaining protein toxins from tobacco cells useful as therapeutic agent,
PT   by transforming a cell suspension with a DNA construct comprising a
PT   signal sequence for the secretion of the proteins.
XX
PS   Example; Col 29-32; 19pp; English.
XX
CC   The present invention relates to obtaining secretable plant protein
CC   toxins from plant cells. The invention is useful for obtaining
CC   commercially useful and higher quantities of plant protein toxins. These
CC   proteins may be used as a therapeutic agent or cytotoxin directed against
CC   specific cancer cells by covalently linking the toxin to an antibody that
CC   recognizes a particular antigenic determinant associated with the cancer
CC   cell. The new method allows production of relatively large quantities of
CC   polypeptide toxins in a heterologous expression system, where the
CC   specific yield and concentration of the desired protein are markedly
CC   higher than those reporter in previous methods. (Updated on 06-AUG-2003
CC   to correct OS field.)
XX
SQ   Sequence 1499 BP; 418 A; 348 C; 337 G; 396 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.14e-13      Length:          1499
Score:                    179.50        Matches:         44
Percent Similarity:       54.5%         Conservative:    34
Best Local Similarity:    30.8%         Mismatches:      58
Query Match:              23.4%         Indels:          7
DB:                       4             Gaps:            3

US-10-758-902-9 (1-149) x AAC60429 (1-1499)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||:::::|||
Db          9 GTGAGCTTTCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 68

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::         :::|||
Db         69 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 128

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::       |||:::   |||:::  :::|||      :::  :::|||:::
Db        129 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 188

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||:::::||||||
Db        189 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 236

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||   :::   |||   ::::::                  :::|||   :::|||
```

```
Db        237 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 296

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                  :::||||||||||   :::   |||:::|||::::::|||      |||
Db        297 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 356

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||          |||:::::::::   ||||||:::      |||:::   :::|||
Db        357 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 416

Qy        141 AlaIleTrp 143
                :::::
Db        417 ACTTTGTAT 425

RESULT 36
AAV51343
ID   AAV51343 standard; DNA; 756 BP.
XX
AC   AAV51343;
XX
DT   23-OCT-1998  (first entry)
XX
DE   Mistletoe rMLA variant DNA.
XX
KW   Lectin A-chain; mistletoe; rMLA; fusion protein; effector; cytotoxic;
KW   intracellular; processing module; protease recognition; targeting module;
KW   internalisation; treatment; disorder; cell proliferation; activation;
KW   autoimmune disease; allergy; tumour; ricin; translocation; ss.
XX
OS   Viscum album.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .756
FT                   /*tag=  a
FT                   /product= "lectin A-chain"
FT                   /note= "Partial sequence"
XX
PN   WO9829540-A2.
XX
PD   09-JUL-1998.
XX
PF   02-JAN-1998;   98WO-EP000009.
XX
PR   02-JAN-1997;   97EP-00100012.
XX
PA   (BRAI-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.
XX
PI   Eck J,  Schmidt A,  Zinke H;
XX
DR   WPI; 1998-388122/33.
XX
PT   Nucleic acid encoding fusion protein containing mistletoe lectin A chain
PT   - useful for treatment of proliferative and autoimmune diseases,
PT   allergies and tumours.
XX
PS   Disclosure; Fig 11a'; 115pp; German.
XX
CC   This sequence encodes a variant mistletoe lectin A-chain, rMLA. This
CC   sequence can be used in the construction of a fusion protein which
CC   comprises an effector module that is cytotoxic intracellularly, a
CC   processing module covalently bonded to the effector module and containing
CC   a protease recognition sequence, and a targeting module covalently bonded
CC   to the processing module, able to bind specifically to the surface of a
CC   cell so as to mediate internalisation of the fusion protein. Such a
CC   fusion protein can be used for treating disorders involving proliferation
CC   and/or elevated activation of cells, especially autoimmune disease,
CC   allergy and tumours. The proteins can be administered e.g. by injection
CC   or topically but especially by intravenous injection, at 1 ng to 500 mu
CC   g/kg/day, or for ex vivo use at 1 pg to 500 ng/ml. Fusion proteins can
CC   develop toxic activity in a wide range of target cells. The processing
CC   module prevents extracellular dissociation, and fusion proteins based on
CC   mistletoe lectin A-chain are far more active than those based on ricin
CC   and do have the associated problems of non-specific toxicity. The protein
CC   may be expressed in a non-glycosylated form that does not bind to sugar
CC   receptors in the liver, and which has a long half-life in the blood.
CC   Where the mistletoe lectin B-chain is used, it actively assists in
CC   translocation of the ML A-chain from the endoplasmic reticulum to the
CC   cytoplasm
XX
SQ   Sequence 756 BP; 167 A; 229 C; 181 G; 179 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.91e-13      Length:          756
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     2             Gaps:            4

US-10-758-902-9 (1-149) x AAV51343 (1-756)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::       |||:::         ::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::      |||||||||||||||::::::
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::||||||||||      |||          |||          |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 37
AAV51341
ID   AAV51341 standard; DNA; 762 BP.
XX
AC   AAV51341;
XX
DT   23-OCT-1998  (first entry)
XX
DE   Mistletoe rMLA DNA.
XX
KW   Lectin A-chain; mistletoe; rMLA; fusion protein; effector; cytotoxic;
KW   intracellular; processing module; protease recognition; targeting module;
KW   internalisation; treatment; disorder; cell proliferation; activation;
KW   autoimmune disease; allergy; tumour; ricin; translocation; ss.
XX
OS   Viscum album.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .759
FT                   /*tag=  a
FT                   /product= "lectin A-chain"
FT                   /note= "Partial sequence"
XX
PN   WO9829540-A2.
XX
PD   09-JUL-1998.
XX
```

```
PF   02-JAN-1998;   98WO-EP000009.
XX
PR   02-JAN-1997;   97EP-00100012.
XX
PA   (BRAI-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.
XX
PI   Eck J,  Schmidt A,  Zinke H;
XX
DR   WPI; 1998-388122/33.
DR   P-PSDB; AAW64659.
XX
PT   Nucleic acid encoding fusion protein containing mistletoe lectin A chain
PT   - useful for treatment of proliferative and autoimmune diseases,
PT   allergies and tumours.
XX
PS   Disclosure; Fig 11a; 115pp; German.
XX
CC   This sequence encodes a lectin A-chain, rMLA, isolated from mistletoe.
CC   This sequence can be used in the construction of a fusion protein which
CC   comprises an effector module that is cytotoxic intracellularly, a
CC   processing module covalently bonded to the effector module and containing
CC   a protease recognition sequence, and a targeting module covalently bonded
CC   to the processing module, able to bind specifically to the surface of a
CC   cell so as to mediate internalisation of the fusion protein. Such a
CC   fusion protein can be used for treating disorders involving proliferation
CC   and/or elevated activation of cells, especially autoimmune disease,
CC   allergy and tumours. The proteins can be administered e.g. by injection
CC   or topically but especially by intravenous injection, at 1 ng to 500 mu
CC   g/kg/day, or for ex vivo use at 1 pg to 500 ng/ml. Fusion proteins can
CC   develop toxic activity in a wide range of target cells. The processing
CC   module prevents extracellular dissociation, and fusion proteins based on
CC   mistletoe lectin A-chain are far more active than those based on ricin
CC   and do have the associated problems of non-specific toxicity. The protein
CC   may be expressed in a non-glycosylated form that does not bind to sugar
CC   receptors in the liver, and which has a long half-life in the blood.
CC   Where the mistletoe lectin B-chain is used, it actively assists in
CC   translocation of the ML A-chain from the endoplasmic reticulum to the
CC   cytoplasm
XX
SQ   Sequence 762 BP; 169 A; 230 C; 183 G; 180 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8e-13          Length:          762
Score:                    176.50         Matches:         49
Percent Similarity:       57.1%          Conservative:    27
Best Local Similarity:    36.8%          Mismatches:      48
Query Match:              23.0%          Indels:          9
DB:                       2              Gaps:            4

US-10-758-902-9 (1-149) x AAV51341 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||               ::::::     |||||||||||||||::::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                ||||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
```

```
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              |||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 38
AAT91660
ID   AAT91660 standard; DNA; 774 BP.
XX
AC   AAT91660;
XX
DT   18-DEC-1997  (first entry)
XX
DE   Prepro mistletoe lectin A chain.
XX
KW   Mistletoe; lectin; cytotoxic; A chain; B chain; dimer; ss.
XX
OS   Viscum album.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .765
FT                   /*tag=  a
XX
PN   EP751221-A1.
XX
PD   02-JAN-1997.
XX
PF   26-JUN-1995;   95EP-00109949.
XX
PR   26-JUN-1995;   95EP-00109949.
XX
PA   (MADU ) MADAUS KOELN AG.
XX
PI   Lentzen H,  Eck J,  Baur A,  Zinke H;
XX
DR   WPI; 1997-054678/06.
DR   P-PSDB; AAW10022.
XX
PT   Nucleic acid encoding pre:pro form of mistletoe lectin - for therapeutic
PT   or diagnostic use.
XX
PS   Claim 2; Fig 4A; 30pp; German.
XX
CC   Mistletoe lectin is a cytotoxic agent that has been used for tumour
CC   therapy. It can be used in immunotoxins and medicaments. Nucleic acid
CC   fragments can be used in diagnostic methods. Mistletoe lectin ( AAT91659)
CC   comprises an A chain (AAT91660) and a B chain (AAT91661)
XX
SQ   Sequence 774 BP; 173 A; 232 C; 185 G; 184 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.17e-13       Length:          774
Score:                    176.50         Matches:         49
Percent Similarity:       57.1%          Conservative:    27
Best Local Similarity:    36.8%          Mismatches:      48
Query Match:              23.0%          Indels:          9
DB:                       2              Gaps:            4

US-10-758-902-9 (1-149) x AAT91660 (1-774)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||               ::::::     |||||||||||||||::::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231
```

```
Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||       |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||       |||         |||         |||       :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 39
AAV74180
ID   AAV74180 standard; DNA; 774 BP.
XX
AC   AAV74180;
XX
DT   20-MAR-2003  (revised)
DT   30-APR-1999  (first entry)
XX
DE   Mistletoe ML A-chain DNA.
XX
KW   ML; mistletoe; lectin; MLA; A-chain; transgenic plant; glycosylation;
KW   dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
KW   cancer; ss.
XX
OS   Viscum album.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .765
FT                   /*tag=  a
FT                   /product= "mistletoe lectin"
XX
PN   EP884388-A1.
XX
PD   16-DEC-1998.
XX
PF   26-JUN-1995;   98EP-00105660.
XX
PR   26-JUN-1995;   95EP-00109949.
XX
PA   (MADU ) MADAUS KOELN AG.
XX
PI   Lentzen H,  Eck J,  Baur A,  Zinke H;
XX
DR   WPI; 1999-026582/03.
DR   P-PSDB; AAW90125.
XX
PT   New transgenic plant expressing mistletoe lectin - useful for producing
PT   recombinant lectin in e.g. cancer diagnosis and therapy.
XX
PS   Claim 2; Fig 4a; 30pp; German.
XX
CC   This invention describes a novel transgenic plant transformed with a
CC   vector capable of encoding a mistletoe (Viscum album) lectin
CC   preproprotein or a biologically active fragment. The specification also
CC   describes a polypeptide produced by a plant where the polypeptide
CC   exhibits at least one enzymatic modification other than the glycosylation
CC   that occurs in Viscum album or the polypeptide is a fusion protein, a
CC   mistletoe lectin polypeptide dimer and an immunotoxin comprising the
CC   polypeptide or the polypeptide dimer. The plants are used for large-scale
CC   production of mistletoe lectin for diagnostic or therapeutic purposes
CC   (e.g. in cancer therapy). This sequence encodes the mistletoe lectin A-
CC   chain which is contained in expression vector pT7MLA. (Updated on 20-MAR-
CC   2003 to correct PF field.)
XX
SQ   Sequence 774 BP; 173 A; 232 C; 185 G; 184 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.17e-13        Length:         774
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     2               Gaps:           4

US-10-758-902-9 (1-149) x AAV74180 (1-774)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::      |||||||||||||||:::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||       |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||       |||         |||         |||       :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 40
ACC85526
ID   ACC85526 standard; DNA; 855 BP.
XX
AC   ACC85526;
XX
DT   29-SEP-2003  (first entry)
XX
DE   Mistletoe lectin coding sequence SEQ ID NO: 1.
XX
KW   Mistletoe; lectin; responsiveness; receptor; N-acetylneuraminic acid;
KW   Neu5Ac; galactose; Gal; glycosidic alpha2-6 bond; cytostatic; virucide;
KW   immunosuppressive; neuroprotective; anti-HIV; anticancer agent; cancer;
KW   proliferative disease; viral infection; autoimmune disease;
KW   neurological disease; gene; ds.
XX
OS   Viscum album.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .855
FT                   /*tag=  a
FT                   /product= "lectin"
FT                   /partial
FT                   /note= "no stop codon"
XX
PN   WO2003054544-A2.
XX
PD   03-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-EP014682.
XX
PR   21-DEC-2001; 2001EP-00130745.
XX
PA   (VISC-) VISCUM AG.
XX
```

PI Muething J, Peter-Katalinic J, Langer M, Moeckel B, Eck J;
XX
DR WPI; 2003-577377/54.
DR P-PSDB; ABR63710.
XX
PT In vitro determination of response to mistletoe lectin, useful for
PT selecting tumor therapy, also anticancer agents that bind to the
PT mistletoe lectin receptor.
XX
PS Claim 8; Page 73-74; 83pp; German.
XX
CC The present invention relates to a method of determining the response of
CC a subject in vitro to misteltoe lectin, or its individual chains, by
CC specific quantitative and/or qualitative determination of membrane-bound
CC receptors that are characterised by a terminal N-acetylneuraminic acid
CC (Neu5Ac) bound to galactose (Gal) through a glycosidic alpha2-6 bond. The
CC method is useful for determining the response of a subject to misteltoe
CC lectin, in order to determine if the lectin is suitable for use as an
CC anticancer agent. Agents that recognise, or bind to, the mistletoe lectin
CC receptor are useful for diagnostic detection of the receptor, especially
CC on tumour cells, e.g. present in a biopsy sample or blood, and for
CC treatment of proliferative, viral (HIV or herpes), autoimmune or
CC neurological diseases. The present sequence is a coding sequence of
CC mistletoe lectin
XX
SQ Sequence 855 BP; 195 A; 243 C; 213 G; 204 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.34e-13	Length:	855
Score:	176.50	Matches:	49
Percent Similarity:	57.1%	Conservative:	27
Best Local Similarity:	36.8%	Mismatches:	48
Query Match:	23.0%	Indels:	9
DB:	9	Gaps:	4

US-10-758-902-9 (1-149) x ACC85526 (1-855)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db        145 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 204

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
Db        205 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 264

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::      ||||||||||||||::::::
Db        265 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 324

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        325 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 372

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        373 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 429

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        430 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 486

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        487 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 525
```

Search completed: February 20, 2006, 07:54:55
Job time : 744.011 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:19:21 ; Search time 226.413 Seconds
(without alignments)
1169.792 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160806_3773/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss08 -USER=US10758902_@CGN_1_1_237_@runat_17022006_160806_3773 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	609	79.3	363	3	US-09-445-160B-8	Sequence 8, Appli
2	221.5	28.8	756	2	US-07-854-845B-1	Sequence 1, Appli
3	220.5	28.7	913	2	US-07-901-707-13	Sequence 13, Appl
4	220.5	28.7	913	2	US-07-988-430-13	Sequence 13, Appl
5	220.5	28.7	913	2	US-08-425-336-13	Sequence 13, Appl
6	220.5	28.7	913	2	US-08-488-113B-13	Sequence 13, Appl
7	220.5	28.7	913	2	US-08-477-484B-13	Sequence 13, Appl
8	220.5	28.7	913	2	US-08-646-360-13	Sequence 13, Appl
9	220.5	28.7	913	3	US-08-839-765-13	Sequence 13, Appl
10	220.5	28.7	913	3	US-09-136-389-13	Sequence 13, Appl
11	220.5	28.7	913	3	US-09-610-838-13	Sequence 13, Appl
12	220.5	28.7	913	3	US-09-711-485-13	Sequence 13, Appl
13	220.5	28.7	913	6	PCT-US92-09487-13	Sequence 13, Appl
14	211.5	27.5	762	2	US-07-854-845B-9	Sequence 9, Appli
15	190.5	24.8	962	2	US-08-324-301-14	Sequence 14, Appl
16	183.5	23.9	886	2	US-07-923-692C-3	Sequence 3, Appli
17	183.5	23.9	886	2	US-08-184-237-3	Sequence 3, Appli
18	183.5	23.9	886	2	US-08-482-920-3	Sequence 3, Appli
19	183.5	23.9	886	3	US-08-484-341-3	Sequence 3, Appli
20	183.5	23.9	886	3	US-08-483-502-3	Sequence 3, Appli
21	183.5	23.9	886	3	US-09-726-651A-3	Sequence 3, Appli
22	179.5	23.4	758	3	US-08-902-486-6	Sequence 6, Appli
23	179.5	23.4	762	3	US-09-601-667C-16	Sequence 16, Appl
24	179.5	23.4	762	3	US-09-601-667C-19	Sequence 19, Appl
25	179.5	23.4	768	3	US-09-601-667C-17	Sequence 17, Appl
26	179.5	23.4	768	3	US-09-601-667C-20	Sequence 20, Appl
27	179.5	23.4	1094	2	US-08-245-754A-1	Sequence 1, Appli
28	179.5	23.4	1094	2	US-08-597-731-1	Sequence 1, Appli
29	179.5	23.4	1499	3	US-08-902-486-14	Sequence 14, Appl
30	176.5	23.0	774	3	US-08-776-059-30	Sequence 30, Appl
31	176.5	23.0	1596	3	US-09-601-667C-15	Sequence 15, Appl
32	176.5	23.0	1596	3	US-09-601-667C-18	Sequence 18, Appl
33	176.5	23.0	1923	3	US-08-776-059-34	Sequence 34, Appl
34	174.5	22.7	837	3	US-09-627-165E-15	Sequence 15, Appl
35	171.5	22.3	762	3	US-09-627-165E-3	Sequence 3, Appli
36	169.5	22.1	705	3	US-08-776-059-38	Sequence 38, Appl
37	169	22.0	807	2	US-08-356-786-7	Sequence 7, Appli
38	169	22.0	1140	2	US-08-218-303-15	Sequence 15, Appl
39	169	22.0	1140	2	US-08-338-793D-60	Sequence 60, Appl
40	169	22.0	1605	2	US-08-356-786-9	Sequence 9, Appli
41	169	22.0	1731	3	US-09-785-921A-2	Sequence 2, Appli
42	169	22.0	1731	3	US-09-785-921A-3	Sequence 3, Appli
43	169	22.0	1805	3	US-09-785-921A-10	Sequence 10, Appl
44	168.5	21.9	762	3	US-09-627-165E-1	Sequence 1, Appli
45	168.5	21.9	852	2	US-09-069-330-1	Sequence 1, Appli
46	167	21.7	1698	3	US-09-785-921A-1	Sequence 1, Appli
47	167	21.7	1855	3	US-09-147-208-33	Sequence 33, Appl
48	167	21.7	1855	3	US-09-147-208-40	Sequence 40, Appl
49	167	21.7	1855	3	US-09-147-208-47	Sequence 47, Appl
50	167	21.7	1855	3	US-09-147-208-54	Sequence 54, Appl
51	167	21.7	1855	3	US-09-550-117A-33	Sequence 33, Appl
52	167	21.7	1855	3	US-09-550-117A-40	Sequence 40, Appl
53	167	21.7	1855	3	US-09-550-117A-47	Sequence 47, Appl
54	167	21.7	1855	3	US-09-550-117A-54	Sequence 54, Appl
55	167	21.7	1855	3	US-09-403-752A-3	Sequence 3, Appli
56	167	21.7	1855	3	US-09-403-752A-5	Sequence 5, Appli
57	167	21.7	1855	3	US-09-403-752A-7	Sequence 7, Appli
58	167	21.7	1855	3	US-09-403-752A-9	Sequence 9, Appli
59	167	21.7	1855	3	US-09-403-752A-13	Sequence 13, Appl
60	167	21.7	1855	3	US-09-403-752A-15	Sequence 15, Appl
61	167	21.7	1855	3	US-09-403-752A-17	Sequence 17, Appl
62	167	21.7	1855	3	US-09-403-752A-19	Sequence 19, Appl
63	167	21.7	1855	3	US-09-403-752A-21	Sequence 21, Appl
64	167	21.7	1855	3	US-09-403-752A-23	Sequence 23, Appl
65	167	21.7	1855	3	US-09-403-752A-25	Sequence 25, Appl
66	167	21.7	1855	3	US-09-403-752A-27	Sequence 27, Appl
67	167	21.7	1855	3	US-09-403-752A-29	Sequence 29, Appl
68	167	21.7	1855	3	US-09-403-752A-31	Sequence 31, Appl
69	167	21.7	1855	3	US-09-403-752A-33	Sequence 33, Appl
70	167	21.7	1855	3	US-09-403-752A-35	Sequence 35, Appl
71	167	21.7	1855	3	US-09-403-752A-37	Sequence 37, Appl
72	167	21.7	1855	3	US-09-403-752A-39	Sequence 39, Appl
73	167	21.7	1855	3	US-09-403-752A-48	Sequence 48, Appl
74	167	21.7	1855	3	US-09-403-752A-50	Sequence 50, Appl
75	167	21.7	1855	3	US-09-403-752A-52	Sequence 52, Appl
76	167	21.7	1855	3	US-09-403-752A-54	Sequence 54, Appl
77	167	21.7	1855	3	US-09-403-752A-74	Sequence 74, Appl
78	167	21.7	1855	3	US-09-403-752A-77	Sequence 77, Appl
79	167	21.7	1855	3	US-09-403-752A-80	Sequence 80, Appl
80	167	21.7	1855	3	US-09-403-752A-83	Sequence 83, Appl
81	167	21.7	1855	3	US-09-403-752A-86	Sequence 86, Appl
82	167	21.7	1855	3	US-09-403-752A-89	Sequence 89, Appl

83	167	21.7	1855	3	US-09-403-752A-92	Sequence 92, Appl
84	167	21.7	1855	3	US-09-403-752A-95	Sequence 95, Appl
85	167	21.7	1855	3	US-09-403-752A-98	Sequence 98, Appl
86	167	21.7	1855	3	US-09-403-752A-101	Sequence 101, App
87	167	21.7	1855	3	US-09-403-752A-104	Sequence 104, App
88	167	21.7	1855	3	US-09-403-752A-110	Sequence 110, App
89	167	21.7	1855	3	US-09-403-752A-113	Sequence 113, App
90	167	21.7	1855	3	US-09-403-752A-116	Sequence 116, App
91	167	21.7	1855	3	US-09-403-752A-119	Sequence 119, App
92	167	21.7	1855	3	US-09-403-752A-122	Sequence 122, App
93	167	21.7	1855	3	US-09-403-752A-125	Sequence 125, App
94	167	21.7	1855	3	US-09-551-151A-3	Sequence 3, Appli
95	167	21.7	1855	3	US-09-551-151A-5	Sequence 5, Appli
96	167	21.7	1855	3	US-09-551-151A-7	Sequence 7, Appli
97	167	21.7	1855	3	US-09-551-151A-9	Sequence 9, Appli
98	167	21.7	1855	3	US-09-551-151A-13	Sequence 13, Appl
99	167	21.7	1855	3	US-09-551-151A-15	Sequence 15, Appl
100	167	21.7	1855	3	US-09-551-151A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-445-160B-8
; Sequence 8, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenza
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
; FILE REFERENCE: Stirpe
; CURRENT APPLICATION NUMBER: US/09/445,160B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/NL98/00336
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 8
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Bougainvillea spectrabilis
; PUBLICATION INFORMATION:
US-09-445-160B-8

Alignment Scores:

Pred. No.:	2.17e-73	Length:	363
Score:	609.00	Matches:	120
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	79.3%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-9 (1-149) x US-09-445-160B-8 (1-363)

```
Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361
```

RESULT 2
US-07-854-845B-1
; Sequence 1, Application US/07854845B
; Patent No. 5340732
; GENERAL INFORMATION:
; APPLICANT: HABUKA, No. 5340732iyuki
; APPLICANT: MIYANO, Masashi
; APPLICANT: MATSUMOTO, Takashi
; APPLICANT: NOMA, Masana
; TITLE OF INVENTION: ANTIVIRAL PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH, & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/854,845B
; FILING DATE: 20-MAR-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 42-194P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mirabilis jalapa
US-07-854-845B-1

Alignment Scores:

Pred. No.:	1.8e-20	Length:	756
Score:	221.50	Matches:	54
Percent Similarity:	55.9%	Conservative:	27
Best Local Similarity:	37.2%	Mismatches:	55
Query Match:	28.8%	Indels:	9
DB:	2	Gaps:	4

US-10-758-902-9 (1-149) x US-07-854-845B-1 (1-756)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||           |||   :::||||||   ::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 84
```

```
Qy          25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
               :::|||     |||      |||          |||:::|||   |||:::
Db          85 GTCGCAGACAAAACCGAACAGTGT-----------ACCATCCAGAAAATCTCTAAAACC 132

Qy          44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                  :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db         133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy          63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
               |||||||||:::   |||:::||||||:::|||||   |||      :::   |||
Db         193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy          83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
               ||||||   |||      |||          :::      |||||||||
Db         253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy         103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                    |||||||||:::   |||||||||   |||||||||       |||
Db         313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372

Qy         121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                  :::   |||||||||       |||||:::::::::::||||||   ||||||
Db         373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429

Qy         141 AlaIleTrpGlyLys 145
               |||:::||||||
Db         430 AACATTTATGGCAAA 444

RESULT 3
US-07-901-707-13
; Sequence 13, Application US/07901707
; Patent No. 5376546
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Composition and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/901,707
;      FILING DATE:  19920619
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5376546and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27129/30910
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-5750
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-901-707-13

Alignment Scores:
Pred. No.:                3.21e-20        Length:          913
Score:                    220.50          Matches:         52
Percent Similarity:       59.9%           Conservative:    33
Best Local Similarity:    36.6%           Mismatches:      50
Query Match:              28.7%           Indels:          7
DB:                       2               Gaps:            3

US-10-758-902-9 (1-149) x US-07-901-707-13 (1-913)

Qy           4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
               |||:::|||:::|||             |||      |||      |||||||:::|||
Db          82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy          22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
               |||      |||                |||      :::|||:::          ||||||
Db         142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy          42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
               :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db         202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy          62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
               ||||||||||||||||||:::||||||||||||   |||:::              :::
Db         262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy          82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
               |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db         310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy         102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db         370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                        |||:::::::::::|||||:::      |||      :::|||
Db         427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy         142 IleTrp 143
               ::::::
Db         487 TTGTTT 492

RESULT 4
US-07-988-430-13
; Sequence 13, Application US/07988430
; Patent No. 5416202
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,430
;      FILING DATE:  19921209
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5416202and, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-988-430-13

Alignment Scores:
Pred. No.:              3.21e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-07-988-430-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||             |||       |||       ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||                 |||       :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                 :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
              |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::::::||||||:::     |||       :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 5
US-08-425-336-13
; Sequence 13, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-425-336-13

Alignment Scores:
Pred. No.:              3.21e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-08-425-336-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||             |||       |||       ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||                 |||       :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                 :::
```

```
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101

Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121

Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141

Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143

Db        487 TTGTTT 492

RESULT 6
US-08-488-113B-13
; Sequence 13, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-488-113B-13

Alignment Scores:
Pred. No.:                3.21e-20        Length:          913
Score:                    220.50          Matches:         52
Percent Similarity:       59.9%           Conservative:    33
Best Local Similarity:    36.6%           Mismatches:      50
Query Match:              28.7%           Indels:          7
DB:                       2               Gaps:            3

US-10-758-902-9 (1-149) x US-08-488-113B-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21

Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41

Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61

Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81

Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101

Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121

Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141

Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143

Db        487 TTGTTT 492

RESULT 7
US-08-477-484B-13
; Sequence 13, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-477-484B-13

Alignment Scores:
Pred. No.:              3.21e-20      Length:         913
Score:                  220.50        Matches:        52
Percent Similarity:     59.9%         Conservative:   33
Best Local Similarity:  36.6%         Mismatches:     50
Query Match:            28.7%         Indels:         7
DB:                     2             Gaps:           3

US-10-758-902-9 (1-149) x US-08-477-484B-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||           |||       |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||           |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC------------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492
```

```
RESULT 8
US-08-646-360-13
; Sequence 13, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-646-360-13

Alignment Scores:
Pred. No.:              3.21e-20      Length:         913
Score:                  220.50        Matches:        52
Percent Similarity:     59.9%         Conservative:   33
Best Local Similarity:  36.6%         Mismatches:     50
Query Match:            28.7%         Indels:         7
DB:                     2             Gaps:           3

US-10-758-902-9 (1-149) x US-08-646-360-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||           |||       |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141
```

```
Qy          22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
               |||      |||                |||      :::|||:::         ||||||
Db         142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy          42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
               :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db         202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy          62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
               ||||||||||||||||||::||||||||||||   |||:::                :::
Db         262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy          82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
               |||  :::  |||      :::  |||      |||  :::  ||||||  |||
Db         310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy         102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  |||  ::::::||||||   :::  |||:::|||:::  |||      ||||||
Db         370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                     |||::::::::::::||||||:::      |||      :::|||
Db         427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy         142 IleTrp 143
               ::::::
Db         487 TTGTTT 492

RESULT 9
US-08-839-765-13
; Sequence 13, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-839-765-13

Alignment Scores:
Pred. No.:                3.21e-20        Length:          913
Score:                    220.50          Matches:         52
Percent Similarity:       59.9%           Conservative:    33
Best Local Similarity:    36.6%           Mismatches:      50
Query Match:              28.7%           Indels:          7
DB:                       3               Gaps:            3

US-10-758-902-9 (1-149) x US-08-839-765-13 (1-913)

Qy           4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
               |||:::|||:::|||          |||      |||      ||||||:::|||
Db          82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy          22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
               |||      |||                |||      :::|||:::         ||||||
Db         142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy          42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
               :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db         202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy          62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
               ||||||||||||||||||::||||||||||||   |||:::                :::
Db         262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy          82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
               |||  :::  |||      :::  |||      |||  :::  ||||||  |||
Db         310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy         102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  |||  ::::::||||||   :::  |||:::|||:::  |||      ||||||
Db         370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                     |||::::::::::::||||||:::      |||      :::|||
Db         427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy         142 IleTrp 143
               ::::::
Db         487 TTGTTT 492

RESULT 10
US-09-136-389-13
; Sequence 13, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
```

```
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-136-389-13

Alignment Scores:
Pred. No.:              3.21e-20      Length:          913
Score:                  220.50        Matches:         52
Percent Similarity:     59.9%         Conservative:    33
Best Local Similarity:  36.6%         Mismatches:      50
Query Match:            28.7%         Indels:          7
DB:                     3             Gaps:            3

US-10-758-902-9 (1-149) x US-09-136-389-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||           |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||:::||||||||||||   |||:::               :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||

Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
                 ::::::
Db        487 TTGTTT 492

RESULT 11
US-09-610-838-13
; Sequence 13, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/610,838
;      FILING DATE:  06-JUL-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:  18-AUG-1998
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-610-838-13

Alignment Scores:
Pred. No.:              3.21e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     3               Gaps:           3

US-10-758-902-9 (1-149) x US-09-610-838-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||           |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||           |||      :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::              :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 12
US-09-711-485-13
; Sequence 13, Application US/09711485
; Patent No. 6649742
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/711,485
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/839,765
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-711-485-13

Alignment Scores:
Pred. No.:              3.21e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     3               Gaps:           3

US-10-758-902-9 (1-149) x US-09-711-485-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||           |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||           |||      :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::              :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492
```

```
RESULT 13
PCT-US92-09487-13
; Sequence 13, Application PC/TUS9209487
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/09487
;      FILING DATE:  19921104
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US92-09487-13

Alignment Scores:
Pred. No.:          3.21e-20        Length:         913
Score:              220.50          Matches:        52
Percent Similarity: 59.9%           Conservative:   33
Best Local Similarity: 36.6%        Mismatches:     50
Query Match:        28.7%           Indels:         7
DB:                 6               Gaps:           3

US-10-758-902-9 (1-149) x PCT-US92-09487-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||      |||     |||     ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||     |||          |||     :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::               :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 14
US-07-854-845B-9
; Sequence 9, Application US/07854845B
; Patent No. 5340732
;  GENERAL INFORMATION:
;    APPLICANT:  HABUKA, No. 5340732iyuki
;    APPLICANT:  MIYANO, Masashi
;    APPLICANT:  MATSUMOTO, Takashi
;    APPLICANT:  NOMA, Masana
;    TITLE OF INVENTION:  ANTIVIRAL PROTEIN
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH, & BIRCH
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22042
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/854,845B
;      FILING DATE:  20-MAR-1992
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy Jr., Gerald M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  42-194P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-205-8000
;      TELEFAX:  703-205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  762 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Mirabilis jalapa
US-07-854-845B-9

Alignment Scores:
Pred. No.:          4.12e-19        Length:         762
```

```
Score:                 211.50        Matches:       53
Percent Similarity:    55.2%         Conservative:  27
Best Local Similarity: 36.6%         Mismatches:    56
Query Match:           27.5%         Indels:        9
DB:                    2             Gaps:          4

US-10-758-902-9 (1-149) x US-07-854-845B-9 (1-762)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||                |||   :::||||||   ::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 84

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||     |||                  |||:::|||   |||:::
Db         85 GTCGCAGACAAAACCGAA-----------CAGTCGACCATCCAGAAAATCTCTAAAACC 132

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                  :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||||:::   |||:::||||||:::||||||   |||     :::    |||
Db        193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              ||||||   |||       |||                :::      |||||||||
Db        253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||       |||
Db        313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                 :::   |||||||||      ||||||:::::::::||||||   ||||||
Db        373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429

Qy        141 AlaIleTrpGlyLys 145
                 |||:::|||||
Db        430 AACATTTATGGCAAA 444

RESULT 15
US-08-324-301-14
; Sequence 14, Application US/08324301
; Patent No. 5597569
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    APPLICANT:  Gawlak, Susan L.
;    APPLICANT:  Marquardt, Hans
;    TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;    TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONICA DIOICA
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,301
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/141,891
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0109A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-728-4800
;      TELEFAX:  206-727-3601
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  962 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
;      TISSUE TYPE:  leaf
US-08-324-301-14

Alignment Scores:
Pred. No.:             3.99e-16      Length:        962
Score:                 190.50        Matches:       50
Percent Similarity:    57.8%         Conservative:  24
Best Local Similarity: 39.1%         Mismatches:    47
Query Match:           24.8%         Indels:        7
DB:                    2             Gaps:          4

US-10-758-902-9 (1-149) x US-08-324-301-14 (1-962)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro---ValCys 32
              |||   |||||||||:::::|||||   :::|||      ||||||||   |||
Db        133 TACAAAACTTTTATAAGGAATCTGCGCACCAAACTCACGGTTGGAACTCCAAGGGTGTAC 192

Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
                 :::|||||               |||          ||||||   ||||||   :::
Db        193 GATATACCTGTCCTGAGAAACGCAGCAGCCGGGCTCGCGCGCTTTCAATTAGTTACCCTC 252

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
              |||       :::   ::::::|||   |||||||:::||||||   :::||||||||||||
Db        253 ACAAATTACAATGGCGAATCTGTCACTGTGGCTTTAGATGTAGTGAACGTGTACGTTGTT 312

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
              |||:::                 :::   |||   ||||||                |||
Db        313 GCATATCGA------------GCTGGAAACACTGCTTACTTTCTCGCAGATGCATCAACA 360

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||   |||:::   |||   |||   |||   :::   |||
Db        361 GAAGCCAACAATGTGTTGTTTGCAGGCATC---AATCATGTAAGACTTCCTTATGGAGGG 417

Qy        113 SerTyrGlnLysLeuValAsnAlaAla---LysValAspArgLysAspLeuGluLeuGly 131
              :::|||     |||       ||||||   ::::::   |||:::::::::||||||||
Db        418 AATTACGATGGCCTTGAGACAGCTGCAGGCAGAATTTCGAGGGAAAATATTGAACTTGGA 477

Qy        132 ValTyrLysLeuGluPheSerIle 139
                    ::::::      :::|||
Db        478 TTTTCCGAAATAAGTAGTGCCATT 501

RESULT 16
US-07-923-692C-3
; Sequence 3, Application US/07923692C
; Patent No. 5316931
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William 0.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Limbach & Limbach
;      STREET:  2001 Ferry Building
```

```
;      CITY:  San Francisco
;      STATE:  CAL
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent in Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,692C
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  BIOG-20121
;      REFERENCE/DOCKET NUMBER:  USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-433-4150
;      TELEFAX:  415-433-8716
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  886 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chinese cucumber
;    IMMEDIATE SOURCE:
;      CLONE:  alpha-trichosanthin
;    FEATURE:
;      NAME/KEY:  CDS (B) LOCATION: 8. .877
;      LOCATION:  8. .877
US-07-923-692C-3

Alignment Scores:
Pred. No.:              3.15e-15      Length:         886
Score:                  183.50        Matches:        44
Percent Similarity:     53.5%         Conservative:   32
Best Local Similarity:  31.0%         Mismatches:     61
Query Match:            23.9%         Indels:         5
DB:                     2             Gaps:           2

US-10-758-902-9 (1-149) x US-07-923-692C-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
                 |||||||||   |||      |||             |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
                 |||      |||                 :::      :::|||:::          ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
                 ||||||||||||||||:::||||||:::::||||||:::              |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                      |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::||||||||||   :::   |||:::|||:::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                 ::::::
Db        491 TTGTTT 496

RESULT 17
US-08-184-237-3
; Sequence 3, Application US/08184237
; Patent No. 5589367
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Limbach & Limbach
;      STREET:  2001 Ferry Building
;      CITY:  San Francisco
;      STATE:  CAL
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent in Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,237
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 923,692
;      FILING DATE:  31-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  BIOG-20121  USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-433-4150
;      TELEFAX:  415-433-8716
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  886 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chinese cucumber
;    IMMEDIATE SOURCE:
;      CLONE:  alpha-trichosanthin
;    FEATURE:
;      NAME/KEY:  CDS (B) LOCATION: 8. .877
;      LOCATION:  8. .877
US-08-184-237-3

Alignment Scores:
Pred. No.:              3.15e-15      Length:          886
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     2             Gaps:            2

US-10-758-902-9 (1-149) x US-08-184-237-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||     |||          |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||              :::      :::|||:::          ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::  :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||:::||||||:::::||||||:::            |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
                        |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||:::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                        |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                 ::::::
Db        491 TTGTTT 496

RESULT 18
US-08-482-920-3
; Sequence 3, Application US/08482920
; Patent No. 5866785
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent in Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,920
;      FILING DATE:  07-JUNE-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 184,237
;      FILING DATE:  19-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  8129-112
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  886 base pairs
```

```
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Chinese cucumber
;     IMMEDIATE SOURCE:
;       CLONE:  alpha-trichosanthin
;     FEATURE:
;       NAME/KEY:  CDS (B) LOCATION: 8. .877
;       LOCATION:  8. .877
US-08-482-920-3

Alignment Scores:
Pred. No.:              3.15e-15        Length:         886
Score:                  183.50          Matches:        44
Percent Similarity:     53.5%           Conservative:   32
Best Local Similarity:  31.0%           Mismatches:     61
Query Match:            23.9%           Indels:         5
DB:                     2               Gaps:           2

US-10-758-902-9 (1-149) x US-08-482-920-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||       |||             |||       ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||              :::       :::|||:::          ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                     :::|||:::   |||:::   :::|||       :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::           |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                        |||   :::          |||   |||          :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                     :::|||||||||   :::   |||:::|||:::::|||       ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                     |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496

RESULT 19
US-08-484-341-3
; Sequence 3, Application US/08484341
;   GENERAL INFORMATION:
;       APPLICANT: Donson, Jon
;                  Dawson, William O.
;                  Grantham, George L.
;                  Turpen, Thomas H.
;                  Turpen, Ann Myers
;                  Garger, Stephen J.
;                  Grill, Laurence K.
;       TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;       NUMBER OF SEQUENCES: 11
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Limbach & Limbach
;            STREET: 2001 Ferry Building
;            CITY: San Francisco
;            STATE: CAL
;            ZIP: 94111
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: Patent in Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/484,341
;            FILING DATE: 07-Jun-1995
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/184,237
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: US 600,244
;            FILING DATE: 22-OCT-1990
;            APPLICATION NUMBER: US 641,617
;            FILING DATE: 16-JAN-1991
;            APPLICATION NUMBER: US 310,881
;            FILING DATE: 17-FEB-1989
;            APPLICATION NUMBER: US 160,766
;            FILING DATE: 26-FEB-1988
;            APPLICATION NUMBER: US 160,771
;            FILING DATE: 26-FEB-1988
;            APPLICATION NUMBER: US 347,637
;            FILING DATE: 05-MAY-1989
;            APPLICATION NUMBER: US 363,138
;            FILING DATE: 08-JUN-1989
;            APPLICATION NUMBER: US 219,279
;            FILING DATE: 15-JUL-1988
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Halluin, Albert P.
;            REGISTRATION NUMBER: 28,957
;            REFERENCE/DOCKET NUMBER: BIOG-20121  USA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-433-4150
;            TELEFAX: 415-433-8716
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 886 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;            ORGANISM: Chinese cucumber
;       IMMEDIATE SOURCE:
;            CLONE: alpha-trichosanthin
;       FEATURE:
;            NAME/KEY:  CDS (B) LOCATION: 8. .877
;            LOCATION:  8. .877
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-484-341-3

Alignment Scores:
Pred. No.:              3.15e-15        Length:         886
Score:                  183.50          Matches:        44
Percent Similarity:     53.5%           Conservative:   32
Best Local Similarity:  31.0%           Mismatches:     61
Query Match:            23.9%           Indels:         5
DB:                     3               Gaps:           2

US-10-758-902-9 (1-149) x US-08-484-341-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||       |||             |||       ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||              :::       :::|||:::          ::::::
```

```
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61

Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81

Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101

Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121

Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141

Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143

Db        491 TTGTTT 496
```

```
RESULT 20
US-08-483-502-3
; Sequence 3, Application US/08483502
; Patent No. 6284492
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Venable, Baetjer, Howard & Civiletti
;      STREET:  1201 New York Avenue N.W., Suite 1000
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,502
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/739,143
;      FILING DATE:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ihnen, Jeffrey L.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  18604-090574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-962-4810
;      TELEFAX:  202-962-8300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  886 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chinese cucumber
;    IMMEDIATE SOURCE:
;      CLONE:  alpha-trichosanthin
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  8..877
US-08-483-502-3

Alignment Scores:
Pred. No.:              3.15e-15        Length:         886
Score:                  183.50          Matches:        44
Percent Similarity:     53.5%           Conservative:   32
Best Local Similarity:  31.0%           Mismatches:     61
Query Match:            23.9%           Indels:         5
DB:                     3               Gaps:           2

US-10-758-902-9 (1-149) x US-08-483-502-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21

Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41

Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61

Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81

Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101

Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121

Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141

Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
```

```
                ::::::
Db        491 TTGTTT 496

RESULT 21
US-09-726-651A-3
; Sequence 3, Application US/09726651A
; Patent No. 6448046
; GENERAL INFORMATION:
;  APPLICANT: Donson, Jon
;  APPLICANT:  DAWSON, William O.
;  APPLICANT:  GRANTHAM, GEORGE L.
;  APPLICANT:  TURPEN, Thomas H.
;  APPLICANT:  TURPEN, Ann M.
;  APPLICANT:  GARGER, Stephen J.
;  APPLICANT:  GRILL, Laurence K.
;  TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
;  FILE REFERENCE: 008010023CNUS01
;  CURRENT APPLICATION NUMBER: US/09/726,651A
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: 08/483,502
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/184,237
;  PRIOR FILING DATE: 1994-01-19
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 886
;   TYPE: DNA
;   ORGANISM: Chinese Cucumber
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (8)...(877)
;   OTHER INFORMATION: Clone:alpha-trichosanthin
US-09-726-651A-3

Alignment Scores:
Pred. No.:              3.15e-15      Length:          886
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     3             Gaps:            2

US-10-758-902-9 (1-149) x US-09-726-651A-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||            |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||            :::     :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::::||||||:::          |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::       |||   |||       :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                ::::::
Db        491 TTGTTT 496

RESULT 22
US-08-902-486-6
; Sequence 6, Application US/08902486
; Patent No. 6140075
;  GENERAL INFORMATION:
;    APPLICANT:  Russel, David R.
;    APPLICANT:  Fuller, James T.
;    TITLE OF INVENTION:  METHOD FOR PRODUCING ANTIBODIES AND
;    TITLE OF INVENTION:  PROTEIN TOXINS IN PLANT CELLS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/902,486
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  670513.90261
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  758 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..748
US-08-902-486-6

Alignment Scores:
Pred. No.:              8.82e-15      Length:          758
Score:                  179.50        Matches:         44
Percent Similarity:     54.5%         Conservative:    34
Best Local Similarity:  30.8%         Mismatches:      58
Query Match:            23.4%         Indels:          7
DB:                     3             Gaps:            3

US-10-758-902-9 (1-149) x US-08-902-486-6 (1-758)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||            |||      ||||||::::|||
Db          9 GTGAGCTTTCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 68

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||            |||      :::|||:::         :::|||
```

```
Db         69 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 128

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::          |||:::   |||:::   :::|||       :::   :::|||:::
Db        129 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 188

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||::::::||||||
Db        189 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 236

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||   :::   |||   ::::::                  :::|||   :::|||
Db        237 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 296

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                       :::|||||||||   :::   |||:::|||::::::|||       |||
Db        297 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 356

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||          |||:::::::::   ||||||:::      |||:::   :::|||
Db        357 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 416

Qy        141 AlaIleTrp 143
                 ::::::
Db        417 ACTTTGTAT 425
```

RESULT 23
US-09-601-667C-16
; Sequence 16, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667C
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 16
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin A1
US-09-601-667C-16

Alignment Scores:

Pred. No.:	8.89e-15	Length:	762
Score:	179.50	Matches:	50
Percent Similarity:	57.1%	Conservative:	26
Best Local Similarity:	37.6%	Mismatches:	48
Query Match:	23.4%	Indels:	9
DB:	3	Gaps:	4

US-10-758-902-9 (1-149) x US-09-601-667C-16 (1-762)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||       ||||||       |||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::       |||:::         :::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||          :::   :::|||       ||||||||||||||:::
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGGTTACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                        |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||       |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||       |||           |||           |||       :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||       |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426
```

RESULT 24
US-09-601-667C-19
; Sequence 19, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667C
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 19
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin A1
US-09-601-667C-19

Alignment Scores:

Pred. No.:	8.89e-15	Length:	762
Score:	179.50	Matches:	50
Percent Similarity:	57.1%	Conservative:	26
Best Local Similarity:	37.6%	Mismatches:	48
Query Match:	23.4%	Indels:	9
DB:	3	Gaps:	4

US-10-758-902-9 (1-149) x US-09-601-667C-19 (1-762)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||       ||||||       |||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::       |||:::         :::::::|||   :::|||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||          :::   :::|||       ||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTGTTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                        |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||       |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330
```

```
Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||         |||      :::
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 25
US-09-601-667C-17
; Sequence 17, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 2$841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 17
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-09-601-667C-17

Alignment Scores:
Pred. No.:              8.98e-15      Length:          768
Score:                  179.50        Matches:         49
Percent Similarity:     56.7%         Conservative:    27
Best Local Similarity:  36.6%         Mismatches:      49
Query Match:            23.4%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-601-667C-17 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   ::::::      |||||||||||||||:::
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGATCACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThr---AsnArgValThrLeu 108
              |||      |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGCACCACCCGAGATAGATCCTCTCTC 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||      |||          |||         |||      :::
Db        334 CCATTCACTGGAAGCTACACCGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATC 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCTCTCGGTATAGAGCAACTCATTCAATCCGTCTCTGCGCTT 432

RESULT 26
US-09-601-667C-20
; Sequence 20, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 20
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-09-601-667C-20

Alignment Scores:
Pred. No.:              8.98e-15      Length:          768
Score:                  179.50        Matches:         49
Percent Similarity:     56.7%         Conservative:    27
Best Local Similarity:  36.6%         Mismatches:      49
Query Match:            23.4%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-601-667C-20 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   ::::::      |||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTATTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThr---AsnArgValThrLeu 108
              |||      |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGTACAACACGGGATAGAAGTTCTTTG 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||      |||          |||         |||      :::
Db        334 CCTTTTACTGGTTCTTATACAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATT 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCATTGGGAATTGAGCAGTTGATCCAGAGTGTTTCTGCTTTG 432

RESULT 27
US-08-245-754A-1
; Sequence 1, Application US/08245754A
; Patent No. 5541110
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    TITLE OF INVENTION:  Cloning and Expression of a Gene
;    TITLE OF INVENTION:  Encoding Bryodin 1 From Bryonia dioica
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Bristol-Myers Squibb Company
;       STREET:  3005 First Aveune
;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  USA
;       ZIP:  98121
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/245,754A
;       FILING DATE:  06-MAY-1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poor, Brian W.
;       REGISTRATION NUMBER:  32,928
;       REFERENCE/DOCKET NUMBER:  ON0124
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 728-4800
;       TELEFAX:  (206) 727-3601
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1094 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Bryonia dioica
US-08-245-754A-1

Alignment Scores:
Pred. No.:              1.47e-14        Length:         1094
Score:                  179.50          Matches:        44
Percent Similarity:     54.5%           Conservative:   34
Best Local Similarity:  30.8%           Mismatches:     58
Query Match:            23.4%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-08-245-754A-1 (1-1094)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||::::::|||
Db        116 GTTAGCTTCCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 175

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                |||      :::|||:::         :::|||
Db        176 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 235

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::      |||:::   |||:::  :::|||      :::   :::|||:::
Db        236 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 295

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::|||||:::::::||||||
Db        296 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 343

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||  :::  |||  ::::::                  :::|||   :::|||
Db        344 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 403

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                  :::||||||||||   :::   |||:::|||:::::|||      |||
Db        404 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 463

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||         |||:::::::::   ||||||:::      |||:::   :::|||
Db        464 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 523

Qy        141 AlaIleTrp 143
```

```
              ::::::
Db        524 ACTTTGTAT 532

RESULT 28
US-08-597-731-1
; Sequence 1, Application US/08597731
; Patent No. 5932447
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    TITLE OF INVENTION:  Cloning and Expression of a Gene
;    TITLE OF INVENTION:  Encoding Bryodin 1 From Bryonia dioica
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Aveune
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/597,731
;      FILING DATE:  07-FEB-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/245,754
;      FILING DATE:  06-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0124
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 728-4800
;      TELEFAX:  (206) 727-3601
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1094 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
US-08-597-731-1

Alignment Scores:
Pred. No.:              1.47e-14        Length:         1094
Score:                  179.50          Matches:        44
Percent Similarity:     54.5%           Conservative:   34
Best Local Similarity:  30.8%           Mismatches:     58
Query Match:            23.4%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-08-597-731-1 (1-1094)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||::::::|||
Db        116 GTTAGCTTCCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 175

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                |||      :::|||:::         :::|||
Db        176 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 235

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::      |||:::   |||:::  :::|||      :::   :::|||:::
Db        236 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 295

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
```

```
                ||||||:::|||||||||:::||||||::::::||||||
Db        296 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 343

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
               |||   :::   |||   ::::::                 :::|||   :::|||
Db        344 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 403

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                      :::||||||||||   :::   |||:::|||::::::|||       |||
Db        404 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 463

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
               |||          |||:::::::::   ||||||:::      |||:::   :::|||
Db        464 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 523

Qy        141 AlaIleTrp 143
                 ::::::
Db        524 ACTTTGTAT 532

RESULT 29
US-08-902-486-14
; Sequence 14, Application US/08902486
; Patent No. 6140075
;  GENERAL INFORMATION:
;    APPLICANT:  Russel, David R.
;    APPLICANT:  Fuller, James T.
;    TITLE OF INVENTION:  METHOD FOR PRODUCING ANTIBODIES AND
;    TITLE OF INVENTION:  PROTEIN TOXINS IN PLANT CELLS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/902,486
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  670513.90261
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1499 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..1493
US-08-902-486-14

Alignment Scores:
Pred. No.:                2.29e-14        Length:         1499
Score:                    179.50          Matches:        44
Percent Similarity:       54.5%           Conservative:   34
Best Local Similarity:    30.8%           Mismatches:     58
Query Match:              23.4%           Indels:         7
DB:                       3               Gaps:           3

US-10-758-902-9 (1-149) x US-08-902-486-14 (1-1499)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||       |||             |||       ||||||::::::|||
Db          9 GTGAGCTTTCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 68

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||             |||       :::|||:::         :::|||
Db         69 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 128

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::         |||:::   |||:::   :::|||       :::   :::|||:::
Db        129 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 188

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||::::::||||||
Db        189 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 236

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||   :::   |||   ::::::                 :::|||   :::|||
Db        237 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 296

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                      :::||||||||||   :::   |||:::|||::::::|||       |||
Db        297 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 356

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||          |||:::::::::   ||||||:::      |||:::   :::|||
Db        357 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 416

Qy        141 AlaIleTrp 143
                 ::::::
Db        417 ACTTTGTAT 425

RESULT 30
US-08-776-059-30
; Sequence 30, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
;  APPLICANT: LENTZEN, Hans
;  APPLICANT: ECK, Jurgen
;  APPLICANT: BAUR, Axel
;  APPLICANT: ZINKE, Holger
;  TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
;  FILE REFERENCE: 674503-2003
;  CURRENT APPLICATION NUMBER: US/08/776,059B
;  CURRENT FILING DATE: 1999-06-19
;  EARLIER APPLICATION NUMBER: PCT/EP96/02273
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 95109949.8
;  EARLIER FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Viscum album
US-08-776-059-30

Alignment Scores:
Pred. No.:                2.31e-14        Length:         774
Score:                    176.50          Matches:        49
Percent Similarity:       57.1%           Conservative:   27
Best Local Similarity:    36.8%           Mismatches:     48
Query Match:              23.0%           Indels:         9
DB:                       3               Gaps:           4

US-10-758-902-9 (1-149) x US-08-776-059-30 (1-774)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
```

```
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
Db        232 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThr 109
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 31
US-09-601-667C-15
; Sequence 15, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 15
;   LENGTH: 1596
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MLA-I
US-09-601-667C-15

Alignment Scores:
Pred. No.:              6.37e-14      Length:          1596
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-601-667C-15 (1-1596)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
Db        226 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThr 109
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 32
US-09-601-667C-18
; Sequence 18, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 18
;   LENGTH: 1596
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MLI (matched)
US-09-601-667C-18

Alignment Scores:
Pred. No.:              6.37e-14      Length:          1596
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-601-667C-18 (1-1596)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
Db        166 GTTGAATTGACTAACCAAGGAGGTGATAGTATTACTGCTGCTATTGATGTGACTAACCTT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
Db        226 TATGTTGTTGCATATCAG------------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThr 109
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387
```

```
Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 33
US-08-776-059-34
; Sequence 34, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
;  APPLICANT: LENTZEN, Hans
;  APPLICANT: ECK, Jurgen
;  APPLICANT: BAUR, Axel
;  APPLICANT: ZINKE, Holger
;  TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
;  FILE REFERENCE: 674503-2003
;  CURRENT APPLICATION NUMBER: US/08/776,059B
;  CURRENT FILING DATE: 1999-06-19
;  EARLIER APPLICATION NUMBER: PCT/EP96/02273
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 95109949.8
;  EARLIER FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
;   LENGTH: 1923
;   TYPE: DNA
;   ORGANISM: Viscum album
US-08-776-059-34

Alignment Scores:
Pred. No.:              8.27e-14      Length:         1923
Score:                  176.50        Matches:        49
Percent Similarity:     57.1%         Conservative:   27
Best Local Similarity:  36.8%         Mismatches:     48
Query Match:            23.0%         Indels:         9
DB:                     3             Gaps:           4

US-10-758-902-9 (1-149) x US-08-776-059-34 (1-1923)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db        199 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 258

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||||
Db        259 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 318

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||             ::::::      |||||||||||||||::::::
Db        319 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 378

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||              |||::::::   ||||||
Db        379 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 426

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||:     |||   :::   ||||||   |||   |||   |||   :::|||
Db        427 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 483

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||             |||             |||      :::
Db        484 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 540

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        541 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 579

RESULT 34
US-09-627-165E-15
; Sequence 15, Application US/09627165E
; Patent No. 6846913
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jong-Bae
;  TITLE OF INVENTION: CRUDE EXTRACT FROM Viscum album coloratum, AND PROTEINS
;  TITLE OF INVENTION:  AND LECTINS ISOLATED THEREFROM
;  FILE REFERENCE: Korean Mistletoe Lectin
;  CURRENT APPLICATION NUMBER: US/09/627,165E
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 15
;   LENGTH: 837
;   TYPE: DNA
;   ORGANISM: Viscum album coloratum
US-09-627-165E-15

Alignment Scores:
Pred. No.:              4.82e-14      Length:         837
Score:                  174.50        Matches:        49
Percent Similarity:     55.6%         Conservative:   25
Best Local Similarity:  36.8%         Mismatches:     50
Query Match:            22.7%         Indels:         9
DB:                     3             Gaps:           4

US-10-758-902-9 (1-149) x US-09-627-165E-15 (1-837)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         19 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 78

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||||
Db         79 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCGGATGCGCAAAGATTTGTGTTG 138

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||             ::::::      |||||||||||||||::::::
Db        139 GTGGAACTCACCAATCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 198

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||              |||::::::   ||||||
Db        199 TACGTGGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 246

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||      |||      ||||||   |||   |||   |||   :::|||
Db        247 GCACCAGACGGCGCGGAAAGGCATCTCTTCACCGGC---ACCACCAGATCCTCTCTCCCA 303

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||   |||||||||      |||      |||      |||      :::
Db        304 TTCACCGGAAGCTACACAGATCTGGAGCGATACGCCGGT---CATAGGGACCAGATCCCT 360

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        361 CTGGGTATAGAGGAACTCATTCAATCCGTCTCGGCGCTT 399

RESULT 35
US-09-627-165E-3
; Sequence 3, Application US/09627165E
; Patent No. 6846913
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jong-Bae
;  TITLE OF INVENTION: CRUDE EXTRACT FROM Viscum album coloratum, AND PROTEINS
;  TITLE OF INVENTION:  AND LECTINS ISOLATED THEREFROM
;  FILE REFERENCE: Korean Mistletoe Lectin
;  CURRENT APPLICATION NUMBER: US/09/627,165E
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 3
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Viscum album coloratum
;   FEATURE:
US-09-627-165E-3

Alignment Scores:
Pred. No.:              1.08e-13      Length:         762
Score:                  171.50        Matches:        47
```

```
Percent Similarity:     57.1%          Conservative:  29
Best Local Similarity:  35.3%          Mismatches:    48
Query Match:            22.3%          Indels:        9
DB:                     3              Gaps:          4

US-10-758-902-9 (1-149) x US-09-627-165E-3 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              :::|||      ||||||      ||||||:::   ::::::   |||:::
Db         46 CAATATTTCAAGTTCATCACGCTTCTCCGAGATCATGTCTCAAGCGGAAGCTTGTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              |||:::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 CAAATACCACTCTTGCGGCAGTCTACTGTCCCCGTCTCGGATACGCAGAGATTTGTGTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||:::::::::                ::::::      ||||||||||||||::::::
Db        166 GTGGAACTCAGCAATCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                ::::::::::   ||||||
Db        226 TACGTGGTGGCTTACCAA-----------GCAGGCAACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||       |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCTCGCGGCGCGGAAACGTATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCTCGGCCCTT 426

RESULT 36
US-08-776-059-38
; Sequence 38, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
;  APPLICANT: LENTZEN, Hans
;  APPLICANT: ECK, Jurgen
;  APPLICANT: BAUR, Axel
;  APPLICANT: ZINKE, Holger
;  TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
;  FILE REFERENCE: 674503-2003
;  CURRENT APPLICATION NUMBER: US/08/776,059B
;  CURRENT FILING DATE: 1999-06-19
;  EARLIER APPLICATION NUMBER: PCT/EP96/02273
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 95109949.8
;  EARLIER FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
;   LENGTH: 705
;   TYPE: DNA
;   ORGANISM: Viscum album
US-08-776-059-38

Alignment Scores:
Pred. No.:              1.8e-13        Length:        705
Score:                  169.50         Matches:       47
Percent Similarity:     57.4%          Conservative:  27
Best Local Similarity:  36.4%          Mismatches:    46
Query Match:            22.1%          Indels:        9
DB:                     3              Gaps:          4

US-10-758-902-9 (1-149) x US-08-776-059-38 (1-705)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||      ||||||:::   ::::::   |||:::         ::::::|||:::
Db          7 TTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAATGAGATACCACTC 66

Qy         37 ThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeuValAspIleThr 53
              |||:::         ::::::|||   :::||||||||||||||::::::|||
Db         67 TTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTGGTGGAGCTCACC 126

Qy         54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73
                        ::::::      ||||||||||||||::::::|||||||||
Db        127 AACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTGTACGTCGTGGCT 186

Qy         74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93
              ||||||                  |||::::::   ||||||          |||
Db        187 TACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGACGCACCACGCGGC 234

Qy         94 AlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
              |||   :::   ||||||   |||   |||   |||   :::|||   |||:::||||||
Db        235 GCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCATTCAACGGAAGC 291

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
              |||       |||          |||          |||      :::   ||||||:::
Db        292 TACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCTCTCGGTATAGAC 348

Qy        134 LysLeuGluPheSerIleGluAlaIle 142
              :::|||      |||:::   |||:::
Db        349 CAACTCATTCAATCCGTCACGGCGCTT 375

RESULT 37
US-08-356-786-7
; Sequence 7, Application US/08356786
; Patent No. 5877305
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Protein for Cancer
;    TITLE OF INVENTION:  Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,786
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/831,967
;      FILING DATE:  06-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  807 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..807
```

```
;      OTHER INFORMATION:  /note= "product = "Ricin-A chain"
US-08-356-786-7

Alignment Scores:
Pred. No.:              2.54e-13        Length:         807
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     2               Gaps:           6

US-10-758-902-9 (1-149) x US-08-356-786-7 (1-807)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db         19 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 78

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||    |||     |||     |||      ::::::||||||
Db         79 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 138

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        139 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 198

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        199 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 258

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                     :::   |||   |||           ::::::
Db        259 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 306

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||     |||   ||||||   |||      |||   |||
Db        307 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 366

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        367 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAAATATCGAGTTGGGAAAT 426

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::          |||   ||||||
Db        427 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 483

RESULT 38
US-08-218-303-15
; Sequence 15, Application US/08218303
; Patent No. 5547867
;  GENERAL INFORMATION:
;    APPLICANT:  Kara, Bhuphendra V.
;    APPLICANT:  Hockney, Robert C.
;    APPLICANT:  Fitton, John E.
;    TITLE OF INVENTION:  FERMENTATION PROCESS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1615 L Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20036-5601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/218,303
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/841,533
;      FILING DATE:  26-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  PNK/3893/94908/MJW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1140 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  143..943
US-08-218-303-15

Alignment Scores:
Pred. No.:              4.12e-13        Length:         1140
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     2               Gaps:           6

US-10-758-902-9 (1-149) x US-08-218-303-15 (1-1140)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        158 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 217

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||    |||     |||     |||      ::::::||||||
Db        218 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 277

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        278 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 337

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        338 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 397

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                     :::   |||   |||           ::::::
Db        398 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 445

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||     |||   ||||||   |||      |||   |||
Db        446 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 505

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        506 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAAATATCGAGTTGGGAAAT 565

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::          |||   ||||||
Db        566 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 622

RESULT 39
US-08-338-793D-60
; Sequence 60, Application US/08338793D
; Patent No. 5840521
;  GENERAL INFORMATION:
;    APPLICANT:  Barth, Peter Thomas
;    TITLE OF INVENTION:  VECTOR
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN DARBY CUSHMAN
```

```
;       ADDRESSEE:  INTELLECTUAL PROPERTY GROUP OF
;       ADDRESSEE:  PILLSBURY MADISON & SUTRO, L.L.P.
;       STREET:  1100 New York Avenue, N.W.
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005-3918
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
;       COMPUTER:  IBM PC/XT/AT Compatibles
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  Microsoft Word or ASCII editors
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/338,793D
;       FILING DATE:  08-No. 5840521-94
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/842,081
;       FILING DATE:  26-Feb-92
;       CLASSIFICATION:  435
;       APPLICATION NUMBER:  9104017.0
;       FILING DATE:  26-Feb-91
;       APPLICATION NUMBER:  9109188.4
;       FILING DATE:  29-Apr-91
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kokulis, Paul N.
;       REGISTRATION NUMBER:  16,773
;       REFERENCE/DOCKET NUMBER:  DJB/9901/215431/TGW
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-861-3000
;       TELEFAX:  202-822-0944
;       TELEX:  6714627 CUSH
;   INFORMATION FOR SEQ ID NO:  60:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1140
;       TYPE:  Nucleic acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
US-08-338-793D-60

Alignment Scores:
Pred. No.:              4.12e-13        Length:         1140
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     2               Gaps:           6

US-10-758-902-9 (1-149) x US-08-338-793D-60 (1-1140)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||            |||          |||      ||||||
Db        158 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 217

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||     ::::::||||||
Db        218 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 277

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::              ::::::|||||:::||||||:::::::::
Db        278 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 337

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        338 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 397

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||                    ::::::
Db        398 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 445

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        446 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 505

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        506 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 565

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        566 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 622

RESULT 40
US-08-356-786-9
; Sequence 9, Application US/08356786
; Patent No. 5877305
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Protein for Cancer
;    TITLE OF INVENTION:  Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,786
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/831,967
;      FILING DATE:  06-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1605 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1605
;      OTHER INFORMATION:  /note= "product = "G-FIT""
US-08-356-786-9

Alignment Scores:
Pred. No.:              6.66e-13        Length:         1605
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     2               Gaps:           6

US-10-758-902-9 (1-149) x US-08-356-786-9 (1-1605)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||            |||          |||      ||||||
Db         25 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 84
```

```
Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db         85 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 144

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::             ::::::||||||:::||||||:::::::::
Db        145 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 204

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        205 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 264

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||            ::::::
Db        265 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 312

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        313 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 372

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        373 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 432

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                 ||||||   :::|||   |||::::::          |||   ||||||
Db        433 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 489


Search completed: February 20, 2006, 00:54:17
Job time : 229.413 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:21:03 ; Search time 1117.92 Seconds
(without alignments)
1102.173 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160808_3828/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03p
-USER=US10758902_@CGN_1_1_2064_@runat_17022006_160808_3828 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	726	94.5	2404	10	US-11-084-080-15	Sequence 15, Appl
2	726	94.5	2404	10	US-11-084-080-19	Sequence 19, Appl
3	726	94.5	2404	10	US-11-084-080-21	Sequence 21, Appl
4	726	94.5	2404	10	US-11-084-080-23	Sequence 23, Appl
5	726	94.5	2431	10	US-11-084-080-27	Sequence 27, Appl
6	609	79.3	363	8	US-10-758-902-8	Sequence 8, Appli
7	220.5	28.7	913	6	US-10-127-890-13	Sequence 13, Appl
8	220.5	28.7	913	9	US-10-717-243-13	Sequence 13, Appl
9	183.5	23.9	870	3	US-09-905-247-2	Sequence 2, Appli
10	183.5	23.9	886	6	US-10-280-679B-3	Sequence 3, Appli
11	183.5	23.9	886	7	US-10-280-725B-3	Sequence 3, Appli
12	179.5	23.4	762	10	US-11-042-707-16	Sequence 16, Appl
13	179.5	23.4	762	10	US-11-042-707-19	Sequence 19, Appl
14	179.5	23.4	768	10	US-11-042-707-17	Sequence 17, Appl
15	179.5	23.4	768	10	US-11-042-707-20	Sequence 20, Appl
16	176.5	23.0	756	3	US-09-347-064-7	Sequence 7, Appli
17	176.5	23.0	762	3	US-09-347-064-1	Sequence 1, Appli
18	176.5	23.0	855	9	US-10-499-297-1	Sequence 1, Appli
19	176.5	23.0	1596	10	US-11-042-707-15	Sequence 15, Appl
20	176.5	23.0	1596	10	US-11-042-707-18	Sequence 18, Appl
21	176.5	23.0	1958	9	US-10-499-297-5	Sequence 5, Appli
22	173	22.5	2788	9	US-10-800-052-35	Sequence 35, Appl
23	173	22.5	2803	9	US-10-800-052-2	Sequence 2, Appli
24	173	22.5	2805	9	US-10-800-052-37	Sequence 37, Appl
25	173	22.5	2869	9	US-10-800-052-20	Sequence 20, Appl
26	173	22.5	2878	9	US-10-800-052-26	Sequence 26, Appl
27	169	22.0	1731	3	US-09-785-921A-2	Sequence 2, Appli
28	169	22.0	1731	3	US-09-785-921A-3	Sequence 3, Appli
29	169	22.0	1731	7	US-10-618-560-2	Sequence 2, Appli
30	169	22.0	1731	7	US-10-618-560-3	Sequence 3, Appli
31	169	22.0	1805	3	US-09-785-921A-10	Sequence 10, Appl
32	169	22.0	1805	7	US-10-618-560-10	Sequence 10, Appl
33	168	21.9	7306	9	US-10-477-373A-2	Sequence 2, Appli
34	168	21.9	8155	9	US-10-477-373A-1	Sequence 1, Appli
35	167	21.7	1698	3	US-09-785-921A-1	Sequence 1, Appli
36	167	21.7	1698	7	US-10-618-560-1	Sequence 1, Appli
37	167	21.7	1855	6	US-10-394-511-3	Sequence 3, Appli
38	167	21.7	1855	6	US-10-394-511-5	Sequence 5, Appli
39	167	21.7	1855	6	US-10-394-511-7	Sequence 7, Appli
40	167	21.7	1855	6	US-10-394-511-9	Sequence 9, Appli
41	167	21.7	1855	6	US-10-394-511-13	Sequence 13, Appl
42	167	21.7	1855	6	US-10-394-511-15	Sequence 15, Appl
43	167	21.7	1855	6	US-10-394-511-17	Sequence 17, Appl
44	167	21.7	1855	6	US-10-394-511-19	Sequence 19, Appl
45	167	21.7	1855	6	US-10-394-511-21	Sequence 21, Appl
46	167	21.7	1855	6	US-10-394-511-23	Sequence 23, Appl
47	167	21.7	1855	6	US-10-394-511-25	Sequence 25, Appl
48	167	21.7	1855	6	US-10-394-511-27	Sequence 27, Appl
49	167	21.7	1855	6	US-10-394-511-29	Sequence 29, Appl
50	167	21.7	1855	6	US-10-394-511-31	Sequence 31, Appl
51	167	21.7	1855	6	US-10-394-511-33	Sequence 33, Appl
52	167	21.7	1855	6	US-10-394-511-35	Sequence 35, Appl
53	167	21.7	1855	6	US-10-394-511-37	Sequence 37, Appl
54	167	21.7	1855	6	US-10-394-511-39	Sequence 39, Appl
55	167	21.7	1855	6	US-10-394-511-48	Sequence 48, Appl
56	167	21.7	1855	6	US-10-394-511-50	Sequence 50, Appl
57	167	21.7	1855	6	US-10-394-511-52	Sequence 52, Appl
58	167	21.7	1855	6	US-10-394-511-54	Sequence 54, Appl
59	167	21.7	1855	6	US-10-394-511-74	Sequence 74, Appl
60	167	21.7	1855	6	US-10-394-511-77	Sequence 77, Appl
61	167	21.7	1855	6	US-10-394-511-80	Sequence 80, Appl
62	167	21.7	1855	6	US-10-394-511-83	Sequence 83, Appl
63	167	21.7	1855	6	US-10-394-511-86	Sequence 86, Appl
64	167	21.7	1855	6	US-10-394-511-89	Sequence 89, Appl
65	167	21.7	1855	6	US-10-394-511-92	Sequence 92, Appl
66	167	21.7	1855	6	US-10-394-511-95	Sequence 95, Appl
67	167	21.7	1855	6	US-10-394-511-98	Sequence 98, Appl
68	167	21.7	1855	6	US-10-394-511-101	Sequence 101, App
69	167	21.7	1855	6	US-10-394-511-104	Sequence 104, App
70	167	21.7	1855	6	US-10-394-511-110	Sequence 110, App
71	167	21.7	1855	6	US-10-394-511-113	Sequence 113, App
72	167	21.7	1855	6	US-10-394-511-116	Sequence 116, App
73	167	21.7	1855	6	US-10-394-511-119	Sequence 119, App
74	167	21.7	1855	6	US-10-394-511-122	Sequence 122, App
75	167	21.7	1855	6	US-10-394-511-125	Sequence 125, App
76	167	21.7	1861	6	US-10-394-511-11	Sequence 11, Appl
77	167	21.7	1912	6	US-10-394-511-107	Sequence 107, App
78	159.5	20.8	763	10	US-11-042-707-13	Sequence 13, Appl
79	159.5	20.8	1598	10	US-11-042-707-12	Sequence 12, Appl
80	156.5	20.4	813	3	US-09-765-527-246	Sequence 246, App

81	156.5	20.4	813	6	US-10-127-890-11	Sequence 11, Appl
82	156.5	20.4	813	9	US-10-717-243-11	Sequence 11, Appl
83	156.5	20.4	1176	6	US-10-074-596-2	Sequence 2, Appli
84	156.5	20.4	1500	9	US-10-964-195-12	Sequence 12, Appl
85	156.5	20.4	1527	6	US-10-074-596-10	Sequence 10, Appl
86	156.5	20.4	2407	10	US-11-084-080-25	Sequence 25, Appl
87	154	20.1	1379	3	US-09-978-274A-30	Sequence 30, Appl
88	154	20.1	1379	10	US-11-106-187-1	Sequence 1, Appli
89	153.5	20.0	955	3	US-09-765-527-258	Sequence 258, App
90	153.5	20.0	1003	3	US-09-765-527-252	Sequence 252, App
91	153.5	20.0	1072	3	US-09-765-527-250	Sequence 250, App
92	147	19.1	1517	9	US-10-964-195-10	Sequence 10, Appl
93	146	19.0	1368	3	US-09-978-274A-31	Sequence 31, Appl
94	145	18.9	1542	9	US-10-926-731A-11	Sequence 11, Appl
95	143.5	18.7	1376	8	US-10-467-009-1	Sequence 1, Appli
96	127	16.5	792	3	US-09-978-274A-3	Sequence 3, Appli
97	127	16.5	945	3	US-09-978-274A-1	Sequence 1, Appli
98	127	16.5	1092	3	US-09-978-274A-19	Sequence 19, Appl
99	124	16.1	465	3	US-09-978-274A-5	Sequence 5, Appli
100	111	14.5	65	8	US-10-758-902-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-11-084-080-15
; Sequence 15, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845
US-11-084-080-15

Alignment Scores:

Pred. No.:	1.19e-90	Length:	2404
Score:	726.00	Matches:	144
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	5
Query Match:	94.5%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-9 (1-149) x US-11-084-080-15 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 884

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 944

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1004

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1064

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1124

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1184

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||  ||||||||  ||||||||||||||  ||||||||||||||||||||
Db       1185 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 1244

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||  |||||||||  ||||||
Db       1245 GCAATCCATGGTAAAACGATAAATGGT 1271
```

RESULT 2
US-11-084-080-19
; Sequence 19, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Alignment Scores:

Pred. No.:	1.19e-90	Length:	2404
Score:	726.00	Matches:	144
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	5
Query Match:	94.5%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-9 (1-149) x US-11-084-080-19 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1643 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1702

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1703 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 1762

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1763 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1822

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1823 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1882

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1883 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1942

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1943 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 2002

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||  |||||||||  ||||||||||||||  ||||||||||||||||||||||||
Db       2003 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 2062

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||   |||||||||   ||||||
Db       2063 GCAATCCATGGTAAAACGATAAATGGT 2089

RESULT 3
US-11-084-080-21
; Sequence 21, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-21

Alignment Scores:
Pred. No.:              1.19e-90        Length:         2404
Score:                  726.00          Matches:        144
Percent Similarity:     96.6%           Conservative:   0
Best Local Similarity:  96.6%           Mismatches:     5
Query Match:            94.5%           Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-9 (1-149) x US-11-084-080-21 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 191

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 251

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 311

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 371

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 431

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 491

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||  |||||||||  ||||||||||||||  ||||||||||||||||||||||||
Db        492 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 551

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||   |||||||||   ||||||
Db        552 GCAATCCATGGTAAAACGATAAATGGT 578

RESULT 4
US-11-084-080-23
; Sequence 23, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Alignment Scores:
Pred. No.:              1.19e-90        Length:         2404
Score:                  726.00          Matches:        144
Percent Similarity:     96.6%           Conservative:   0
Best Local Similarity:  96.6%           Mismatches:     5
Query Match:            94.5%           Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-9 (1-149) x US-11-084-080-23 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        950 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1009
```

```
Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1010 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 1069

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1129

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1130 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1189

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1190 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1249

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1250 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1309

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||  |||||||||  ||||||||||||||||  ||||||||||||||||||||||
Db       1310 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 1369

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||  |||||||||  ||||||
Db       1370 GCAATCCATGGTAAAACGATAAATGGT 1396

RESULT 5
US-11-084-080-27
; Sequence 27, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 2431
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-011
US-11-084-080-27

Alignment Scores:
Pred. No.:              1.21e-90        Length:         2431
Score:                  726.00          Matches:        144
Percent Similarity:     96.6%           Conservative:   0
Best Local Similarity:  96.6%           Mismatches:     5
Query Match:            94.5%           Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-9 (1-149) x US-11-084-080-27 (1-2431)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 911

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        912 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 971

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1031

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1091

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1092 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1151

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1152 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1211

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||  |||||||||  ||||||||||||||||  ||||||||||||||||||||||
Db       1212 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 1271

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||  |||||||||  ||||||
Db       1272 GCAATCCATGGTAAAACGATAAATGGT 1298

RESULT 6
US-10-758-902-8
; Sequence 8, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)...(361)
US-10-758-902-8

Alignment Scores:
Pred. No.:              1.99e-75        Length:         363
Score:                  609.00          Matches:        120
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            79.3%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-9 (1-149) x US-10-758-902-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361

RESULT 7
US-10-127-890-13
; Sequence 13, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 913 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-127-890-13

Alignment Scores:
Pred. No.:              3.04e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     6               Gaps:           3

US-10-758-902-9 (1-149) x US-10-127-890-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||             |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||             |||      :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::|||||||||||   |||:::                :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||::::::::::::|||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 8
US-10-717-243-13
; Sequence 13, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
```

```
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 913 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-717-243-13

Alignment Scores:
Pred. No.:              3.04e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     9               Gaps:           3

US-10-758-902-9 (1-149) x US-10-717-243-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||            |||     |||     ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||     |||                 |||     :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::               :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||     :::   |||     |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||::::::::::::||||||:::     |||     :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 9
```

```
US-09-905-247-2
; Sequence 2, Application US/09905247
; Publication No. US20040197853A1
; GENERAL INFORMATION:
;  APPLICANT: KE, YI-BAO
;  APPLICANT:  NIE, HUI-LING
;  TITLE OF INVENTION: Mutant Trichosanthin
;  FILE REFERENCE: 04399/000J615-US0
;  CURRENT APPLICATION NUMBER: US/09/905,247
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: CN 00119553.0
;  PRIOR FILING DATE: 2000-08-02
;  PRIOR APPLICATION NUMBER: CN 01103102.6
;  PRIOR FILING DATE: 2001-01-18
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 870
;   TYPE: DNA
;   ORGANISM: Trichosanthes Kirilowii M.
US-09-905-247-2

Alignment Scores:
Pred. No.:              4.48e-15        Length:         870
Score:                  183.50          Matches:        44
Percent Similarity:     53.5%           Conservative:   32
Best Local Similarity:  31.0%           Mismatches:     61
Query Match:            23.9%           Indels:         5
DB:                     3               Gaps:           2

US-10-758-902-9 (1-149) x US-09-905-247-2 (1-870)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||     |||             |||     ||||||   :::|||
Db         73 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 132

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||     |||               :::     :::|||:::         ::::::
Db        133 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCAGTCTT 192

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||:::   |||:::   :::|||     :::   :::|||:::
Db        193 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 252

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::            |||
Db        253 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 303

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                        |||   ::      |||   |||         :::|||
Db        304 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 363

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::||||||||   :::   |||:::|||::::::|||       ||||||
Db        364 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCA 423

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                       |||:::::::::   ||||||:::      |||:::   :::|||
Db        424 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCTGCTTTGGACAGTGCCATTACCACT 483

Qy        142 IleTrp 143
              ::::::
Db        484 TTGTTT 489

RESULT 10
US-10-280-679B-3
; Sequence 3, Application US/10280679B
; Publication No. US20030150019A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
;  FILE REFERENCE: LSBC-0109-US03
;  CURRENT APPLICATION NUMBER: US/10/280,679B
```

```
;  CURRENT FILING DATE:  2000-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;    LENGTH: 886
;    TYPE: DNA
;    ORGANISM: Chinese Cucumber
;    FEATURE:
;    NAME/KEY: exon
;    LOCATION: (8)..(877)
;    OTHER INFORMATION:
US-10-280-679B-3

Alignment Scores:
Pred. No.:              4.6e-15        Length:          886
Score:                  183.50         Matches:         44
Percent Similarity:     53.5%          Conservative:    32
Best Local Similarity:  31.0%          Mismatches:      61
Query Match:            23.9%          Indels:          5
DB:                     6              Gaps:            2

US-10-758-902-9 (1-149) x US-10-280-679B-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||       |||             |||       ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||                  :::       :::|||:::          ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::    |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::::||||||:::             |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::       |||   |||       :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::||||||||||   :::   |||:::|||:::::|||       ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::     |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
```

```
              ::::::
Db        491 TTGTTT 496

RESULT 11
US-10-280-725B-3
; Sequence 3, Application US/10280725B
; Publication No. US20040049025A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Recombinant Viral Nucleic Acids
;  FILE REFERENCE: LSBC-0109-US02
;  CURRENT APPLICATION NUMBER: US/10/280,725B
;  CURRENT FILING DATE:  2002-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;    LENGTH: 886
;    TYPE: DNA
;    ORGANISM: Chinese Cucumber
;    FEATURE:
;    NAME/KEY: exon
;    LOCATION: (8)..(877)
;    OTHER INFORMATION:
US-10-280-725B-3

Alignment Scores:
Pred. No.:              4.6e-15        Length:          886
Score:                  183.50         Matches:         44
Percent Similarity:     53.5%          Conservative:    32
Best Local Similarity:  31.0%          Mismatches:      61
Query Match:            23.9%          Indels:          5
DB:                     7              Gaps:            2

US-10-758-902-9 (1-149) x US-10-280-725B-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||       |||             |||       ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||                  :::       :::|||:::          ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::    |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::::||||||:::             |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
```

```
                    |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
              :::||||||||||   :::   |||:::|||:::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                 ::::::
Db        491 TTGTTT 496

RESULT 12
US-11-042-707-16
; Sequence 16, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 16
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1
US-11-042-707-16

Alignment Scores:
Pred. No.:              1.34e-14      Length:          762
Score:                  179.50        Matches:         50
Percent Similarity:     57.1%         Conservative:    26
Best Local Similarity:  37.6%         Mismatches:      48
Query Match:            23.4%         Indels:          9
DB:                     10            Gaps:            4

US-10-758-902-9 (1-149) x US-11-042-707-16 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   :::|||      ||||||||||||||:::
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGGTTACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                ||:::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 13
US-11-042-707-19
; Sequence 19, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 19
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1
US-11-042-707-19

Alignment Scores:
Pred. No.:              1.34e-14      Length:          762
Score:                  179.50        Matches:         50
Percent Similarity:     57.1%         Conservative:    26
Best Local Similarity:  37.6%         Mismatches:      48
Query Match:            23.4%         Indels:          9
DB:                     10            Gaps:            4

US-10-758-902-9 (1-149) x US-11-042-707-19 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   :::|||      ||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTGTTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                ||:::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 14
US-11-042-707-17
; Sequence 17, Application US/11042707
```

```
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 17
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-11-042-707-17
```

Alignment Scores:			
Pred. No.:	1.36e-14	Length:	768
Score:	179.50	Matches:	49
Percent Similarity:	56.7%	Conservative:	27
Best Local Similarity:	36.6%	Mismatches:	49
Query Match:	23.4%	Indels:	9
DB:	10	Gaps:	4

US-10-758-902-9 (1-149) x US-11-042-707-17 (1-768)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::||   :::|||||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   ::::::     |||||||||||||||:::
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGATCACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||      |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThr---AsnArgValThrLeu 108
              |||       |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGCACCACCCGAGATAGATCCTCTCTC 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||       |||         |||         |||       :::
Db        334 CCATTCACTGGAAGCTACACCGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATC 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCTCTCGGTATAGAGCAACTCATTCAATCCGTCTCTGCGCTT 432
```

```
RESULT 15
US-11-042-707-20
; Sequence 20, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 20
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-11-042-707-20
```

Alignment Scores:			
Pred. No.:	1.36e-14	Length:	768
Score:	179.50	Matches:	49
Percent Similarity:	56.7%	Conservative:	27
Best Local Similarity:	36.6%	Mismatches:	49
Query Match:	23.4%	Indels:	9
DB:	10	Gaps:	4

US-10-758-902-9 (1-149) x US-11-042-707-20 (1-768)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::||   :::|||||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   ::::::     |||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTATTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||      |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThr---AsnArgValThrLeu 108
              |||       |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGTACAACACGGGATAGAAGTTCTTTG 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||       |||         |||         |||       :::
Db        334 CCTTTTACTGGTTCTTATACAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATT 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCATTGGGAATTGAGCAGTTGATCCAGAGTGTTTCTGCTTTG 432
```

```
RESULT 16
US-09-347-064-7
; Sequence 7, Application US/09347064A
; Patent No. US20020045208A1
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
```

```
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064-7

Alignment Scores:
Pred. No.:              3.5e-14       Length:          756
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-347-064-7 (1-756)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                 ::::::      |||||||||||||||::::::
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::||||||||||      |||         |||         |||       :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 17
US-09-347-064-1
; Sequence 1, Application US/09347064A
; Patent No. US20020045208A1
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064-1

Alignment Scores:
Pred. No.:              3.55e-14      Length:          762
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-347-064-1 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                 ::::::      |||||||||||||||::::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::||||||||||      |||         |||         |||       :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 18
US-10-499-297-1
; Sequence 1, Application US/10499297
; Publication No. US20050221380A1
; GENERAL INFORMATION:
;  APPLICANT: Muthing, Johannes
;  APPLICANT:  Peter-Katalinic, Jasna
;  APPLICANT:  Langer, Martin
;  APPLICANT:  Mockel, Babette
;  APPLICANT:  Eck, Jurgen
;  TITLE OF INVENTION: METHOD FOR DETERMINATION OF THE
;  TITLE OF INVENTION:  RESPONSIVENESS OF AN INDIVIDUAL TO MISTLETOE LECTIN
;  FILE REFERENCE: VOSS-P01-010
;  CURRENT APPLICATION NUMBER: US/10/499,297
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: EP 01130745.1
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 855
;   TYPE: DNA
;   ORGANISM: Viscum album
US-10-499-297-1

Alignment Scores:
Pred. No.:              4.21e-14      Length:          855
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     9             Gaps:            4

US-10-758-902-9 (1-149) x US-10-499-297-1 (1-855)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db        145 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 204
```

```
Qy          33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
               ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db         205 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 264

Qy          50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
               |||::::::|||                :::::      |||||||||||||||::::::
Db         265 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 324

Qy          70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
               |||||||||  ||||||           |||::::::   ||||||
Db         325 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 372

Qy          90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
               |||     |||  :::   ||||||  |||  |||  |||   :::|||
Db         373 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 429

Qy         110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
               |||:::|||||||||      |||         |||         |||      :::
Db         430 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 486

Qy         130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
               ||||||:::   :::|||      |||:::   |||:::
Db         487 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 525

RESULT 19
US-11-042-707-15
; Sequence 15, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 15
;   LENGTH: 1596
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: MLA-I
US-11-042-707-15

Alignment Scores:
Pred. No.:              1.06e-13      Length:          1596
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     10            Gaps:            4

US-10-758-902-9 (1-149) x US-11-042-707-15 (1-1596)

Qy          13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
               ||||||      ||||||      ||||||:::   ::::::   |||:::
Db          46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy          33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
               ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db         106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy          50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
               |||::::::|||                :::::      |||||||||||||||::::::
Db         166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy          70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
               |||||||||  ||||||           |||::::::   ||||||
Db         226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy          90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
               |||     |||  :::   ||||||  |||  |||  |||   :::|||
Db         274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy         110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
               |||:::|||||||||      |||         |||         |||      :::
Db         331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy         130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
               ||||||:::   :::|||      |||:::   |||:::
Db         388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 20
US-11-042-707-18
; Sequence 18, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 18
;   LENGTH: 1596
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: MLI (matched)
US-11-042-707-18

Alignment Scores:
Pred. No.:              1.06e-13      Length:          1596
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     10            Gaps:            4

US-10-758-902-9 (1-149) x US-11-042-707-18 (1-1596)

Qy          13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
               ||||||      ||||||      ||||||:::   ::::::   |||:::
Db          46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy          33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
               ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db         106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy          50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
               |||::::::|||                :::::      |||||||||||||||::::::
Db         166 GTTGAATTGACTAACCAAGGAGGTGATAGTATTACTGCTGCTATTGATGTGACTAACCTT 225

Qy          70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
               |||||||||  ||||||           |||::::::   ||||||
Db         226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy          90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
               |||     |||  :::   ||||||  |||  |||  |||   :::|||
Db         274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330

Qy         110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
               |||:::|||||||||      |||         |||         |||      :::
```

```
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 21
US-10-499-297-5
; Sequence 5, Application US/10499297
; Publication No. US20050221380A1
; GENERAL INFORMATION:
;  APPLICANT: Muthing, Johannes
;  APPLICANT:  Peter-Katalinic, Jasna
;  APPLICANT:  Langer, Martin
;  APPLICANT:  Mockel, Babette
;  APPLICANT:  Eck, Jurgen
;  TITLE OF INVENTION: METHOD FOR DETERMINATION OF THE
;  TITLE OF INVENTION:  RESPONSIVENESS OF AN INDIVIDUAL TO MISTLETOE LECTIN
;  FILE REFERENCE: VOSS-P01-010
;  CURRENT APPLICATION NUMBER: US/10/499,297
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: EP 01130745.1
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1958
;   TYPE: DNA
;   ORGANISM: Viscum album
US-10-499-297-5

Alignment Scores:
Pred. No.:              1.44e-13      Length:         1958
Score:                  176.50        Matches:        49
Percent Similarity:     57.1%         Conservative:   27
Best Local Similarity:  36.8%         Mismatches:     48
Query Match:            23.0%         Indels:         9
DB:                     9             Gaps:           4

US-10-758-902-9 (1-149) x US-10-499-297-5 (1-1958)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db        199 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 258

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||
Db        259 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 318

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::      ||||||||||||||::::::
Db        319 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 378

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                        |||::::::   ||||||
Db        379 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 426

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||       |||   :::   ||||||   |||   |||   |||   :::|||
Db        427 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 483

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        484 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 540

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        541 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 579

RESULT 22
US-10-800-052-35
; Sequence 35, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 2788
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: pWKK-21
US-10-800-052-35

Alignment Scores:
Pred. No.:              7.54e-13      Length:         2788
Score:                  173.00        Matches:        52
Percent Similarity:     52.2%         Conservative:   31
Best Local Similarity:  32.7%         Mismatches:     60
Query Match:            22.5%         Indels:         16
DB:                     9             Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-35 (1-2788)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db       1288 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1347

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db       1348 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1407

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||||::::::
Db       1408 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1467

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db       1468 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1527

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||            ::::::
Db       1528 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1575

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db       1576 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1635

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db       1636 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1695

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db       1696 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1752

RESULT 23
US-10-800-052-2
; Sequence 2, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 2803
;   TYPE: DNA
```

```
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Plasmid pWKK-500.
US-10-800-052-2

Alignment Scores:
Pred. No.:              7.6e-13         Length:         2803
Score:                  173.00          Matches:        52
Percent Similarity:     52.2%           Conservative:   31
Best Local Similarity:  32.7%           Mismatches:     60
Query Match:            22.5%           Indels:         16
DB:                     9               Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-2 (1-2803)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db       1402 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1461

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db       1462 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1521

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::|||||||||::::::
Db       1522 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1581

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db       1582 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1641

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db       1642 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1689

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db       1690 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1749

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db       1750 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1809

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db       1810 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1866

RESULT 24
US-10-800-052-37
; Sequence 37, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 2805
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: pWKK-15
US-10-800-052-37

Alignment Scores:
Pred. No.:              7.61e-13        Length:         2805
Score:                  173.00          Matches:        52
Percent Similarity:     52.2%           Conservative:   31
Best Local Similarity:  32.7%           Mismatches:     60
Query Match:            22.5%           Indels:         16
DB:                     9               Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-37 (1-2805)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db       1405 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1464

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db       1465 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1524

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::|||||||||::::::
Db       1525 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1584

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db       1585 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1644

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db       1645 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1692

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db       1693 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1752

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db       1753 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1812

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db       1813 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1869

RESULT 25
US-10-800-052-20
; Sequence 20, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2869
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Coding region of pWKK-700.
US-10-800-052-20

Alignment Scores:
Pred. No.:              7.87e-13        Length:         2869
Score:                  173.00          Matches:        52
Percent Similarity:     52.2%           Conservative:   31
Best Local Similarity:  32.7%           Mismatches:     60
Query Match:            22.5%           Indels:         16
DB:                     9               Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-20 (1-2869)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db       1486 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1545

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db       1546 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1605
```

```
Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           :::::|||||||:::|||||||||:::::::
Db       1606 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1665

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db       1666 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1725

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db       1726 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1773

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db       1774 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1833

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db       1834 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1893

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db       1894 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1950

RESULT 26
US-10-800-052-26
; Sequence 26, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 2878
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: pWKK-800
US-10-800-052-26

Alignment Scores:
Pred. No.:              7.9e-13       Length:          2878
Score:                  173.00        Matches:         52
Percent Similarity:     52.2%         Conservative:    31
Best Local Similarity:  32.7%         Mismatches:      60
Query Match:            22.5%         Indels:          16
DB:                     9             Gaps:            6

US-10-758-902-9 (1-149) x US-10-800-052-26 (1-2878)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||          |||      ||||||
Db       1495 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1554

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db       1555 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1614

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           :::::|||||||:::|||||||||:::::::
Db       1615 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1674

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db       1675 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1734

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
```

```
Db       1735 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1782

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db       1783 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1842

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db       1843 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1902

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db       1903 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1959

RESULT 27
US-09-785-921A-2
; Sequence 2, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 2
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-2

Alignment Scores:
Pred. No.:              1.36e-12      Length:          1731
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-785-921A-2 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||          |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           :::::|||||||:::|||||||||:::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        361 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGAGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
```

```
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 28
US-09-785-921A-3
; Sequence 3, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 3
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-3

Alignment Scores:
Pred. No.:              1.36e-12      Length:         1731
Score:                  169.00        Matches:        51
Percent Similarity:     52.2%         Conservative:   32
Best Local Similarity:  32.1%         Mismatches:     60
Query Match:            22.0%         Indels:         16
DB:                     3             Gaps:           6

US-10-758-902-9 (1-149) x US-09-785-921A-3 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||          |||          |||       ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::|||||||:::|||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        361 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 29
US-10-618-560-2
; Sequence 2, Application US/10618560
; Publication No. US20040048784A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 2
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-2

Alignment Scores:
Pred. No.:              1.36e-12      Length:         1731
Score:                  169.00        Matches:        51
Percent Similarity:     52.2%         Conservative:   32
Best Local Similarity:  32.1%         Mismatches:     60
Query Match:            22.0%         Indels:         16
DB:                     7             Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-2 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||          |||          |||       ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::|||||||:::|||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        361 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGAGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 30
US-10-618-560-3
; Sequence 3, Application US/10618560
; Publication No. US20040048784A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 3
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-3
```

```
Alignment Scores:
Pred. No.:              1.36e-12        Length:         1731
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-3 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||           |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        301 GCAGAGGTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        361 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 31
US-09-785-921A-10
; Sequence 10, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 10
;   LENGTH: 1805
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-10

Alignment Scores:
Pred. No.:              1.44e-12        Length:         1805
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-785-921A-10 (1-1805)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||           |||      ||||||
Db        129 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 188

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        189 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 248

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||:::::::::
Db        249 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 308

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        309 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 368

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        369 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 416

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        417 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 476

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        477 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 536

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        537 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 593

RESULT 32
US-10-618-560-10
; Sequence 10, Application US/10618560
; Publication No. US20040048784A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 10
;   LENGTH: 1805
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-10

Alignment Scores:
Pred. No.:              1.44e-12        Length:         1805
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-10 (1-1805)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||           |||      ||||||
Db        129 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 188

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        189 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 248

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||:::::::::
Db        249 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 308
```

```
Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               :::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db         309 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 368

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db         369 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 416

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::  ||||||     |||  ||||||  |||      |||   |||
Db         417 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 476

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         477 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 536

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::            |||   ||||||
Db         537 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 593

RESULT 33
US-10-477-373A-2
; Sequence 2, Application US/10477373A
; Publication No. US20050191626A1
; GENERAL INFORMATION:
;  APPLICANT: TAIRA Kazunari
;  APPLICANT:  FUJITA Satoshi
;  APPLICANT:  YOSHIZAKI Shinya
;  APPLICANT:  WARASHINA Masaki
;  TITLE OF INVENTION: METHODS FOR FORMING A STABLE COMPLEX BETWEEN THE TRANSCRIPT AND
;  TITLE OF INVENTION:  TRANSLATION PRODUCT OF A DNA ENCODING AN ARBITRARY POLYPEPTIDE,
;  TITLE OF INVENTION:  CONSTRUCTS TO BE USED IN THESE METHODS, COMPLEXES FORMED BY THE
;  TITLE OF INVENTION:  OF THESE METHODS TO SCREEN FOR FUNCTIONAL PROTEINS, AND mRNAs AN
;  TITLE OF INVENTION:  ENCODING THESE PROTEINS
;  FILE REFERENCE: 6235-67303-01
;  CURRENT APPLICATION NUMBER: US/10/477,373A
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: PCT/JP02/04582
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: JP 2001-141594
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: JP 2002-62751
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 2
;   LENGTH: 7306
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant expression vector for streptavidin fused with the Ric
;   OTHER INFORMATION: communis Ricin-A chain (short spacer).
US-10-477-373A-2

Alignment Scores:
Pred. No.:              1.59e-11      Length:         7306
Score:                  168.00        Matches:        51
Percent Similarity:     52.2%         Conservative:   32
Best Local Similarity:  32.1%         Mismatches:     60
Query Match:            21.9%         Indels:         16
DB:                     9             Gaps:           6

US-10-758-902-9 (1-149) x US-10-477-373A-2 (1-7306)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||     ::::::|||          |||          |||      ||||||
Db        5787 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 5846

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                  :::   :::|||      |||      |||      |||      ::::::||||||
Db        5847 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 5906

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::||||||:::||||||:::::::::
Db        5907 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 5966

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        5967 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 6026

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        6027 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 6074

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::  ||||||     |||  ||||||  |||      |||   |||
Db        6075 GAAGCAATCACTTATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 6134

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db        6135 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 6194

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::            |||   ||||||
Db        6195 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 6251

RESULT 34
US-10-477-373A-1
; Sequence 1, Application US/10477373A
; Publication No. US20050191626A1
; GENERAL INFORMATION:
;  APPLICANT: TAIRA Kazunari
;  APPLICANT:  FUJITA Satoshi
;  APPLICANT:  YOSHIZAKI Shinya
;  APPLICANT:  WARASHINA Masaki
;  TITLE OF INVENTION: METHODS FOR FORMING A STABLE COMPLEX BETWEEN THE TRANSCRIPT AND
;  TITLE OF INVENTION:  TRANSLATION PRODUCT OF A DNA ENCODING AN ARBITRARY POLYPEPTIDE,
;  TITLE OF INVENTION:  CONSTRUCTS TO BE USED IN THESE METHODS, COMPLEXES FORMED BY THE
;  TITLE OF INVENTION:  OF THESE METHODS TO SCREEN FOR FUNCTIONAL PROTEINS, AND mRNAs A
;  TITLE OF INVENTION:  ENCODING THESE PROTEINS
;  FILE REFERENCE: 6235-67303-01
;  CURRENT APPLICATION NUMBER: US/10/477,373A
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: PCT/JP02/04582
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: JP 2001-141594
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: JP 2002-62751
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 1
;   LENGTH: 8155
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant expression vector for streptavidin fused with the Ri
;   OTHER INFORMATION: communis Ricin-A chain (long spacer).
US-10-477-373A-1

Alignment Scores:
Pred. No.:              1.87e-11      Length:         8155
Score:                  168.00        Matches:        51
Percent Similarity:     52.2%         Conservative:   32
Best Local Similarity:  32.1%         Mismatches:     60
Query Match:            21.9%         Indels:         16
DB:                     9             Gaps:           6

US-10-758-902-9 (1-149) x US-10-477-373A-1 (1-8155)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||     ::::::|||          |||          |||      ||||||
Db        5787 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 5846

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                  :::   :::|||      |||      |||      |||      ::::::||||||
Db        5847 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 5906
```

```
Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           :::::||||||:::||||||:::::::::
Db       5907 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 5966

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::::: :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db       5967 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 6026

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db       6027 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 6074

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db       6075 GAAGCAATCACTTATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 6134

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||::::::::::|||||||||
Db       6135 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 6194

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db       6195 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 6251

RESULT 35
US-09-785-921A-1
; Sequence 1, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
;   LENGTH: 1698
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-1

Alignment Scores:
Pred. No.:              2.52e-12        Length:         1698
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-785-921A-1 (1-1698)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db         88 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 147

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        148 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 207

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           :::::||||||:::||||||:::::::::
Db        208 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 267

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::::: :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        268 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 327

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        328 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 375

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        376 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 435

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||::::::::::|||||||||
Db        436 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 495

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        496 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 552

RESULT 36
US-10-618-560-1
; Sequence 1, Application US/10618560
; Publication No. US20040048784A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
;   LENGTH: 1698
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-1

Alignment Scores:
Pred. No.:              2.52e-12        Length:         1698
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-1 (1-1698)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db         88 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 147

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        148 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 207

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           :::::||||||:::||||||:::::::::
Db        208 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 267

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::::: :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        268 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 327

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        328 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 375

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        376 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 435

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||::::::::::|||||||||
Db        436 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 495

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
```

```
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        496 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 552

RESULT 37
US-10-394-511-3
; Sequence 3, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Cathepsin B linker regions of pAP-214
US-10-394-511-3

Alignment Scores:
Pred. No.:              2.87e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     6               Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-3 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||       |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 38
US-10-394-511-5
; Sequence 5, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-216 insert
US-10-394-511-5

Alignment Scores:
Pred. No.:              2.87e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     6               Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-5 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||       |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 39
US-10-394-511-7
; Sequence 7, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-218 insert
US-10-394-511-7

Alignment Scores:
Pred. No.:              2.87e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     6             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-7 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||        :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 40
US-10-394-511-9
; Sequence 9, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-220 insert
US-10-394-511-9

Alignment Scores:
Pred. No.:              2.87e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     6             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-9 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||        :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

Search completed: February 20, 2006, 02:30:27
Job time : 1130.92 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:49:47 ; Search time 443.67 Seconds
(without alignments)
712.890 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160811_3886/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss08
-USER=US10758902_@CGN_1_1_380_@runat_17022006_160811_3886 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	169	22.0	807	12	US-11-010-795-23	Sequence 23, Appl
2	169	22.0	1623	8	US-10-893-584-273	Sequence 273, App
3	169	22.0	1807	8	US-10-893-584-196	Sequence 196, App
4	169	22.0	1810	8	US-10-893-584-168	Sequence 168, App
5	169	22.0	1813	8	US-10-893-584-245	Sequence 245, App
6	169	22.0	1819	8	US-10-893-584-238	Sequence 238, App
7	169	22.0	1822	8	US-10-893-584-175	Sequence 175, App
8	169	22.0	1822	8	US-10-893-584-182	Sequence 182, App
9	169	22.0	1825	8	US-10-893-584-231	Sequence 231, App
10	169	22.0	1828	8	US-10-893-584-210	Sequence 210, App
11	169	22.0	1831	8	US-10-893-584-161	Sequence 161, App
12	169	22.0	1831	8	US-10-893-584-203	Sequence 203, App
13	169	22.0	1834	8	US-10-893-584-154	Sequence 154, App
14	169	22.0	1837	8	US-10-893-584-266	Sequence 266, App
15	169	22.0	1843	8	US-10-893-584-259	Sequence 259, App
16	169	22.0	1849	8	US-10-893-584-252	Sequence 252, App
17	169	22.0	1855	8	US-10-893-584-147	Sequence 147, App
18	169	22.0	1855	8	US-10-893-584-189	Sequence 189, App
19	169	22.0	1855	8	US-10-893-584-217	Sequence 217, App
20	169	22.0	1855	8	US-10-893-584-224	Sequence 224, App
21	167	21.7	1855	8	US-10-893-584-3	Sequence 3, Appli
22	167	21.7	1855	8	US-10-893-584-5	Sequence 5, Appli
23	167	21.7	1855	8	US-10-893-584-7	Sequence 7, Appli
24	167	21.7	1855	8	US-10-893-584-9	Sequence 9, Appli
25	167	21.7	1855	8	US-10-893-584-13	Sequence 13, Appl
26	167	21.7	1855	8	US-10-893-584-15	Sequence 15, Appl
27	167	21.7	1855	8	US-10-893-584-17	Sequence 17, Appl
28	167	21.7	1855	8	US-10-893-584-19	Sequence 19, Appl
29	167	21.7	1855	8	US-10-893-584-21	Sequence 21, Appl
30	167	21.7	1855	8	US-10-893-584-23	Sequence 23, Appl
31	167	21.7	1855	8	US-10-893-584-25	Sequence 25, Appl
32	167	21.7	1855	8	US-10-893-584-27	Sequence 27, Appl
33	167	21.7	1855	8	US-10-893-584-29	Sequence 29, Appl
34	167	21.7	1855	8	US-10-893-584-31	Sequence 31, Appl
35	167	21.7	1855	8	US-10-893-584-33	Sequence 33, Appl
36	167	21.7	1855	8	US-10-893-584-35	Sequence 35, Appl
37	167	21.7	1855	8	US-10-893-584-37	Sequence 37, Appl
38	167	21.7	1855	8	US-10-893-584-39	Sequence 39, Appl
39	167	21.7	1855	8	US-10-893-584-48	Sequence 48, Appl
40	167	21.7	1855	8	US-10-893-584-50	Sequence 50, Appl
41	167	21.7	1855	8	US-10-893-584-52	Sequence 52, Appl
42	167	21.7	1855	8	US-10-893-584-54	Sequence 54, Appl
43	167	21.7	1855	8	US-10-893-584-74	Sequence 74, Appl
44	167	21.7	1855	8	US-10-893-584-77	Sequence 77, Appl
45	167	21.7	1855	8	US-10-893-584-80	Sequence 80, Appl
46	167	21.7	1855	8	US-10-893-584-83	Sequence 83, Appl
47	167	21.7	1855	8	US-10-893-584-86	Sequence 86, Appl
48	167	21.7	1855	8	US-10-893-584-89	Sequence 89, Appl
49	167	21.7	1855	8	US-10-893-584-92	Sequence 92, Appl
50	167	21.7	1855	8	US-10-893-584-95	Sequence 95, Appl
51	167	21.7	1855	8	US-10-893-584-98	Sequence 98, Appl
52	167	21.7	1855	8	US-10-893-584-101	Sequence 101, App
53	167	21.7	1855	8	US-10-893-584-104	Sequence 104, App
54	167	21.7	1855	8	US-10-893-584-110	Sequence 110, App
55	167	21.7	1855	8	US-10-893-584-113	Sequence 113, App
56	167	21.7	1855	8	US-10-893-584-116	Sequence 116, App
57	167	21.7	1855	8	US-10-893-584-119	Sequence 119, App
58	167	21.7	1855	8	US-10-893-584-122	Sequence 122, App
59	167	21.7	1855	8	US-10-893-584-125	Sequence 125, App
60	167	21.7	1861	8	US-10-893-584-11	Sequence 11, Appl
61	167	21.7	1912	8	US-10-893-584-107	Sequence 107, App
62	154	20.1	1360	12	US-11-010-795-19	Sequence 19, Appl
63	103	13.4	934	12	US-11-010-795-21	Sequence 21, Appl
64	81	10.5	6159	12	US-11-013-759-8	Sequence 8, Appli
65	76.5	10.0	611	6	US-09-925-065A-931079	Sequence 931079,
66	75	9.8	1095	8	US-10-793-626-1093	Sequence 1093, Ap
c 67	75	9.8	2796	8	US-10-793-626-3806	Sequence 3806, Ap
68	74	9.6	6702	8	US-10-873-528-209	Sequence 209, App
69	73	9.5	960	12	US-11-098-686-9041	Sequence 9041, Ap
70	73	9.5	1457619	12	US-11-098-686-8739	Sequence 8739, Ap
71	72.5	9.4	2766	8	US-10-880-144-1	Sequence 1, Appli
72	72.5	9.4	5037	12	US-11-136-527-3036	Sequence 3036, Ap
c 73	72	9.4	1626	6	US-09-925-065A-41965	Sequence 41965, A
c 74	72	9.4	1626	6	US-09-925-065A-41966	Sequence 41966, A
c 75	72	9.4	1626	6	US-09-925-065A-41967	Sequence 41967, A
c 76	72	9.4	1626	6	US-09-925-065A-41968	Sequence 41968, A
c 77	72	9.4	1626	6	US-09-925-065A-41969	Sequence 41969, A

78	71	9.2	2541	8	US-10-517-939-89	Sequence 89, Appl
79	70.5	9.2	4740	12	US-11-052-554A-393	Sequence 393, App
80	70.5	9.2	5012	12	US-11-136-527-2289	Sequence 2289, Ap
c 81	70	9.1	566	6	US-09-925-065A-575622	Sequence 575622,
82	69.5	9.0	960	12	US-11-010-795-25	Sequence 25, Appl
83	69.5	9.0	1299	8	US-10-793-626-2941	Sequence 2941, Ap
84	69.5	9.0	3219	8	US-10-793-626-3405	Sequence 3405, Ap
c 85	69.5	9.0	4453	12	US-11-000-688-1248	Sequence 1248, Ap
c 86	69	9.0	3085	8	US-10-485-517-89	Sequence 89, Appl
87	69	9.0	4000	8	US-10-750-185-38457	Sequence 38457, A
88	69	9.0	4000	8	US-10-750-623-38457	Sequence 38457, A
89	68.5	8.9	2140	8	US-10-510-386-75	Sequence 75, Appl
c 90	68.5	8.9	3432	8	US-10-793-626-3596	Sequence 3596, Ap
91	68.5	8.9	3456	8	US-10-793-626-2447	Sequence 2447, Ap
92	67.5	8.8	948	11	US-11-082-389-275	Sequence 275, App
93	67.5	8.8	948	12	US-11-010-795-27	Sequence 27, Appl
c 94	67.5	8.8	1411	6	US-09-925-065A-707084	Sequence 707084,
95	67.5	8.8	2085	6	US-09-925-065A-681476	Sequence 681476,
c 96	67.5	8.8	2110	8	US-10-750-185-38190	Sequence 38190, A
c 97	67.5	8.8	2110	8	US-10-750-623-38190	Sequence 38190, A
c 98	67	8.7	509	6	US-09-925-065A-283065	Sequence 283065,
99	67	8.7	600	8	US-10-750-185-839	Sequence 839, App
100	67	8.7	600	8	US-10-750-623-839	Sequence 839, App

ALIGNMENTS

RESULT 1
US-11-010-795-23
; Sequence 23, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Ricinus communis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(804)
US-11-010-795-23

Alignment Scores:

Pred. No.:	2.57e-13	Length:	807
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	12	Gaps:	6

US-10-758-902-9 (1-149) x US-11-010-795-23 (1-807)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db         19 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 78

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||     ::::::||||||
Db         79 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 138

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::|||||||:::::::::
Db        139 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 198

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        199 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 258

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::  |||   |||             ::::::
Db        259 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 306

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        307 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 366

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        367 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 426

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        427 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 483
```

RESULT 2
US-10-893-584-273
; Sequence 273, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 273
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ricin-like toxin (TST10054)
US-10-893-584-273

Alignment Scores:

Pred. No.:	6.21e-13	Length:	1623
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-273 (1-1623)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db         16 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 75

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||     ::::::||||||
Db         76 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 135

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::|||||||:::::::::
Db        136 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 195
```

```
Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         196 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 255

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||            ::::::
Db         256 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 303

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db         304 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 363

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         364 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 423

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::            |||   ||||||
Db         424 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 480
```

RESULT 3
US-10-893-584-196
; Sequence 196, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-196

Alignment Scores:

Pred. No.:	7.11e-13	Length:	1807
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-196 (1-1807)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||          |||          |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                          :::           ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||            ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::            |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 4
US-10-893-584-168
; Sequence 168, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 168
; LENGTH: 1810
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-168

Alignment Scores:

Pred. No.:	7.13e-13	Length:	1810
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-168 (1-1810)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||          |||          |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                          :::           ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||            ::::::
```

```
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 5
US-10-893-584-245
; Sequence 245, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
;   LENGTH: 1813
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-245

Alignment Scores:
Pred. No.:              7.14e-13        Length:         1813
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-245 (1-1813)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||            ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 6
US-10-893-584-238
; Sequence 238, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
;   LENGTH: 1819
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-238

Alignment Scores:
Pred. No.:              7.17e-13        Length:         1819
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-238 (1-1819)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||            ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474
```

```
Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||       |||       |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 7
US-10-893-584-175
; Sequence 175, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-175

Alignment Scores:
Pred. No.:              7.19e-13        Length:         1822
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-175 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||       ::::::|||       |||         |||       ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||       |||       |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 8
US-10-893-584-182
; Sequence 182, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-182

Alignment Scores:
Pred. No.:              7.19e-13        Length:         1822
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-182 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||       ::::::|||       |||         |||       ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||       |||       |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
```

```
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 9
US-10-893-584-231
; Sequence 231, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 231
;   LENGTH: 1825
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-231

Alignment Scores:
Pred. No.:              7.2e-13       Length:          1825
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-231 (1-1825)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||       |||       |||       |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 10
US-10-893-584-210
; Sequence 210, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
;   LENGTH: 1828
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-210

Alignment Scores:
Pred. No.:              7.22e-13      Length:          1828
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-210 (1-1828)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||       |||       |||       |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 11
US-10-893-584-161
; Sequence 161, Application US/10893584
; Publication No. US20050272048A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 161
;   LENGTH: 1831
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-161

Alignment Scores:
Pred. No.:                7.23e-13        Length:          1831
Score:                    169.00          Matches:         51
Percent Similarity:       52.2%           Conservative:    32
Best Local Similarity:    32.1%           Mismatches:      60
Query Match:              22.0%           Indels:          16
DB:                       8               Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-161 (1-1831)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 12
US-10-893-584-203
; Sequence 203, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
;   LENGTH: 1831
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-203

Alignment Scores:
Pred. No.:                7.23e-13        Length:          1831
Score:                    169.00          Matches:         51
Percent Similarity:       52.2%           Conservative:    32
Best Local Similarity:    32.1%           Mismatches:      60
Query Match:              22.0%           Indels:          16
DB:                       8               Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-203 (1-1831)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 13
US-10-893-584-154
; Sequence 154, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
```

```
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
;   LENGTH: 1834
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-154

Alignment Scores:
Pred. No.:              7.25e-13      Length:         1834
Score:                  169.00        Matches:        51
Percent Similarity:     52.2%         Conservative:   32
Best Local Similarity:  32.1%         Mismatches:     60
Query Match:            22.0%         Indels:         16
DB:                     8             Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-154 (1-1834)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||      |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 14
US-10-893-584-266
; Sequence 266, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-266

Alignment Scores:
Pred. No.:              7.26e-13      Length:         1837
Score:                  169.00        Matches:        51
Percent Similarity:     52.2%         Conservative:   32
Best Local Similarity:  32.1%         Mismatches:     60
Query Match:            22.0%         Indels:         16
DB:                     8             Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-266 (1-1837)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||      |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 15
US-10-893-584-259
; Sequence 259, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
```

```
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 259
;   LENGTH: 1843
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-259

Alignment Scores:
Pred. No.:              7.29e-13        Length:         1843
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-259 (1-1843)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::          ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 16
US-10-893-584-252
; Sequence 252, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 252
;   LENGTH: 1849
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-252

Alignment Scores:
Pred. No.:              7.32e-13        Length:         1849
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-252 (1-1849)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::          ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 17
US-10-893-584-147
; Sequence 147, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 147
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-147

Alignment Scores:
Pred. No.:              7.35e-13        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-147 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 18
US-10-893-584-189
; Sequence 189, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-189

Alignment Scores:
Pred. No.:              7.35e-13        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-189 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 19
US-10-893-584-217
; Sequence 217, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-217
```

```
Alignment Scores:
Pred. No.:              7.35e-13        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-217 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||                  ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 20
US-10-893-584-224
; Sequence 224, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-224

Alignment Scores:
Pred. No.:              7.35e-13        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-224 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||                  ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 21
US-10-893-584-3
; Sequence 3, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Cathepsin B linker regions of pAP-214
US-10-893-584-3

Alignment Scores:
Pred. No.:              1.4e-12         Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
```

```
Best Local Similarity:  32.1%          Mismatches:    61
Query Match:            21.7%          Indels:        16
DB:                     8              Gaps:          6

US-10-758-902-9 (1-149) x US-10-893-584-3 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||      |||      |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 22
US-10-893-584-5
; Sequence 5, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-216 insert
US-10-893-584-5

Alignment Scores:
Pred. No.:              1.4e-12        Length:        1855
Score:                  167.00         Matches:       51
Percent Similarity:     51.6%          Conservative:  31
Best Local Similarity:  32.1%          Mismatches:    61
Query Match:            21.7%          Indels:        16
DB:                     8              Gaps:          6

US-10-758-902-9 (1-149) x US-10-893-584-5 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||      |||      |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 23
US-10-893-584-7
; Sequence 7, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-218 insert
US-10-893-584-7

Alignment Scores:
Pred. No.:              1.4e-12        Length:        1855
Score:                  167.00         Matches:       51
Percent Similarity:     51.6%          Conservative:  31
Best Local Similarity:  32.1%          Mismatches:    61
Query Match:            21.7%          Indels:        16
```

```
DB:                 8             Gaps:          6

US-10-758-902-9 (1-149) x US-10-893-584-7 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||       :::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||       |||       |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||:::|||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||           |||           |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 24
US-10-893-584-9
; Sequence 9, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-220 insert
US-10-893-584-9

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-9 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||       :::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||       |||       |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||:::|||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||           |||           |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 25
US-10-893-584-13
; Sequence 13, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-224 insert
US-10-893-584-13

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6
```

US-10-758-902-9 (1-149) x US-10-893-584-13 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 26
US-10-893-584-15
; Sequence 15, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-226 insert
US-10-893-584-15

Alignment Scores:

Pred. No.:	1.4e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-15 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::|||||||:::|||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 27
US-10-893-584-17
; Sequence 17, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-228 insert
US-10-893-584-17

Alignment Scores:

Pred. No.:	1.4e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-17 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::|||||:::|||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||  |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 28
US-10-893-584-19
; Sequence 19, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-230 insert
US-10-893-584-19

Alignment Scores:

Pred. No.:	1.4e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-19 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::|||||:::|||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||  |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 29
US-10-893-584-21
; Sequence 21, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-232 insert
US-10-893-584-21

Alignment Scores:

Pred. No.:	1.4e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-21 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
```

```
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 30
US-10-893-584-23
; Sequence 23, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-234 insert
US-10-893-584-23

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-23 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 31
US-10-893-584-25
; Sequence 25, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-236 insert
US-10-893-584-25

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-25 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186
```

```
Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||         :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                     :::   |||   |||                  ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||          |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
               ||||||   :::|||   |||::::::          |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 32
US-10-893-584-27
; Sequence 27, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-238 insert
US-10-893-584-27

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-27 (1-1855)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||            |||           |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||         :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                     :::   |||   |||                  ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||          |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
               ||||||   :::|||   |||::::::          |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 33
US-10-893-584-29
; Sequence 29, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-240 insert
US-10-893-584-29

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-29 (1-1855)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||            |||           |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||         :::||||||
```

```
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::               :::::::::::::::::::::::::::::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 34
US-10-893-584-31
; Sequence 31, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-242 insert
US-10-893-584-31

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-31 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::               :::::::::::::::::::::::::::::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 35
US-10-893-584-33
; Sequence 33, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-244 insert
US-10-893-584-33

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-33 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246
```

```
Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||           |||           |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 36
US-10-893-584-35
; Sequence 35, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-246 insert
US-10-893-584-35

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-35 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||   :   ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                 :::   :::|||       |||       |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||           |||           |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 37
US-10-893-584-37
; Sequence 37, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pPA-248 insert
US-10-893-584-37

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-37 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||   :   ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                 :::   :::|||       |||       |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           ::::::||||||:::||||||:::::::::
```

```
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                         :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 38
US-10-893-584-39
; Sequence 39, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-250 insert
US-10-893-584-39

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-39 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                         :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 39
US-10-893-584-48
; Sequence 48, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-254 insert
US-10-893-584-48

Alignment Scores:
Pred. No.:              1.4e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-48 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306
```

```
Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||           ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
               ||||||   :::|||   |||::::::             |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 40
US-10-893-584-50
; Sequence 50, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-258 insert
US-10-893-584-50

Alignment Scores:
Pred. No.:              1.4e-12        Length:         1855
Score:                  167.00         Matches:        51
Percent Similarity:     51.6%          Conservative:   31
Best Local Similarity:  32.1%          Mismatches:     61
Query Match:            21.7%          Indels:         16
DB:                     8              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-50 (1-1855)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||           |||           |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||         :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                      :::           ::::::||||||:::||||||::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||           ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
               ||||||   :::|||   |||::::::             |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

Search completed: February 20, 2006, 01:03:13
Job time : 447.67 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:12:50 ; Search time 5243.3 Seconds
(without alignments)
1329.558 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160802_3709/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10758902_@CGN_1_1_10172_@runat_17022006_160802_3709 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	386	50.3	1021	2	BE036639	BE036639 MP03B03 M
2	372	48.4	667	6	CA838446	CA838446 MCT016F04
3	372	48.4	678	6	CA840373	CA840373 MCT036G03
4	372	48.4	698	6	CA838926	CA838926 MCT021H09
5	361	47.0	811	2	BE034055	BE034055 MG04C05 M
6	346.5	45.1	837	1	AW053634	AW053634 L30-1401T
7	345	44.9	644	6	CA838401	CA838401 MCT016B04
8	304	39.6	672	1	AW053585	AW053585 L30-2143T
9	269	35.0	1038	2	BE033546	BE033546 MF03A09 M
10	244.5	31.8	603	5	BQ590856	BQ590856 E012599-0
11	206	26.8	1033	2	BE036541	BE036541 MP01B07 M
12	202.5	26.4	546	5	BQ588856	BQ588856 E012534-0
13	201	26.2	506	1	AI043519	AI043519 L30-519T3
14	181	23.6	658	5	BQ583480	BQ583480 E011979-0
15	172	22.4	611	5	BQ490182	BQ490182 34-E9435-
16	156	20.3	621	7	CV052755	CV052755 EST 12203
17	153	19.9	504	5	BQ594182	BQ594182 E012758-0
18	150.5	19.6	494	7	CN600715	CN600715 EG-F01_00
c 19	145.5	18.9	993	2	BE035039	BE035039 MM02A03 M
20	145	18.9	829	7	CN782289	CN782289 EST00385
21	143.5	18.7	472	8	DN953953	DN953953 it66g11.g
22	140.5	18.3	841	7	CO121195	CO121195 GR__Eb02E
23	140.5	18.3	903	7	CO103587	CO103587 GR__Eb003
24	138.5	18.0	661	6	CA835532	CA835532 MCS038A11
25	138.5	18.0	689	6	CA833333	CA833333 MCS021A09
26	138.5	18.0	689	6	CA833383	CA833383 MCS021F04
27	134	17.4	661	6	CF227046	CF227046 IH202 sub
28	134	17.4	662	6	CF227047	CF227047 IH215 sub
29	131.5	17.1	639	6	CA835855	CA835855 MCS004G12
30	128.5	16.7	671	7	CN846973	CN846973 PG07022B0
31	128	16.7	665	6	CF227084	CF227084 IHSLP22 s
32	124.5	16.2	669	7	CN848288	CN848288 PG07019B0
33	118.5	15.4	649	6	CA838757	CA838757 MCT020B02
34	118.5	15.4	649	6	CA839330	CA839330 MCT026C11
35	118.5	15.4	671	6	CA839511	CA839511 MCT028D04
36	116.5	15.2	672	8	CX175757	CX175757 G06_69-68
37	115	15.0	502	7	CF974701	CF974701 PSU_weup3
38	114	14.8	560	7	CF974192	CF974192 PSU_meup2
39	111.5	14.5	644	8	DN501509	DN501509 UR108TF08
40	109.5	14.3	491	8	DN142823	DN142823 5054_D09_
41	109.5	14.3	503	8	DN142727	DN142727 5053_C01_
42	109.5	14.3	648	1	AJ645897	AJ645897 AJ645897
43	109.5	14.3	660	7	CK113535	CK113535 UR108TF08
44	104	13.5	267	1	AA856221	AA856221 L30-242T3
45	103	13.4	716	1	AJ716669	AJ716669 AJ716669
46	100	13.0	489	2	BE130330	BE130330 L48-484T3
47	97.5	12.7	875	2	BG369793	BG369793 HVSMEi002
48	96	12.5	414	7	CN848216	CN848216 PG07009B0
49	96	12.5	498	5	BQ588134	BQ588134 E012337-0
50	96	12.5	555	6	CF649484	CF649484 3530_1_70
51	96	12.5	824	8	DR820041	DR820041 ZM_BFb005
52	96	12.5	889	8	DR829642	DR829642 ZM_BFb007
53	95.5	12.4	459	2	BE422496	BE422496 WHE0056_E
54	95.5	12.4	499	2	BG366828	BG366828 HVSMEi000
55	94.5	12.3	500	2	BG366751	BG366751 HVSMEi000
56	94.5	12.3	555	2	BG368381	BG368381 HVSMEi001
57	94.5	12.3	567	5	BQ755834	BQ755834 EBed07_SQ
58	94.5	12.3	602	2	BG368548	BG368548 HVSMEi001
59	94.5	12.3	617	2	BG368487	BG368487 HVSMEi001
60	94.5	12.3	665	3	BM441651	BM441651 EBed07_SQ
61	94.5	12.3	713	2	BG367523	BG367523 HVSMEi001
62	94.5	12.3	757	2	BE193626	BE193626 HVSMEh008
63	94.5	12.3	775	2	BG368290	BG368290 HVSMEi001
64	94.5	12.3	802	2	BG368986	BG368986 HVSMEi002
65	94.5	12.3	804	2	BG366929	BG366929 HVSMEi000
66	94.5	12.3	817	2	BG369108	BG369108 HVSMEi002
67	94.5	12.3	839	2	BE195528	BE195528 HVSMEh008
68	94.5	12.3	890	2	BG369007	BG369007 HVSMEi002
69	94.5	12.3	913	2	BE195990	BE195990 HVSMEh009
70	94.5	12.3	1014	3	BI947737	BI947737 HVSMEl000
71	94.5	12.3	1104	3	BI957852	BI957852 HVSMEn001
72	94	12.2	575	5	BQ471219	BQ471219 HV01J21T
73	93.5	12.2	492	5	BQ755729	BQ755729 EBed07_SQ
74	93.5	12.2	552	2	BG367753	BG367753 HVSMEi001
75	93.5	12.2	601	6	CD913194	CD913194 G550.117C
76	92.5	12.0	520	6	CD909306	CD909306 G468.112F
77	92.5	12.0	544	2	BE424607	BE424607 WHE0085_G
78	92.5	12.0	551	6	CD912264	CD912264 G550.113M
79	92.5	12.0	600	6	CD909654	CD909654 G468.113D
80	92	12.0	554	5	CA025172	CA025172 HZ51G16r

	81	92	12.0	634	5	CA018466	CA018466 HV08L09r
	82	92	12.0	635	1	AV933468	AV933468 AV933468
	83	92	12.0	638	3	BJ469278	BJ469278 BJ469278
	84	92	12.0	646	5	BQ472125	BQ472125 HV04H17r
	85	92	12.0	752	7	CV159416	CV159416 SCARABAEU
	86	92	12.0	752	7	CV159446	CV159446 SCARABAEU
	87	90.5	11.8	412	5	BQ488744	BQ488744 01-E8455-
	88	90.5	11.8	1119	7	CK209315	CK209315 FGAS02107
	89	89.5	11.7	646	5	BQ739798	BQ739798 HB03D06 H
	90	89.5	11.7	646	5	BQ739823	BQ739823 HB03D12 H
	91	89.5	11.7	646	5	BQ740218	BQ740218 HC114H06
	92	88.5	11.5	505	3	BI947482	BI947482 HVSMEl000
	93	88	11.5	560	1	AV912821	AV912821 AV912821
c	94	87.5	11.4	534	11	TA86F03P	AL462033 T. brucei
c	95	87.5	11.4	742	6	CD916444	CD916444 G608.001M
	96	86.5	11.3	435	2	BE424802	BE424802 WHE0090_G
c	97	86	11.2	422	6	CF227044	CF227044 IH198 sub
	98	86	11.2	686	9	BZ669202	BZ669202 PUBBV50TD
	99	85.5	11.1	818	2	BG299694	BG299694 HVSMEa002
c	100	85	11.1	796	10	CZ292876	CZ292876 cp83g12.r

ALIGNMENTS

RESULT 1
BE036639
LOCUS BE036639 1021 bp mRNA linear EST 07-JUN-2000
DEFINITION MP03B03 MP Mesembryanthemum crystallinum cDNA 5' similar to ribosome-inactivating protein gelonin, mRNA sequence.
ACCESSION BE036639
VERSION BE036639.1 GI:8331648
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 1021)
AUTHORS Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
TITLE Functional Genomics of Plant Stress Tolerance
JOURNAL Unpublished (2000)
COMMENT Contact: Michalowski,C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
An open reading frame exists.
Insert Length: 1 Std Error: 0.00.
FEATURES Location/Qualifiers
source 1. .1021
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"
ORIGIN

Alignment Scores:
Pred. No.: 1.09e-41 Length: 1021
Score: 386.00 Matches: 82
Percent Similarity: 70.1% Conservative: 21
Best Local Similarity: 55.8% Mismatches: 42
Query Match: 50.3% Indels: 2
DB: 2 Gaps: 2

US-10-758-902-9 (1-149) x BE036639 (1-1021)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||||||||   :::         |||   ||||||:::
Db        216 TACAACACCGTGACATTCAACCTCGCCCAACCCAACACATATTCCACATTCATGACATCT 275

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||   :::|||:::   ||||||      ||||||:::|||||||||      |||
Db        276 CTCCGAGCTCAACTCTCT---GGCACAACCGCATGTCAAATCCCCGTGACACGGTCAACC 332

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
                 |||   :::||||||||||||||||||:::   |||||||||:::||||||:::
Db        333 GCACCGGATCTCCAACGATTCGTCCTCGTCGACCTCAAAACAACCTCGCAAAAGACCATC 392

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              :::|||||||||||||||   ||||||||||||   |||:::||||||      |||
Db        393 ACACTCGCAATCGACGTGACAAGCGTCTATGTCGTGGCCTACCGCGACAAGCTTGGCGGA 452

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProPro 100
              ||||||||||||   ||||||          ||||||||||||   :::   ||||||
Db        453 AAAGACCGTGCCAACTTCCTTAGCGATGCTCCCACGGTCGCTAGGAACAACCTCTTCAAG 512

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              |||   |||   |||      :::   |||   |||||||||      |||      |||
Db        513 GGCGCGACGGTTCGG---AACATTGCGTTCGGAGGGAGTTACATAGCCTTAGAGAAGGCT 569

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||      |||      :::||||||||||||   ||||||||||||:::||||||
Db        570 GCAAAGCAAGGCCGAAATGCAATAGAGTTAGGGGTGAATAAACTAGAGTTTGCGATCGAG 629

Qy        141 AlaIleTrpGlyLysThrGln 147
              :::::::::|||:::|||:::
Db        630 TCGGTTTTTGGTAGAACCCGA 650
```

RESULT 2
CA838446
LOCUS CA838446 667 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT016F04_166823 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT016F04 5, mRNA sequence.
ACCESSION CA838446
VERSION CA838446.1 GI:26566211
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 667)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 016 row: F column: 04
Seq primer: T3 20mer
High quality sequence stop: 667.
FEATURES Location/Qualifiers
source 1. .667
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT016F04"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression

library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.:	4.99e-40	Length:	667
Score:	372.00	Matches:	83
Percent Similarity:	68.6%	Conservative:	22
Best Local Similarity:	54.2%	Mismatches:	40
Query Match:	48.4%	Indels:	8
DB:	6	Gaps:	4

US-10-758-902-9 (1-149) x CA838446 (1-667)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        200 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 259

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr------Leu 38
              |||:::   ||||||      ||||||      ||||||:::||||||||||
Db        260 CTCCAAACTGAACTATTCTCCGGCACAACCGCATGTCAAATCCCCGTGACACGGGCAACC 319

Qy         39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
                 |||   ::::::|||:::||||||||||||||||||:::   |||   |||:::|||
Db        320 GCAACCACATCCAATGACCAACGATTCGTCCTCGTCGACCTCGAAACACCCTCGCAAAAA 379

Qy         59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
              |||:::   :::|||||||||||||||||||||||||||||   |||:::||||||:::
Db        380 ACCATCACCCTCGCAATCGACGTGACAGACGTCTACGTCGTCGCCTATCGCGACAAGTTC 439

Qy         79 ---------AspGly------LysAspArgAlaValPheLeuAspLysValProThrVal 93
                      ||||||      ||||||||||||   ||||||              ||||||
Db        440 AAAGAAAAGGACGGACAAATGAAGGACCGTGCCAACTTCCTTCAAGATGCATCTACGGTT 499

Qy         94 AlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
              |||         ||||||   |||   |||   |||       |||   |||   |||:::
Db        500 GCGAAGGAGAATCTCTTTCATGGAGCAACAGTTCGG---AACCTTGCGTTCAAAGGGACT 556

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
              |||       |||   ||||||||          |||:::   :::||||||||||
Db        557 TACACATCCTTAGAGAATGCTGCAAACCAACGACGAGAAGCCATAGAGTTAGGGGTGGAT 616

Qy        134 LysLeuGluPheSerIleGluAlaIleTrpGlyLysThr 146
              ||||||||||||:::||||||:::::::::||||||||
Db        617 AAACTAGAGTTTGCGATCGAGTCGGTTTATGGTAAGACA 655
```

RESULT 3
CA840373
LOCUS CA840373 678 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT036G03_173841 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT036G03 5, mRNA sequence.
ACCESSION CA840373
VERSION CA840373.1 GI:26568138
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 678)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 036 row: G column: 03
Seq primer: T3 20mer
High quality sequence stop: 678.
FEATURES Location/Qualifiers
source 1. .678
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT036G03"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.:	5.11e-40	Length:	678
Score:	372.00	Matches:	83
Percent Similarity:	68.6%	Conservative:	22
Best Local Similarity:	54.2%	Mismatches:	40
Query Match:	48.4%	Indels:	8
DB:	6	Gaps:	4

US-10-758-902-9 (1-149) x CA840373 (1-678)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        202 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 261

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr------Leu 38
              |||:::   ||||||      ||||||      ||||||:::||||||||||
Db        262 CTCCAAACTGAACTATTCTCCGGCACAACCGCATGTCAAATCCCCGTGACACGGGCAACC 321

Qy         39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
                 |||   ::::::|||:::||||||||||||||||||:::   |||   |||:::|||
Db        322 GCAACCACATCCAATGACCAACGATTCGTCCTCGTCGACCTCGAAACACCCTCGCAAAAA 381

Qy         59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
              |||:::   :::|||||||||||||||||||||||||||||   |||:::||||||:::
Db        382 ACCATCACCCTCGCAATCGACGTGACAGACGTCTACGTCGTCGCCTATCGCGACAAGTTC 441

Qy         79 ---------AspGly------LysAspArgAlaValPheLeuAspLysValProThrVal 93
                      ||||||      ||||||||||||   ||||||              ||||||
Db        442 AAAGAAAAGGACGGACAAATGAAGGACCGTGCCAACTTCCTTCAAGATGCATCTACGGTT 501

Qy         94 AlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
              |||         ||||||   |||   |||   |||       |||   |||   |||:::
Db        502 GCGAAGGAGAATCTCTTTCATGGAGCAACAGTTCGG---AACCTTGCGTTCAAAGGGACT 558

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
              |||       |||   ||||||||          |||:::   :::||||||||||
Db        559 TACACATCCTTAGAGAATGCTGCAAACCAACGACGAGAAGCCATAGAGTTAGGGGTGGAT 618

Qy        134 LysLeuGluPheSerIleGluAlaIleTrpGlyLysThr 146
              ||||||||||||:::||||||:::::::::||||||||
Db        619 AAACTAGAGTTTGCGATCGAGTCGGTTTATGGTAAGACA 657
```

RESULT 4
CA838926
LOCUS CA838926 698 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT021H09_170947 Ice plant Lambda Uni-Zap XR expression library, 5

```
           days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
           (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT021H09 5,
           mRNA sequence.
ACCESSION  CA838926
VERSION    CA838926.1  GI:26566691
KEYWORDS   EST.
SOURCE     Mesembryanthemum crystallinum (common iceplant)
  ORGANISM Mesembryanthemum crystallinum
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE  1  (bases 1 to 698)
  AUTHORS  Cushman, J.C.
  TITLE    An expressed sequence tag database for the common ice plant,
           Mesembryanthemum crystallinum
  JOURNAL  Unpublished (1997)
COMMENT    Contact: Cushman JC
           Department of Biochemistry
           University of Nevada
           MS200, Reno, NV 89557-0014, USA
           Tel: 775-784-1918
           Fax: 775-784-1650
           Email: jcushman@unr.edu
           PCR PRimers
           FORWARD: T3 20mer
           BACKWARD: T7 21mer
           Plate: 021  row: H  column: 09
           Seq primer: T3 20mer
           High quality sequence stop: 698.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCT021H09"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase IV (5:30 PM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.:              5.32e-40        Length:         698
Score:                  372.00          Matches:        83
Percent Similarity:     68.6%           Conservative:   22
Best Local Similarity:  54.2%           Mismatches:     40
Query Match:            48.4%           Indels:         8
DB:                     6               Gaps:           4

US-10-758-902-9 (1-149) x CA838926 (1-698)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||||||||||||:::|||:::|||   ::::::      |||       ||||||   |||
Db        197 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 256

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr------Leu 38
              |||:::   ||||||      ||||||      ||||||:::|||||||||
Db        257 CTCCAAACTGAACTATTCTCCGGCACAACCGCATGTCAAATCCCCGTGACACGGGCAACC 316

Qy         39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
                 |||   ::::::|||:::|||||||||||||||||||:::   |||   |||:::|||
Db        317 GCAACCACATCCAATGACCAACGATTCGTCCTCGTCGACCTCGAAACACCCTCGCAAAAA 376

Qy         59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
              |||:::   :::|||||||||||||||||||||||||||||   |||:::||||||:::
Db        377 ACCATCACCCTCGCAATCGACGTGACAGACGTCTACGTCGTCGCCTATCGCGACAAGTTC 436

Qy         79 ---------AspGly------LysAspArgAlaValPheLeuAspLysValProThrVal 93
```

```
                    ||||||      ||||||||||||   ||||||           ||||||
Db        437 AAAGAAAAGGACGGACAAATGAAGGACCGTGCCAACTTCCTTCAAGATGCATCTACGGTT 496

Qy         94 AlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
              |||          ||||||  |||  |||  |||      |||  |||  ||:::
Db        497 GCGAAGGAGAATCTCTTTCATGGAGCAACAGTTCGG---AACCTTGCGTTCAAAGGGACT 553

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
              |||      |||  |||||||||          |||:::   :::||||||||||||
Db        554 TACACATCCTTAGAGAATGCTGCAAACCAACGACGAGAAGCCATAGAGTTAGGGGTGGAT 613

Qy        134 LysLeuGluPheSerIleGluAlaIleTrpGlyLysThr 146
              ||||||||||||:::||||||:::::::::|||||||||
Db        614 AAACTAGAGTTTGCGATCGAGTCGGTTTATGGTAAGACA 652
```

```
RESULT 5
BE034055
LOCUS       BE034055                811 bp    mRNA    linear   EST 07-JUN-2000
DEFINITION  MG04C05 MG Mesembryanthemum crystallinum cDNA 5' similar to
            ribosome-inactivating protein gelonin, mRNA sequence.
ACCESSION   BE034055
VERSION     BE034055.1  GI:8329064
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 811)
  AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
  TITLE     Functional Genomics of Plant Stress Tolerance
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Michalowski,C.B.
            University of Arizona
            Bio Sciences West room 513, Tucson, AZ 85721, USA
            Tel: 520-621-7982
            Fax: 520-621-1697
            Email: cbm@u.arizona.edu
            An open reading frame exists.
            Insert Length: 1   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .811
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /tissue_type="roots"
                     /dev_stage="5-6 weeks"
                     /clone_lib="MG"
                     /note="grown in hydroponics, stress 400 mM NaCl (in 0.5
                     Hoagland's), 30 h stress"
ORIGIN

Alignment Scores:
Pred. No.:              2.12e-38        Length:         811
Score:                  361.00          Matches:        81
Percent Similarity:     68.5%           Conservative:   19
Best Local Similarity:  55.5%           Mismatches:     43
Query Match:            47.0%           Indels:         3
DB:                     2               Gaps:           2

US-10-758-902-9 (1-149) x BE034055 (1-811)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||||||||||||:::|||||||||   :::          |||   ||||||:::
Db        243 TACAACACCGTGACATTCAACCTCGCCCAACCCAACACATATTCCACATTCATGACATCT 302

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||   :::|||:::   ||||||      ||||||:::|||||||||       |||
Db        303 CTCCGAGCTCAACTCTCT---GGCACAACCGCATGTCAAATCCCCGTGACACGGTCAACC 359

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
```

```
Db        360 GCACCGGATCTCCAACGATTCGTCCTCGTCGACCTCAAAACAACCTCGCAAAAGACCATC 419

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80

Db        420 ACACTCGCAATCGACGTGACAAGCGTCTATGTCGTGGCCTACCGCGACAAGCTTGGCGGA 479

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100

Db        480 AAAGACCGTGCCAACTTCCTTAGCGATGCTCCCACGGTCGCTAGGAACAACCTCTTCAAG 539

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120

Db        540 GGCGCGACGGTTCGG---AACATTGCGTTCGGAGGGAGTTACATAGCCCTAGAAAAAGCT 596

Qy        121 AlaLysValAspArgLysAspLeu-GluLeuGlyValTyrLysLeuGluPheSerIleGl 140

Db        597 GCAAAGCAAGGCCGAAATGCAATATGAGTTAGGGGTGAATTAACTAGAATTTGCGATCGA 656

Qy        140 uAlaIleTrpGlyLys 145

Db        657 ATCCGTTTTTGGGAAG 672
```

RESULT 6
AW053634
LOCUS AW053634 837 bp mRNA linear EST 20-FEB-2001
DEFINITION L30-1401T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-1401 5', mRNA sequence.
ACCESSION AW053634
VERSION AW053634.1 GI:5916827
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 837)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
Poly(A) tail, 10 nt: 838. .847
PCR PRimers
FORWARD: T7
BACKWARD: T3
Insert Length: 847 Std Error: 5.00
Plate: L30-15 row: A column: 5
Seq primer: T3
High quality sequence stop: 450.
FEATURES Location/Qualifiers
source 1. .837
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L30-1401"
/tissue_type="Leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.: 2.15e-36 Length: 837

Score:	346.50	Matches:	77
Percent Similarity:	68.6%	Conservative:	17
Best Local Similarity:	56.2%	Mismatches:	40
Query Match:	45.1%	Indels:	3
DB:	1	Gaps:	3

US-10-758-902-9 (1-149) x AW053634 (1-837)

```
Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGln 33

Db         11 TATTCCACATTCATGACATCTCTCCGAGCTCAACTCTCT---GGCACAACCGCATGTCAA 67

Qy         34 LeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr 53

Db         68 ATCCCCGTGACACGGTCAACCGCACCGGATCTCCAACGATTCGTCCTCGTCGACCTCAAA 127

Qy         54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73

Db        128 ACAACCTCGCAAAAGACCATCACACTCGCAATCGACGTGACAAGCGTCTATGTCGTGGCC 187

Qy         74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93

Db        188 TACCGCGACAAGCTTGGCGGAAAAGACCGTGCCAACTTCCTTAGCGATGCTCCCACGGTC 247

Qy         94 AlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113

Db        248 GCTAGGAACAACCTCTTCAAGGGCGCGACGGTTCGG---AACATTGCGTTCGGAGGGAGT 304

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133

Db        305 TACATAGCCTTAGAGAAGGCTGCAAAGCAAGGCCGAAATGCAATAGAGTTAGGGGTGAAT 364

Qy        134 LysLeuGluPheSerIleGluAlaIleTrpGlyLysThrGln---AsnGly 149

Db        365 AAACTAGAGTTTGCGATCGAGTCGGTTTTTGGTAAGAACCCGATTAATGGG 415
```

RESULT 7
CA838401
LOCUS CA838401 644 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT016B04_166733 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT016B04 5, mRNA sequence.
ACCESSION CA838401
VERSION CA838401.1 GI:26566166
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 644)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 016 row: B column: 04
Seq primer: T3 20mer
High quality sequence stop: 644.
FEATURES Location/Qualifiers
source 1. .644
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"

/db_xref="taxon:3544"
/clone="MCT016B04"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.:	2.39e-36	Length:	644
Score:	345.00	Matches:	79
Percent Similarity:	66.9%	Conservative:	20
Best Local Similarity:	53.4%	Mismatches:	41
Query Match:	44.9%	Indels:	8
DB:	6	Gaps:	4

US-10-758-902-9 (1-149) x CA838401 (1-644)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        202 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 261

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr------Leu 38
              |||:::  ||||||      ||||||      ||||||:::|||||||||
Db        262 CTCCAAACTGAACTATTCTCCGGCACAACCGCATGTCAAATCCCCGTGACACGGGCAACC 321

Qy         39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
                |||   ::::::|||:::||||||||||||||||||:::   |||   |||:::|||
Db        322 GCAACCACATCCAATGACCAACGATTCGTCCTCGTCGACCTCGAAACACCCTCGCAAAAA 381

Qy         59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
              |||:::   :::||||||||||||||||||||||||||||   |||:::||||||:::
Db        382 ACCATCACCCTCGCAATCGACGTGACAGACGTCTACGTCGTCGCCTATCGCGACAAGTTC 441

Qy         79 ---------AspGly------LysAspArgAlaValPheLeuAspLysValProThrVal 93
                      ||||||      ||||||||||||   ||||||           ||||||
Db        442 AAAGAAAAGGACGGACAAATGAAGGACCGTGCCAACTTCCTTCAAGATGCATCTACGGTT 501

Qy         94 AlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
              |||      ||||||   |||   |||   |||      |||   |||   |||:::
Db        502 GCGAAGGAGAATCTCTTTCATGGAGCAACAGTTCGG---AACCTTGCGTTCAAAGGGACT 558

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
              |||      |||   |||||||||         |||:::   :::||||||||||||
Db        559 TACACATCCTTAGAGAATGCTGCAAACCAACGACGAGAAGCCATAGAGTTAGGGGTGGAT 618

Qy        134 LysLeuGluPheSerIleGluAla 141
                |||||||||:::||||||:::
Db        619 ANACTAGAGTTTGCGATCGAGTCG 642
```

RESULT 8
AW053585

```
LOCUS       AW053585                672 bp    mRNA    linear   EST 20-FEB-2001
DEFINITION  L30-2143T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours
            NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-2143
            5', mRNA sequence.
ACCESSION   AW053585
VERSION     AW053585.1  GI:5916778
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T7
            BACKWARD: T3
            Plate: L30-22  row: D  column: 11
            Seq primer: T3
            High quality sequence stop: 450.
FEATURES             Location/Qualifiers
     source          1. .672
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="L30-2143"
                     /tissue_type="Leaf, 30 h 0.4M NaCl"
                     /dev_stage="Six week old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 30 hours NaCl treatment"
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
ORIGIN
```

Alignment Scores:

Pred. No.:	1.06e-30	Length:	672
Score:	304.00	Matches:	83
Percent Similarity:	66.2%	Conservative:	19
Best Local Similarity:	53.9%	Mismatches:	43
Query Match:	39.6%	Indels:	11
DB:	1	Gaps:	4

US-10-758-902-9 (1-149) x AW053585 (1-672)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        196 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 255

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr------Leu 38
              |||:::  ||||||      ||||||      ||||||:::|||||||||
Db        256 CTCCAAACTGAACTATTCTCCGGCACAACCGCATGTCAAATCCCCGTGACACGGGCAACC 315

Qy         39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
                |||   ::::::|||:::||||||||||||||||||:::   |||   |||:::|||
Db        316 GCAACCACATCCAATGACCAACGATTCGTCCTCGTCGACCTCGAAACACCCTCGCAAAAA 375

Qy         59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
              |||:::   :::||||||||||||||||||||||||||||   |||:::||||||:::
Db        376 ACCATCACCCTCGCAATCGACGTGACAGACGTCTACGTCGTCGCCTATCGCGACAAGTTC 435

Qy         79 ---------AspGly------LysAsp-ArgAlaValPheLeuAspLysValProThrVa 93
                      ||||||      |||||| ||||||   ||||||             |||
Db        436 AAAGAAAAGGACGGACAAATGAAGGACCCGTGCCAACTTCCTTCAAGATGCATCTACGGG 495

Qy         93 lAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySe 113
              |||      ||||||   |||   |||   |||      |||   |||   |||::
Db        496 TGCGAAGGAGAATCTCTTTTATGGAGCAACAGTTCGG---AACCTTGCGTTCAAAGGGAC 552

Qy        113 rTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTy 133
              :|||      |||   |||||||||         |||   |||   ||||||||||||||
Db        553 TTACACATCCTTAGAGAATGCTGCAACCAACGACGAGAAGCC-TTAGAGTTAGGGGTGGA 611

Qy        133 rLysLeuGluPheSerIleGluAlaIleTrpGlyLysThr 146
                |||||||||:::||||||::::::   |||||||||
Db        612 TAA-CTAGAATTTGCGATCGAGTCGGTTATTGGTAAGACA 650
```

RESULT 9
BE033546

```
LOCUS       BE033546                1038 bp    mRNA    linear   EST 07-JUN-2000
```

```
DEFINITION  MF03A09 MF Mesembryanthemum crystallinum cDNA 5' similar to
            ribosome-inactivating protein, mRNA sequence.
ACCESSION   BE033546
VERSION     BE033546.1  GI:8328555
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 1038)
  AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
  TITLE     Functional Genomics of Plant Stress Tolerance
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Michalowski,C.B.
            University of Arizona
            Bio Sciences West room 513, Tucson, AZ 85721, USA
            Tel: 520-621-7982
            Fax: 520-621-1697
            Email: cbm@u.arizona.edu
            An open reading frame exists.
FEATURES             Location/Qualifiers
     source          1. .1038
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /tissue_type="Root"
                     /dev_stage="5-6 weeks old"
                     /clone_lib="MF"
                     /note="Vector: Bluescript SK+; Site_1: EcorI; Site_2:
                     XhoI"
ORIGIN

Alignment Scores:
Pred. No.:                1.23e-25        Length:          1038
Score:                    269.00          Matches:         62
Percent Similarity:       70.4%           Conservative:    14
Best Local Similarity:    57.4%           Mismatches:      29
Query Match:              35.0%           Indels:          3
DB:                       2               Gaps:            2

US-10-758-902-9 (1-149) x BE033546 (1-1038)

Qy          44 AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAla 63
               |||:::|||||||||||||||||||:::   |||||||||:::||||||:::   :::|||
Db          67 GACCAACGATTCGTCCTCGTCGACCTCAAAACAACCTCGCAAAAGACCATCACACTCGCA 126

Qy          64 IleAspValThrAsp-ValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspAr 83
               |||   ||||||::: ||||||||||||   |||:::||||||      ||||||||||
Db         127 ATCGGCGTGACAGAGCGTCTATGTCGTGGCCTACCGCGACAAGCTTGGCGGAAAAGACCG 186

Qy          83 gAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyValTh 103
               ||||   ||||||         ||||||||||||   :::   ||||||   |||   ||
Db         187 TGCCAACTTCCTTAGCGATGCTCCCACGGTCGCTAGGAACAACCTCTTCAAGGGCGCGAC 246

Qy         103 rAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysVa 123
               |   |||      :::   |||   |||||||||      |||      |||||||||
Db         247 GGTTCGG---AACATTGCGTTCGGAGGGAGTTACATAGCCTTAGAGAAGGCTGCAAAGCA 303

Qy         123 lAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTr 143
               |||      :::||||||||||||   ||||||||||||:::||||||:::::::
Db         304 AGGCCGAAATGCAATAGAGTTAGGGGTGAATAAACTAGAGTTCGCGATCGAGTCGGTTTT 363

Qy         143 pGlyLysThrGln---AsnGly 149
               :||||||         ||||||
Db         364 TGGTAAGAACCCGATTAATGGG 385

RESULT 10
BQ590856
LOCUS       BQ590856                603 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012599-024-018-N14-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-018-N14 5-PRIME, mRNA sequence.
ACCESSION   BQ590856
VERSION     BQ590856.1  GI:26120439
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 603)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  PUBMED    12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 603   Std Error: 0.00
            Plate: 18  row: N  column: 14
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .603
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189267"
                     /db_xref="taxon:161934"
                     /clone="024-018-N14"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

Alignment Scores:
Pred. No.:                1.3e-22         Length:          603
Score:                    244.50          Matches:         55
Percent Similarity:       56.9%           Conservative:    27
Best Local Similarity:    38.2%           Mismatches:      59
Query Match:              31.8%           Indels:          3
DB:                       5               Gaps:            1

US-10-758-902-9 (1-149) x BQ590856 (1-603)

Qy            1 TyrAsnThrValSerPheAsnLeuGly---------GluAlaTyrGluTyrProThrPhe 17
                |||||||||||||||:::::|||                      ||||||   |||
Db          171 TACAACACTGTGTCATGGGACCTTTCACTTCCTGATCCTGTAAAATGCTATCCAAAATTC 230

Qy           18 IleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr 37
                :::      |||||||||:::::                :::|||   ||||||   |||
Db          231 TTGACGAGACTGCGAAATCAAGTGGAAGCTCCGATCAGGATCTGCGGCTTACCATCCACG 290

Qy           38 LeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLys 57
                           :::   :::   ::::::   ||||||:::      :::::::::
Db          291 CGACATGCTCCGTTAGAAGGCCAAGAATATATAACAGTGGACCTAAAGATTAGCAACAGA 350

Qy           58 LysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLys 77
```

```
                    |||   :::   |||||||||   |||:::||||||   ||||||||||||||||
Db        351 AATTGGGTGACCATAGGAATAGATGTCATAGATTTGTATGTATGGGGTTATCAAGACAAG 410

Qy         78 TrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys 97
              ::::::|||      |||:::   |||::::::   ||||||      |||   :::
Db        411 TTTAACGGGATACTTCGGTCCACTTTCGTTAATGACGTTCCCCAGGCTGCAAGGAACACC 470

Qy         98 LeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
              ||||||                ||| |||      |||  |||:::|||      |||
Db        471 CTTTTCCAAGATGCGGCAATTAGAAGAACAACTAATTTTGCAGGCAACTACGACAGTCTT 530

Qy        118 ValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPhe 137
                    |||:::   ||||||      |||||||||||||||   ||||||:::
Db        531 GAGCCATACGCTCGAACAGATAGAACAAGGCTTGAATTAGGTGTTGATAAGCTACAGGGT 590

Qy        138 SerIleGluAla 141
              :::|||   :::
Db        591 GCAATCAGAAGT 602

RESULT 11
BE036541
LOCUS       BE036541                1033 bp    mRNA    linear   EST 07-JUN-2000
DEFINITION  MP01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to
            antiviral protein, mRNA sequence.
ACCESSION   BE036541
VERSION     BE036541.1  GI:8331550
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 1033)
  AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
  TITLE     Functional Genomics of Plant Stress Tolerance
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Michalowski,C.B.
            University of Arizona
            Bio Sciences West room 513, Tucson, AZ 85721, USA
            Tel: 520-621-7982
            Fax: 520-621-1697
            Email: cbm@u.arizona.edu
            An open reading frame exists.
FEATURES             Location/Qualifiers
     source          1. .1033
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /tissue_type="apical meristem and leaf primordia"
                     /dev_stage="6 weeks"
                     /clone_lib="MP"
                     /note="3 d 500mM NaCl"
ORIGIN

Alignment Scores:
Pred. No.:              5.27e-17        Length:         1033
Score:                  206.00          Matches:        47
Percent Similarity:     65.1%           Conservative:   9
Best Local Similarity:  54.7%           Mismatches:     28
Query Match:            26.8%           Indels:         2
DB:                     2               Gaps:           2

US-10-758-902-9 (1-149) x BE036541 (1-1033)

Qy         65 AspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAla 84
              :::   |||   ||||||||||||   |||:::||||||      ||||||||||||||
Db         38 GAGGCGACAAGCGTCTATGTCGTGGCCTACCGCGACAAGCTTGGCGGAAAAGACCGTGCC 97

Qy         85 ValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyValThrAsn 104
              ||||||         ||||||||||||   :::   ||||||   |||   |||
Db         98 AACTTCCTTAGCGATGCTCCCACGGTCGCTAGGAACAACCTCTTCAAGGGCGCGACGGTT 157

Qy        105 ArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAsp 124
              |||      :::   |||   |||||||||      |||      |||||||||
Db        158 CGG---AACATTGCGTTCGGAGGGAGTTACATAGCCTTAGAGAAGGCTGCAAAGCAAGGC 214

Qy        125 ArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGly 144
              |||      :::||||||||||||   ||||||||||||:::||||||:::::::::|||
Db        215 CGAAATGCAATAGAGTTAGGGGTGAATAAACTAGAGTTTGCGATCGAGTCGGTTTTTGGT 274

Qy        145 LysThrGln---AsnGly 149
              |||          ||||||
Db        275 AAGAACCCGATTAATGGG 292

RESULT 12
BQ588856
LOCUS       BQ588856                546 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  EO12534-024-014-P10-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-014-P10 5-PRIME, mRNA sequence.
ACCESSION   BQ588856
VERSION     BQ588856.1  GI:26118439
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 546)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 546   Std Error: 0.00
            Plate: 14  row: P  column: 10
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .546
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:187113"
                     /db_xref="taxon:161934"
                     /clone="024-014-P10"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

Alignment Scores:
Pred. No.:              6.49e-17        Length:         546
Score:                  202.50          Matches:        44
Percent Similarity:     55.8%           Conservative:   23
Best Local Similarity:  36.7%           Mismatches:     50
Query Match:            26.4%           Indels:         3
```

```
DB:                 5             Gaps:          1

US-10-758-902-9 (1-149) x BQ588856 (1-546)

Qy          1 TyrAsnThrValSerPheAsnLeuGly---------GluAlaTyrGluTyrProThrPhe 17
              ||||||||||||||||:::::|||                          ||||||   |||
Db        183 TACAACACTGTGTCATGGGACCTTTCACTTCCTGATCCTGTAAAATGCTATCCAAAATTC 242

Qy         18 IleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr 37
              :::      ||||||||||::::::                 :::|||   ||||||   |||
Db        243 TTGACGAGACTGCGAAATCAAGTGGAAGCTCCGATCAGGATCTGCGGCTTACCATCCACG 302

Qy         38 LeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLys 57
                        :::   :::   ::::::   ||||||:::      :::::::::
Db        303 CGACATGCTCCGTTAGAAGGCCAAGAATATATAACAGTGGACCTAAAGATTAGCAACAGA 362

Qy         58 LysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLys 77
                 |||   :::   |||||||||   |||:::||||||   ||||||||||||||||
Db        363 AATTGGGTGACCATAGGAATAGATGTCATAGATTTGTATGTATGGGGTTATCAAGACAAG 422

Qy         78 TrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys 97
              ::::::|||      |||:::   |||::::::   ||||||      |||   :::
Db        423 TTTAACGGGATACTTCGGTCCACTTTCGTTAATGACGTTCCCCAGGCTGCAAGGAACACC 482

Qy         98 LeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
              ||||||                |||   |||       |||   |||:::|||      |||
Db        483 CTTTTCCAAGATGCGGCAATTAGAAGAACAACTAATTTTGCAGGCAACTACGACAGTCTT 542

RESULT 13
AI043519
LOCUS       AI043519                506 bp    mRNA    linear   EST 20-FEB-2001
DEFINITION  L30-519T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours
            NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-519 5',
            mRNA sequence.
ACCESSION   AI043519
VERSION     AI043519.1  GI:3290302
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T7
            BACKWARD: T3
            Plate: L30-6  row: C  column: 3
            Seq primer: T3
            High quality sequence stop: 310.
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="L30-519"
                     /tissue_type="Leaf, 30 h 0.4M NaCl"
                     /dev_stage="Six week old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 30 hours NaCl treatment"
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.:                9.37e-17      Length:          506
Score:                    201.00        Matches:         48
Percent Similarity:       66.3%         Conservative:    15
Best Local Similarity:    50.5%         Mismatches:      24
Query Match:              26.2%         Indels:          9
DB:                       1             Gaps:            2

US-10-758-902-9 (1-149) x AI043519 (1-506)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||:::|||:::|||   ::::::      |||      ||||||   |||
Db        199 TACAACACCGTGACATTCGACCTCGCCCAATCCGACACATATTCCAAGTTCATTGCCGAT 258

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr------Leu 38
              |||:::   ||||||      ||||||      ||||||:::|||||||||
Db        259 CTCCAAACTGAACTATTCTCCGGCACAACCGCATGTCAAATCCCCGTGACACGGGCAACC 318

Qy         39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
                 |||   ::::::|||:::|||||||||||||||||:::   |||   |||:::|||
Db        319 GCAACCACATCCAATGACCAACGATTCGTCCTCGTCGACCTCGAAACACCCTCGCAAAAA 378

Qy         59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
              |||:::   :::|||||||||||||||||||   |||   |||   |||:::|||   :::
Db        379 ACCATCAC-CTCGCAATCGACGTGACAGACTTCTACTTCGTCGCCTATCGCGACAATTTC 437

Qy         79 AspGly-----------------LysAspArgAlaValPheLeu 87
                                     ||||||||||||   ||||||
Db        438 AAAGAAAAAGGACGGGACAAATGAAAGGACCGTGCCAACTTCCTT 482

RESULT 14
BQ583480
LOCUS       BQ583480                658 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E011979-024-005-N05-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-005-N05 5-PRIME, mRNA sequence.
ACCESSION   BQ583480
VERSION     BQ583480.1  GI:26113057
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  PUBMED    12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 658   Std Error: 0.00
            Plate: 5  row: N  column: 05
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:183219"
                     /db_xref="taxon:161934"
                     /clone="024-005-N05"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
```

/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.:	7.48e-14	Length:	658
Score:	181.00	Matches:	52
Percent Similarity:	53.8%	Conservative:	26
Best Local Similarity:	35.9%	Mismatches:	61
Query Match:	23.6%	Indels:	6
DB:	5	Gaps:	5

US-10-758-902-9 (1-149) x BQ583480 (1-658)

```
Qy          1 TyrAsnThrValSerPheAsnLeu---GlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||   |||   :::::::::|||   |||             |||      |||:::
Db        154 TACGCTACTGAAACATACGACCTGAGCGGCGGTACAAAAGGCTACTCTCAATTCTTGACA 213

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGln 39
              :::||||||   :::|||   :::   |||      |||   :::|||||||||
Db        214 AATTTACGCAAAAAATTG---GAAGCAACAAAGGCTTGCAACATGCCAGTGACGCGAGCA 270
                          ;

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
                 :::                 :::||||||||||||:::      |||      :::
Db        271 AACTTACCAGCAGGCGCGGAATATGTTTTAGTGGATCTCAAAGTTACCCCAGTACAATAT 330

Qy         60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp 79
              |||   :::||||||   |||   :::||||||:::|||   |||      :::
Db        331 GTCACCTTAGCTATAAGAGTTAATAATGTGTATCTGGTGGCTTAT------CGTGTTGGC 384

Qy         80 GlyLysAspArgAlaValPheLeuAspLysValPro---ThrValAlaThrSerLysLeu 98
              ||||||   :::      ||||||::::::        |||   |||   |||||||||
Db        385 GGCAAAACTCAAGGCACATTCCTTAATGAGCCAGATGTTACATTTGCCAGGTCTAAGCTT 444

Qy         99 PheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuVal 118
              |||            |||:::   ||||||   :::|||   :::|||         :::
Db        445 TTTGATAAGAATGATAATCAACCAACACTTCGATATGACAGCAACTACGCTAAT---ATA 501

Qy        119 AsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSer 138
                 |||              ||||||||||   ||||||:::   :::|||
Db        502 GAGGCGGTGGGTGGCTCCAGGAAGGACCTTCTCTTGGGGCTTCAGGAATTACGGAAGAGA 561

Qy        139 IleGluAlaIleTrp 143
              |||   |||   :::
Db        562 ATTGTAGCCTTCTTT 576
```

RESULT 15
BQ490182
LOCUS BQ490182 611 bp mRNA linear EST 07-JUN-2002
DEFINITION 34-E9435-006-010-C10-T3 Sugar beet MPIZ-ADIS-006 Lambda Zap II library Beta vulgaris cDNA clone C-10-10, mRNA sequence.
ACCESSION BQ490182
VERSION BQ490182.1 GI:21334802
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 611)
AUTHORS Bellin,D., Werber,M., Theis,T., Weisshaar,B. and Schneider,K.
TITLE EST sequencing, annotation and macroarray expression analysis of more than 3000 sugar beet cDNAs identifies genes with root-specific expression pattern
JOURNAL Unpublished (2002)

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Seq primer: T3 'AATTAACCCTCACTAAAGGG'
High quality sequence stop: 611.
FEATURES Location/Qualifiers
source 1. .611
/organism="Beta vulgaris"
/mol_type="mRNA"
/db_xref="taxon:161934"
/clone="C-10-10"
/dev_stage="4 week old pot-grown plants"
/clone_lib="Sugar beet MPIZ-ADIS-006 Lambda Zap II library"
/note="Organ: shoot and root; Vector: pBluescript SK- from lambda ZAP II; cDNA (lambda ZAP-II) library from sugar beet, whole plant mRNA, Prepared using the Stratagene UniZAP cDNA kit, cloning sites EcoRI-XhoI, primer sites and orientation:
rev-T3-SacI-SK-EcoRI-GGCACGAGG-5pr-cDNA-polyA-XhoI-KpnI-T7-uni"
ORIGIN

Alignment Scores:

Pred. No.:	1.15e-12	Length:	611
Score:	172.00	Matches:	49
Percent Similarity:	54.0%	Conservative:	25
Best Local Similarity:	35.8%	Mismatches:	57
Query Match:	22.4%	Indels:	6
DB:	5	Gaps:	5

US-10-758-902-9 (1-149) x BQ490182 (1-611)

```
Qy          1 TyrAsnThrValSerPheAsnLeu---GlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||   |||   :::::::::|||   |||             |||      |||:::
Db        209 TACGCTACTGAAACATACGACCTGAGCGGCGGTACAAAAGGCTACTCTCAATTCTTGACA 268

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGln 39
              :::||||||   :::|||   :::   |||      |||   :::|||||||||
Db        269 AATTTACGCAAAAAATTG---GAAGCAACAAAGGCTTGCAACATGCCAGTGACGCGAGCA 325

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
                 :::                 :::||||||||||||:::      |||      :::
Db        326 AACTTACCAGCAGGCGCGGAATATGTTTTAGTGGATCTCAAAGTTACCCCAGTACAATAT 385

Qy         60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp 79
              |||   :::||||||   |||   :::||||||:::|||   |||      :::
Db        386 GTCACCTTAGCTATAAGAGTTAATAATGTGTATCTGGTGGCTTAT------CGTGTTGGC 439

Qy         80 GlyLysAspArgAlaValPheLeuAspLysValPro---ThrValAlaThrSerLysLeu 98
              ||||||   :::      ||||||::::::        |||   |||   |||||||||
Db        440 GGCAAAACTCAAGGCACATTCCTTAATGAGCCAGATGTTACATTTGCCAGGTCTAAGCTT 499

Qy         99 PheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuVal 118
              |||            |||:::   ||||||   :::|||   :::|||         :::
Db        500 TTTGATAAGAATGATAATCAACCAACACTTCGATATGACAGCAACTACGCTAAT---ATA 556

Qy        119 AsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
                 |||              |||||||||   ||||||:::   :::|||
Db        557 GAGGCGGTGGGTGGCTCCAGTAAGGACCTTCTCTTGGGGCTTCAGGAATTA 607
```

RESULT 16
CV052755
LOCUS CV052755 621 bp mRNA linear EST 24-AUG-2004
DEFINITION EST 12203 Half-Ripe Apricot Fruit Lambda Zap II Library Prunus armeniaca cDNA clone bge017c17q 5', mRNA sequence.
ACCESSION CV052755
VERSION CV052755.1 GI:51515776
KEYWORDS EST.
SOURCE Prunus armeniaca (apricot)

```
  ORGANISM  Prunus armeniaca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Grimplet,J., Romieu,C., Audergon,J.M., Albagnac,G., Lambert,P.,
            Bouchet,J.P. and Terrier,N.
  TITLE     High Throughput Detection of Isogenes among 5724 3' EST from
            Apricot Fruit(Prunus armeniaca)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Audergon JM
            Unite de genetique et amelioration des fruits et legumes
            Institut National de la Recherche Agronomique
            Domaine Saint-Maurice BP 94 84143 Montfavet cedex
            Tel: 00-33-(0)4-32-72-26-68
            Fax: 00-33-(0)4-32-72-26-62
            Email: audergon@avignon.inra.fr
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Prunus armeniaca"
                     /mol_type="mRNA"
                     /cultivar="Bergeron"
                     /db_xref="taxon:36596"
                     /clone="bge017c17q"
                     /dev_stage="Half-Ripe stage"
                     /clone_lib="Half-Ripe Apricot Fruit Lambda Zap II Library"
                     /note="Organ: Fruit; Vector: Lambda Zap II; Site_1: Eco
                     RI; Site_2: XhoI; Oriented library, construction described
                     in Molecular cloning and expression of a cDNA encoding
                     1-aminocyclopropane-1-carboxylate (ACC) oxidase from
                     apricot fruit (Prunus armeniaca cv. Bergeron) by
                     Mbeguie-Mbeguie D, Chahine H, Gomez RM, Gouble B, Audergon
                     JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant
                     105:294-303 1999"
ORIGIN

Alignment Scores:
Pred. No.:                1.84e-10        Length:          621
Score:                    156.00          Matches:         44
Percent Similarity:       52.5%           Conservative:    18
Best Local Similarity:    37.3%           Mismatches:      42
Query Match:              20.3%           Indels:          14
DB:                       7               Gaps:            6

US-10-758-902-9 (1-149) x CV052755 (1-621)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              :::|||      ||||||:::  ||||||      |||      |||
Db         95 AAATACCGCGACTTCATAGAATCTCTTCGACAGCGACTCACAGCAGGACGATCCACATCA 154

Qy         33 Gln---LeuProVal------ThrLeuGlnThrIleAlaAspAspLysArgPheValLeu 49
                 :::||||||            :::   :::   |||   :::|||||:::|||
Db        155 CACGGTATACCGGTGCTGCCTCGAAGAGAAGATGTGCCGGACGCACAGCGCTTTCTTCTT 214

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              ||||||:::|||   :::         |||:::::::::|||||||||||   :::
Db        215 GTTGATCTCACAAACTCTGGAAACAATACCATCAGGCTCGCAATCGATGTGGTGAACGCT 274

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeu------ 87
              ||||||||||||||||            ||||||      |||:::   ||||||
Db        275 TACGTGGTGGGTTATGCTGCA------GATGGC------CGATCCTACTTTCTTAAAGAA 322

Qy         88 ---------AspLysValProThrValAlaThrSerLysLeuProProGlyValThrAsn 104
                      :::      |||   :::   |||      ||||||          |||
Db        323 AATGCTCGTGAGAATCCGCCTCCAATCCACACC------TTGTTCCGCGACACCACTCGG 376

Qy        105 ArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLys 122
                 |||   |||||||||:::|||      |||      ||||||:::
Db        377 ATGCCTCCTCTGGACTTCGACGGCACCTACACCGGGCTTTCGCGAGCTGCGCAA 430

RESULT 17
BQ594182
```

```
LOCUS       BQ594182                504 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012758-024-025-I18-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-025-I18 5-PRIME, mRNA sequence.
ACCESSION   BQ594182
VERSION     BQ594182.1  GI:26123765
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 504   Std Error: 0.00
            Plate: 25  row: I  column: 18
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:192674"
                     /db_xref="taxon:161934"
                     /clone="024-025-I18"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

Alignment Scores:
Pred. No.:                3.54e-10        Length:          504
Score:                    153.00          Matches:         38
Percent Similarity:       58.8%           Conservative:    19
Best Local Similarity:    39.2%           Mismatches:      36
Query Match:              19.9%           Indels:          4
DB:                       5               Gaps:            3

US-10-758-902-9 (1-149) x BQ594182 (1-504)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---AlaTyrGluTyrProThrPheIleGln 19
              |||   |||||||||||:::|||   :::   |||      |||   ||||||:::
Db        212 TACCAAACTGTAAGTTTTGATCTCGAAGACGGTGCTTCTGGTTACTCAACATTCTTAACA 271

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGln 39
              :::||||||   :::                  |||   ||||||||||||
Db        272 AATTTGCGGCAGAAATTTGAAGGCCCCCTCAAGGCTTGCGGTTTACCAGTAACGCGAGAC 331

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
              |||:::               :::|||||||   |||:::     ::::::   :::
Db        332 ACCCTACCGAAAGGCGGCGAGTATGTACTTGCAGACCTCAAAATTAGCACCACAGAATGG 391
```

```
Qy          60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln------AspLys 77
               |||   ||||||:::   |||||||||:::|||:::|||   |||:::
Db         392 GTTACCGTAGCCTTAAAAGTCACAGATCTGTATTTGGTGGCTTACCGTGTTAACAAACTA 451

Qy          78 TrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAla 94
               :::  ||||||     |||:::||||||::::::   |||   ||||||
Db         452 TATAGTGGCAAGTATCACGCCATTTTTCTTAATGAG---CCAGACGTAGCT 499

RESULT 18
CN600715
LOCUS       CN600715                494 bp    mRNA    linear   EST 31-DEC-2004
DEFINITION  EG-F01_002_D10 Oil palm female inflorescence Lambda Zap Library
            Elaeis guineensis cDNA, mRNA sequence.
ACCESSION   CN600715
VERSION     CN600715.1  GI:56930055
KEYWORDS    EST.
SOURCE      Elaeis guineensis (African oil palm)
  ORGANISM  Elaeis guineensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoideae;
            Cocoeae; Elaeidinae; Elaeis.
REFERENCE   1  (bases 1 to 494)
  AUTHORS   Jouannic,S., Argout,X., Lechauve,F., Fizames,C., Borgel,A.,
            Morcillo,F., Aberlenc-Bertossi,F., Duval,Y. and Tregear,J.
  TITLE     Analysis of expressed sequence tags from oil palm (Elaeis
            guineensis)
  JOURNAL   FEBS Lett. 579 (12), 2709-2714 (2005)
   PUBMED   15862313
COMMENT     Contact: Jouannic S
            UMR1098
            Institut de Recherche pour le Developpement (IRD)
            911, avenue Agropolis, BP64501, F34394 Montpellier cedex 5, FRANCE
            Tel: 00 33 4 67 41 61 93
            Fax: 00 33 4 67 41 61 81
            Email: jouannic@mpl.ird.fr.
FEATURES             Location/Qualifiers
     source          1. .494
                     /organism="Elaeis guineensis"
                     /mol_type="mRNA"
                     /cultivar="tenera LMC17"
                     /db_xref="taxon:51953"
                     /dev_stage="20 cm long inflorescence"
                     /clone_lib="Oil palm female inflorescence Lambda Zap
                     Library"
                     /note="Organ: Female inflorescence; Vector: Lambda Zap;
                     Site_1: EcoRI; Site_2: XhoI; cDNA library constructed from
                     poly(A)+ RNAs using the ZAP-cDNA synthesis kit and the
                     ZAP-cDNA Gigapack(r) III Gold packaging extract
                     (Stratagen)."
ORIGIN

Alignment Scores:
Pred. No.:              7.58e-10        Length:         494
Score:                  150.50          Matches:        41
Percent Similarity:     53.0%           Conservative:   21
Best Local Similarity:  35.0%           Mismatches:     40
Query Match:            19.6%           Indels:         15
DB:                     7               Gaps:           5

US-10-758-902-9 (1-149) x CN600715 (1-494)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIle 18
               ||||||   |||   |||            |||   :::      |||      |||:::
Db         165 TACAACCTGGTGCGCTTCACCACCGTAAATGCCACTAAGGAAAGCTACGCGCAGTTTATG 224

Qy          19 GlnAspLeuArgAsnGluLeuAlaLys--------------GlyThrProValCysGln 33
               :::|||||||:::::|||||                  |||   ||||||  :::
Db         225 AAAGATCTGAGAGATCAATTGGCAAGTGGAGATGAGAGGCATGGAATACCAGTGTTACGT 284

Qy          34 LeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr 53
                  |||           |||:::   |||   :::||||||:::||||||:::::::::
Db         285 GATCCA---------TCCACAGTGCCCGATTCCCAGCGGTTTCTTTTGGTGGAACTCTCA 335

Qy          54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73
                     :::   :::|||   :::|||:::||||||   :::   |||||||||
Db         336 AATTGGGGGGAGGCATCCGTCACATTAGCAGTAGATGTCATCAATGCATATGTGGTGGCT 395

Qy          74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93
               ||||||              |||::::::   |||            |||   :::
Db         396 TATCAG------------GCGGGAGATCAGTCCTACTTCTTTNNAGATGCTCCGGACCTT 443

Qy          94 AlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPhe 110
               |||   |||   ||||||         |||             |||:::|||
Db         444 GCATTTTCTAATCTTTTCACAAAC---ACNNNGCNNNNNNNNCTTTCATTC 491

RESULT 19
BE035039/c
LOCUS       BE035039                993 bp    mRNA    linear   EST 07-JUN-2000
DEFINITION  MM02A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
            antiviral protein, mRNA sequence.
ACCESSION   BE035039
VERSION     BE035039.1  GI:8330048
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
  TITLE     Functional Genomics of Plant Stress Tolerance
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Michalowski,C.B.
            University of Arizona
            Bio Sciences West room 513, Tucson, AZ 85721, USA
            Tel: 520-621-7982
            Fax: 520-621-1697
            Email: cbm@u.arizona.edu
            Insert Length: 1   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /cell_type="epidermal bladder cells"
                     /dev_stage="12 weeks old"
                     /clone_lib="MM"
                     /note="Vector: Bluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Plants stessed 6 weeks in 500mM NaCl"
ORIGIN

Alignment Scores:
Pred. No.:              9.82e-09        Length:         993
Score:                  145.50          Matches:        34
Percent Similarity:     61.2%           Conservative:   7
Best Local Similarity:  50.7%           Mismatches:     25
Query Match:            18.9%           Indels:         1
DB:                     2               Gaps:           1

US-10-758-902-9 (1-149) x BE035039 (1-993)

Qy          79 AspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeu 98
               |||   ||||||||||||   ||||||         ||||||||||||
Db         796 GACAAGAAGGATCGAGCCAACTTCCTTAGCGATGCTCCTACAGTCGCTAAGAAAACCTTC 737

Qy          99 PheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuVal 118
               |||   |||   |||   |||      :::   |||   |||:::|||      |||
Db         736 TTTAAGGGAGCGACCGTTCGA---AACATTCCATTTGGTGGTAACTACATAGCTCTGGAG 680

Qy         119 AsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSer 138
               ||||||         |||      :::||||||||:::   ||||||||||||:::
Db         679 AAAGCTGCCGGTCAAGGACGAAACAGTATTGAGTTGGGGCTTGCTAAACTAGAGTTTGCC 620
```

```
Qy        139 IleGluAlaIleTrpGlyLys 145
              ||||||:::|||:::||||||
Db        619 ATCGAGTCGATTTATGGTAAA 599

RESULT 20
CN782289
LOCUS       CN782289                 829 bp    mRNA    linear   EST 21-MAY-2004
DEFINITION  EST00385 cqseed Chenopodium quinoa cDNA clone S02J22 5' similar to
            antiviral ribosome-inactivating protein CAP30B [Chenopodium album],
            mRNA sequence.
ACCESSION   CN782289
VERSION     CN782289.1  GI:47561753
KEYWORDS    EST.
SOURCE      Chenopodium quinoa (quinoa)
  ORGANISM  Chenopodium quinoa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Amaranthaceae; Chenopodium.
REFERENCE   1  (bases 1 to 829)
  AUTHORS   Coles,N.D., Coleman,C.E., Christensen,S.A., Jellen,E.N.,
            Stevens,M.R., Bonifacio,A., Rojas-Beltran,J.A., Fairbanks,D.J. and
            Maughan,P.J.
  TITLE     Development and use of an expressed sequenced tag library in quinoa
            (Chenopodium quinoa Willd.) for the discovery of single nucleotide
            polymorphisms
  JOURNAL   Plant Sci. 168 (2), 439-447 (2005)
COMMENT     Contact: Coleman, Craig E.
            Department of Plant and Animal Sciences
            Brigham Young University
            275 WIDB, Brigham Young University, Provo, UT 84602, USA
            Tel: (801) 422-5145
            Fax: (801) 422-0008
            Email: craig_coleman@byu.edu
            Plate: 02  row: J  column: 22
            Seq primer: M13 Forward
            High quality sequence stop: 829.
FEATURES             Location/Qualifiers
     source          1. .829
                     /organism="Chenopodium quinoa"
                     /mol_type="mRNA"
                     /cultivar="Real"
                     /db_xref="taxon:63459"
                     /clone="S02J22"
                     /tissue_type="Developing Seed"
                     /lab_host="XL-1 Blue"
                     /clone_lib="cqseed"
                     /note="Vector: pTriplEx2; Site_1: SfiI; Site_2: SfiI;
                     Developing Seed cDNA Library from Chenopodium quinoa"
ORIGIN

Alignment Scores:
Pred. No.:              8.92e-09        Length:         829
Score:                  145.00          Matches:        39
Percent Similarity:     49.7%           Conservative:   32
Best Local Similarity:  27.3%           Mismatches:     54
Query Match:            18.9%           Indels:         18
DB:                     7               Gaps:           5

US-10-758-902-9 (1-149) x CN782289 (1-829)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGlu------------------LeuAlaLys 27
              |||   ||||||:::|||   :::|||::::::                :::   :::
Db        134 TATAACACCTTTCTGCAAAGTATACGCAGCCAAACTAAGGATCCAAGCTTAGTGTATGAA 193

Qy         28 GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPhe 47
              |||   |||:::   :::   |||           |||                 :::
Db        194 GGAATCCCAATGATCCGACCACCAACCAACCCAGATACA------------------TAT 235

Qy         48 ValLeuValAspIleThrThrThrSerLysLysThr---------ValLysValAlaIle 64
              :::||||||||||:::   :::         |||           :::   :::|||:::
Db        236 CTTTTGGTTGACCTTGAATCTAAAAAGGATAAGAATGAGATATTCATTACACTTGCTTTA 295

Qy         65 AspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAla 84
                  |||:::|||||||||   :::   ||||||:::   ||||||   |||
Db        296 AGTAGAAACGACTTGTATGTAGTGGCCTTTGCTGATAAATTTGGAGGCAAAGTTCGCGGC 355

Qy         85 ValPheLeuAsp------LysValProThrVal---AlaThrSerLysLeuPheProGly 101
              |||             :::   |||:::           |||:::||||||
Db        356 CATTTCTTTTCCAATCTTAACATTGACACCATTGATAAGGCAAAGAAAGTTTTTCCAGAA 415

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
              |||         :::   :::|||:::      ||||||   ::::::   :::   |||
Db        416 GTTCAGGTTTTCATAAATATAACGTATGGGGAAAGTTACAGTCAAATCGAAAGCAATGCT 475

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                 :::|||          ||||||          |||:::      :::|||
Db        476 GGTACAAACCGATTAAGTTTTCCGTTGGGGTTTGATAACCTTAAAACTTACATGGAAAAG 535

Qy        142 IleTrpGly 144
              :::::|||
Db        536 GTCTATGGG 544

RESULT 21
DN953953
LOCUS       DN953953                 472 bp    mRNA    linear   EST 04-MAY-2005
DEFINITION  it66g11.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
            sequence.
ACCESSION   DN953953
VERSION     DN953953.1  GI:63026091
KEYWORDS    EST.
SOURCE      Gnetum gnemon
  ORGANISM  Gnetum gnemon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae; Gnetum.
REFERENCE   1  (bases 1 to 472)
  AUTHORS   Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P., Coruzzi,G. and Stevenson,D.
  TITLE     Expressed tag sequences from Gnetum female cone (NYBG)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Seq primer: -21M13UnivRev.
FEATURES             Location/Qualifiers
     source          1. .472
                     /organism="Gnetum gnemon"
                     /mol_type="mRNA"
                     /db_xref="taxon:3382"
                     /sex="female"
                     /clone_lib="Gnetum female cone (NYBG)"
                     /note="Organ: mature, unfertilized reproductive strobili;
                     Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
                     Completed 02/11/02, submitted for sequencing 02/12/02.
                     Library: Stratagene ZAP Express cDNA Synthesis Kit. The
                     library was size-fractionated to enrich for large inserts.
                     Sample: NYBG accession number #436/84"
ORIGIN

Alignment Scores:
Pred. No.:              6.48e-09        Length:         472
Score:                  143.50          Matches:        47
Percent Similarity:     55.1%           Conservative:   23
Best Local Similarity:  37.0%           Mismatches:     46
Query Match:            18.7%           Indels:         11
DB:                     8               Gaps:           5

US-10-758-902-9 (1-149) x DN953953 (1-472)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGlu------TyrProThrPheIleGlnAspLeu 21
              |||   |||:::      :::|||   |||      :::      |||::::::||||||
Db        109 GTCAAGTTTTCAACGAAAGATGCCACTGAGGATACCTTCAGCGACTTCATGAAGGATCTG 168
```

```
Qy         22 ArgAsnGluLeuAlaLys---GlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              |||   ||||||   |||   |||:::           :::||||||
Db        169 AGAACAGAGCTGACCAAAGAAGGAAGCCAACAATACGACATACCAGTG------------ 216

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ::::::   :::|||||||||||||||||||:::   :::      |||   ::::::
Db        217 TTGAGCGTGAACAAGAGGTTCGTACTCGTGGATCTC---TCCAACGATAAGAACAGCATC 273

Qy         61 LysValAlaIleAspValThrAsp-ValTyrVal-ValGlyTyrGlnAspLysTrpAspG 80
              |||||||||:::      ::: |||||||||| :::|||||                |||
Db        274 ACAGTGGCCATCAACGCCGTGGAATGTTTACGTGTCTGGGTTATTGTGCCTGTCAAGATT 333

Qy         80 lyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheP 100
              ||||||   |||   :::                        :::   |||||||
Db        334 CAACCCCGCGAGCCTACTTTTACAACGACACTGCTGATGCCGATATTAACACTCTGTTCC 393

Qy        100 ro---GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValA 119
              ||      |||:::      |||   |||:::|||:::|||   :::|||
Db        394 CCGAGGCCCAGAAGAATAAACGCAAGCTCAATTTCAACGGCACCTACCCGCAACTGGAGA 453

Qy        119 snAlaAlaLysValAsp 124
              |||||||||||||
Db        454 GATTTGCCAAAGTAGAC 470

RESULT 22
CO121195
LOCUS       CO121195                841 bp    mRNA    linear   EST 16-JUN-2004
DEFINITION  GR__Eb02E11.f GR__Eb Gossypium raimondii cDNA clone GR__Eb02E11 5',
            mRNA sequence.
ACCESSION   CO121195
VERSION     CO121195.1  GI:48819882
KEYWORDS    EST.
SOURCE      Gossypium raimondii
  ORGANISM  Gossypium raimondii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 841)
  AUTHORS   Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
            Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
            Wing,R.A.
  TITLE     Global assembly of Cotton ESTs
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            Plate: 02  row: E  column: 11.
FEATURES             Location/Qualifiers
     source          1. .841
                     /organism="Gossypium raimondii"
                     /mol_type="mRNA"
                     /db_xref="taxon:29730"
                     /clone="GR__Eb02E11"
                     /tissue_type="floral"
                     /dev_stage="_3 to +3 DPA"
                     /lab_host="DH10B"
                     /clone_lib="GR__Eb"
                     /note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
                     EcoRV; Library made by Invitrogen with RNA supplied by
                     Wendle lab. Directional cloned into NotI-EV. Colonies
                     plated/picked by AGI. More glycerol clones held in -80."
ORIGIN

Alignment Scores:
Pred. No.:              3.77e-08        Length:         841
Score:                  140.50          Matches:        47
Percent Similarity:     49.7%           Conservative:   26
Best Local Similarity:  32.0%           Mismatches:     55

Query Match:            18.3%           Indels:         19
DB:                     7               Gaps:           7

US-10-758-902-9 (1-149) x CO121195 (1-841)

Qy          3 ThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAsp 20
              ||||||  |||             |||             |||       |||:::::|||
Db         40 ACAGTGAGATTCACCACTGAAAGAGCCACCAGGAACTCTTATCTGATGTTTATGAAGGAT 99

Qy         21 LeuArgAsnGluLeuAlaLys-----------------GlyThrProValCysGlnLeu 34
              |||  |||  |||  :::                          |||:::     |||
Db        100 CTGTACAATGCATTGACAGAGCGTGCAGATAGAAGCGGAGACATGCCGATA------TTG 153

Qy         35 ProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThr 54
              |||                      |||  :::::::::|||||||||:::::   :::
Db        154 CCTCCCCGATCTGCACAGCCTACTGATCCTCGGCAATATGTTCTGGTAGAGCTC---TCA 210

Qy         55 ThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyr 74
                    :::||||||   :::|||:::   |||::::::||||||::::::||||||
Db        211 AATGGTTACCAAACTGTCACATTAGCCTTGCATGTCAGTAATGTGTATATCTTGGGTTAT 270

Qy         75 GlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAla 94
              :::                      :::   |||       ||||||
Db        271 CGT-----------GCAAGTGCGGGCTCCTATTTCTTTAGCGATGTCCCAGACGATGTA 318

Qy         95 ThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyr 114
              :::   ||||||||||||   |||             |||   |||  |||  |||
Db        319 CGTAATGCTTTGTTCCCAGGCAGTACTGGC---------CTACCCTTTACAGGCAGATAT 369

Qy        115 GlnLysLeuValAsnAlaAlaLysVal---AspArgLysAspLeuGluLeuGlyValTyr 133
                 |||      ||||||   |||   ||||||:::::::::   ||||||:::
Db        370 GGGGCACTTGAGGGTGCTGCGGGAGTAGATGACAGAAGGGAAATCCCTCTGGGAATGGAT 429

Qy        134 LysLeuGluPheSerIleGlu 140
              :::|||          |||:::
Db        430 GAACTACGCCAACATATTGAT 450

RESULT 23
CO103587
LOCUS       CO103587                903 bp    mRNA    linear   EST 16-JUN-2004
DEFINITION  GR__Eb0032E01.r GR__Eb Gossypium raimondii cDNA clone GR__Eb0032E01
            3', mRNA sequence.
ACCESSION   CO103587
VERSION     CO103587.1  GI:48802273
KEYWORDS    EST.
SOURCE      Gossypium raimondii
  ORGANISM  Gossypium raimondii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
            Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
            Wing,R.A.
  TITLE     Global assembly of Cotton ESTs
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            Plate: 0032  row: E  column: 01.
FEATURES             Location/Qualifiers
     source          1. .903
                     /organism="Gossypium raimondii"
                     /mol_type="mRNA"
                     /db_xref="taxon:29730"
                     /clone="GR__Eb0032E01"
                     /tissue_type="floral"
                     /dev_stage="_3 to +3 DPA"
                     /lab_host="DH10B"
```

/clone_lib="GR__Eb"
/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2: EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."
ORIGIN

Alignment Scores:

Pred. No.:	4.16e-08	Length:	903
Score:	140.50	Matches:	47
Percent Similarity:	49.7%	Conservative:	26
Best Local Similarity:	32.0%	Mismatches:	55
Query Match:	18.3%	Indels:	19
DB:	7	Gaps:	7

US-10-758-902-9 (1-149) x CO103587 (1-903)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAsp 20
              ||||||   |||          |||          |||       |||::::::|||
Db        178 ACAGTGAGATTCACCACTGAAAGAGCCACCAGGAACTCTTATCTGATGTTTATGAAGGAT 237

Qy         21 LeuArgAsnGluLeuAlaLys-----------------GlyThrProValCysGlnLeu 34
              |||   |||   |||   :::                 |||:::      |||
Db        238 CTGTACAATGCATTGACAGAGCGTGCAGATAGAAGCGGAGACATGCCGATA------TTG 291

Qy         35 ProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThr 54
              |||                |||   :::::::::|||||||||::::::   :::
Db        292 CCTCCCCGATCTGCACAGCCTACTGATCCTCGGCAATATGTTCTGGTAGAGCTC---TCA 348

Qy         55 ThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyr 74
                 :::||||||   :::|||:::   |||::::::||||||::::::||||||
Db        349 AATGGTTACCAAACTGTCACATTAGCCTTGCATGTCAGTAATGTGTATATCTTGGGTTAT 408

Qy         75 GlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAla 94
              :::                     :::   |||          ||||||
Db        409 CGT-----------GCAAGTGCGGGCTCCTATTTCTTTAGCGATGTCCCAGACGATGTA 456

Qy         95 ThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyr 114
                 :::   ||||||||||||   |||          |||   |||   |||   |||
Db        457 CGTAATGCTTTGTTCCCAGGCAGTACTGGC---------CTACCCTTTACAGGCAGATAT 507

Qy        115 GlnLysLeuValAsnAlaAlaLysVal---AspArgLysAspLeuGluLeuGlyValTyr 133
                 |||      ||||||   |||   ||||||:::::::::   ||||||:::
Db        508 GGGGCACTTGAGGGTGCTGCGGGAGTAGATGACAGAAGGGAAATCCCTCTGGGAATGGAT 567

Qy        134 LysLeuGluPheSerIleGlu 140
              :::|||          |||:::
Db        568 GAACTACGCCAACATATTGAT 588
```

RESULT 24
CA835532
LOCUS CA835532 661 bp mRNA linear EST 12-DEC-2002
DEFINITION MCS038A11_160572 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS038A11 5, mRNA sequence.
ACCESSION CA835532
VERSION CA835532.1 GI:26563297
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 661)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 038 row: A column: 11
Seq primer: T3 20mer
High quality sequence stop: 661.
FEATURES Location/Qualifiers
source 1. .661
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS038A11"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:

Pred. No.:	5.04e-08	Length:	661
Score:	138.50	Matches:	32
Percent Similarity:	63.9%	Conservative:	7
Best Local Similarity:	52.5%	Mismatches:	21
Query Match:	18.0%	Indels:	1
DB:	6	Gaps:	1

US-10-758-902-9 (1-149) x CA835532 (1-661)

```
Qy         86 PheLeuAspLysValProThrValAlaThrSerLysLeuProGlyValThrAsnArg 105
              ||||||            |||||||||          ||||||   |||   |||   |||
Db          6 TTCCTTCAAGATGCATCTACGGTTGCGAAGGAGAATCTCTTTCATGGAGCAACAGTTCGG 65

Qy        106 ValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
                 |||   |||   |||:::|||      |||   |||||||||          |||
Db         66 ---AACCTTGCGTTCAAAGGGACTTACACATCCTTAGAGAATGCTGCAAACCAACGACGA 122

Qy        126 LysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGlyLys 145
              :::   :::|||||||||||||   ||||||||||||:::||||||::::::::||||||
Db        123 GAAGCCATAGAGTTAGGGGTGGATAAACTAGAGTTTGCGATCGAGTCGGTTTATGGTAAG 182

Qy        146 Thr 146
              |||
Db        183 ACA 185
```

RESULT 25
CA833333
LOCUS CA833333 689 bp mRNA linear EST 12-DEC-2002
DEFINITION MCS021A09_151944 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021A09 5, mRNA sequence.
ACCESSION CA833333
VERSION CA833333.1 GI:26561098
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 689)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC

```
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 021  row: A  column: 09
            Seq primer: T3 20mer
            High quality sequence stop: 689.
FEATURES              Location/Qualifiers
     source           1. .689
                      /organism="Mesembryanthemum crystallinum"
                      /mol_type="mRNA"
                      /db_xref="taxon:3544"
                      /clone="MCS021A09"
                      /tissue_type="leaf"
                      /dev_stage="five-week-old"
                      /clone_lib="Ice plant Lambda Uni-Zap XR expression
                      library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                      metabolism, phase I (2 AM)."
                      /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                      EcoRI; Site_2: XhoI; Library construction was performed
                      according to Stratagene's recommended protocol for the
                      Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.:              5.35e-08        Length:         689
Score:                  138.50          Matches:        32
Percent Similarity:     63.9%           Conservative:   7
Best Local Similarity:  52.5%           Mismatches:     21
Query Match:            18.0%           Indels:         1
DB:                     6               Gaps:           1

US-10-758-902-9 (1-149) x CA833333 (1-689)

Qy         86 PheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArg 105
              ||||||              |||||||||           ||||||   |||   |||   |||
Db          6 TTCCTTCAAGATGCATCTACGGTTGCGAAGGAGAATCTCTTTCATGGAGCAACAGTTCGG 65

Qy        106 ValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
                 |||   |||   |||:::|||       |||   |||||||||           |||
Db         66 ---AACCTTGCGTTCAAAGGGACTTACACATCCTTAGAGAATGCTGCAAACCAACGACGA 122

Qy        126 LysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGlyLys 145
              :::   :::||||||||||||   ||||||||||||:::||||||::::::::||||||
Db        123 GAAGCCATAGAGTTAGGGGTGGATAAACTAGAGTTTGCGATCGAGTCGGTTTATGGTAAG 182

Qy        146 Thr 146
              |||
Db        183 ACA 185

RESULT 26
CA833383
LOCUS       CA833383                689 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  MCS021F04_152044 Ice plant Lambda Uni-Zap XR expression library, 5
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
            AM). Mesembryanthemum crystallinum cDNA clone MCS021F04 5, mRNA
            sequence.
ACCESSION   CA833383
VERSION     CA833383.1  GI:26561148
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 021  row: F  column: 04
            Seq primer: T3 20mer
            High quality sequence stop: 689.
FEATURES              Location/Qualifiers
     source           1. .689
                      /organism="Mesembryanthemum crystallinum"
                      /mol_type="mRNA"
                      /db_xref="taxon:3544"
                      /clone="MCS021F04"
                      /tissue_type="leaf"
                      /dev_stage="five-week-old"
                      /clone_lib="Ice plant Lambda Uni-Zap XR expression
                      library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                      metabolism, phase I (2 AM)."
                      /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                      EcoRI; Site_2: XhoI; Library construction was performed
                      according to Stratagene's recommended protocol for the
                      Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.:              5.35e-08        Length:         689
Score:                  138.50          Matches:        32
Percent Similarity:     63.9%           Conservative:   7
Best Local Similarity:  52.5%           Mismatches:     21
Query Match:            18.0%           Indels:         1
DB:                     6               Gaps:           1

US-10-758-902-9 (1-149) x CA833383 (1-689)

Qy         86 PheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArg 105
              ||||||              |||||||||           ||||||   |||   |||   |||
Db          6 TTCCTTCAAGATGCATCTACGGTTGCGAAGGAGAATCTCTTTCATGGAGCAACAGTTCGG 65

Qy        106 ValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
                 |||   |||   |||:::|||       |||   |||||||||           |||
Db         66 ---AACCTTGCGTTCAAAGGGACTTACACATCCTTAGAGAATGCTGCAAACCAACGACGA 122

Qy        126 LysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGlyLys 145
              :::   :::||||||||||||   ||||||||||||:::||||||::::::::||||||
Db        123 GAAGCCATAGAGTTAGGGGTGGATAAACTAGAGTTTGCGATCGAGTCGGTTTATGGTAAG 182

Qy        146 Thr 146
              |||
Db        183 ACA 185

RESULT 27
CF227046
LOCUS       CF227046                661 bp    mRNA    linear   EST 04-AUG-2003
DEFINITION  IH202 subtracted Iris tepal cDNA library Iris hollandica cDNA clone
            IH202, mRNA sequence.
ACCESSION   CF227046
VERSION     CF227046.1  GI:33438082
KEYWORDS    EST.
SOURCE      Iris hollandica
  ORGANISM  Iris hollandica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
            Iris.
REFERENCE   1  (bases 1 to 661)
  AUTHORS   van Doorn,W.G., Balk,P.A., van Houwelingen,A.M., Hoeberichts,F.A.,
```

```
            Hall,R.D., Vorst,O., van der Schoot,C. and van Wordragen,M.F.
  TITLE     Gene expression during anthesis and senescence in Iris flowers
  JOURNAL   Plant Mol. Biol. 53 (6), 845-863 (2003)
   PUBMED   15082930
COMMENT     Contact: Wouter G. van Doorn
            Institute for Agrotechnological Research (ATO)
            Wageningen University and Research Centre
            P.O. Box 17, 6700 AA, Wageningen, The Netherlands
            Tel: 0031 317 475105
            Fax: 0031 317 475347
            Email: wouter.vandoorn@wur.nl.
FEATURES             Location/Qualifiers
     source          1. .661
                     /organism="Iris hollandica"
                     /mol_type="mRNA"
                     /cultivar="Blue Magic"
                     /db_xref="taxon:35876"
                     /clone="IH202"
                     /tissue_type="sepals"
                     /clone_lib="subtracted Iris tepal cDNA library"
                     /note="Vector: pGEMT-Easy; mRNA isolated from Iris sepals
                     was subtracted using pedicel material as the driver. Equal
                     amounts of mRNA from each developmental stage were pooled
                     for cDNA synthesis. The pGEM-T Easy Vector System
                     (Promega) was used to construct the cDNA library."
ORIGIN

Alignment Scores:
Pred. No.:                2.09e-07      Length:          661
Score:                    134.00        Matches:         36
Percent Similarity:       48.1%         Conservative:    26
Best Local Similarity:    27.9%         Mismatches:      59
Query Match:              17.4%         Indels:          8
DB:                       6             Gaps:            3

US-10-758-902-9 (1-149) x CF227046 (1-661)

Qy          14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGln 33
               |||      |||:::|||   ||||||      |||:::   |||:::   |||
Db         121 TATAGTGCTTTCCTACAGACCCTACGAACGCGCTTAAGCAGTGGAAGTAGCGTGCATGAT 180

Qy          34 LeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr 53
               :::|||:::                        :::      :::||||||   :::
Db         181 ATTCCTTTGCTGCCTGGGCAATCCGGTTCCCAGCAGGATTTGCTCCTTGTGCAACTCTTT 240

Qy          54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73
                           :::   :::   ::::::      :::   |||:::|||
Db         241 GATTGGGACAACACGCCGATCACGCTGGTGCTTAATCGCGTCAATGCTTATCTGGTAGCT 300

Qy          74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93
               ||||||              |||:::|||        |||         |||
Db         301 TATCAA------------GCTAAAAATCGTTATTACTTGCTTTCCGACACTCCC------ 342

Qy          94 AlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
               |||      :::|||:::             :::|||      |||:::|||   ||||||
Db         343 GCCAATCCTCAGCTTTATGGAAGCAACCCGCACCGC------CTTAGTTTTACAGGCAGC 396

Qy         114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
               |||      |||   |||   ||||||      |||:::::::::::::||||||:::
Db         397 TACATTGCTCTTCAAAATGTTGCGAAAACAAGTAGAGAAAATATTGATCTGGGAATCAAT 456

Qy         134 LysLeuGluPheSerIleGluAlaIle 142
                  |||      :::|||      :::
Db         457 CCACTTGCAACGGCAATCACGACACTC 483

RESULT 28
CF227047
LOCUS       CF227047                662 bp    mRNA    linear   EST 04-AUG-2003
DEFINITION  IH215 subtracted Iris tepal cDNA library Iris hollandica cDNA clone
            IH215, mRNA sequence.
ACCESSION   CF227047
VERSION     CF227047.1  GI:33438083
KEYWORDS    EST.
SOURCE      Iris hollandica
  ORGANISM  Iris hollandica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
            Iris.
REFERENCE   1  (bases 1 to 662)
  AUTHORS   van Doorn,W.G., Balk,P.A., van Houwelingen,A.M., Hoeberichts,F.A.,
            Hall,R.D., Vorst,O., van der Schoot,C. and van Wordragen,M.F.
  TITLE     Gene expression during anthesis and senescence in Iris flowers
  JOURNAL   Plant Mol. Biol. 53 (6), 845-863 (2003)
   PUBMED   15082930
COMMENT     Contact: Wouter G. van Doorn
            Institute for Agrotechnological Research (ATO)
            Wageningen University and Research Centre
            P.O. Box 17, 6700 AA, Wageningen, The Netherlands
            Tel: 0031 317 475105
            Fax: 0031 317 475347
            Email: wouter.vandoorn@wur.nl.
FEATURES             Location/Qualifiers
     source          1. .662
                     /organism="Iris hollandica"
                     /mol_type="mRNA"
                     /cultivar="Blue Magic"
                     /db_xref="taxon:35876"
                     /clone="IH215"
                     /tissue_type="sepals"
                     /clone_lib="subtracted Iris tepal cDNA library"
                     /note="Vector: pGEMT-Easy; mRNA isolated from Iris sepals
                     was subtracted using pedicel material as the driver. Equal
                     amounts of mRNA from each developmental stage were pooled
                     for cDNA synthesis. The pGEM-T Easy Vector System
                     (Promega) was used to construct the cDNA library."
ORIGIN

Alignment Scores:
Pred. No.:                2.09e-07      Length:          662
Score:                    134.00        Matches:         36
Percent Similarity:       48.1%         Conservative:    26
Best Local Similarity:    27.9%         Mismatches:      59
Query Match:              17.4%         Indels:          8
DB:                       6             Gaps:            3

US-10-758-902-9 (1-149) x CF227047 (1-662)

Qy          14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGln 33
               |||      |||:::|||   ||||||      |||:::   |||:::   |||
Db         154 TATAGTGCTTTCCTACAGACCCTACGAACGCGCTTAAGCAGTGGAAGTAGCGTGCATGAT 213

Qy          34 LeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr 53
               :::|||:::                        :::      :::||||||   :::
Db         214 ATTCCTTTGCTGCCTGGGCAATCCGGTTCCCAGCAGGATTTGCTCCTTGTGCAACTCTTT 273

Qy          54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73
                           :::   :::   ::::::      :::   |||:::|||
Db         274 GATTGGGACAACACGCCGATCACGCTGGTGCTTAATCGCGTCAATGCTTATCTGGTAGCT 333

Qy          74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93
               ||||||              |||:::|||        |||         |||
Db         334 TATCAA------------GCTAAAAATCGTTATTACTTGCTTTCCGACACTCCC------ 375

Qy          94 AlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
               |||      :::|||:::             :::|||      |||:::|||   ||||||
Db         376 GCCAATCCTCAGCTTTATGGAAGCAACCCGCACCGC------CTTAGTTTTACAGGCAGC 429

Qy         114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
               |||      |||   |||   ||||||      |||:::::::::::::||||||:::
Db         430 TACATTGCACTTCAAAATGTTGCGAAAACAAGTAGAGAAAATATTGATCTGGGAATCAAT 489

Qy         134 LysLeuGluPheSerIleGluAlaIle 142
                  |||      :::|||      :::
Db         490 CCACTTGCAACGGCAATCACGACACTC 516

RESULT 29
```

```
CA835855
LOCUS       CA835855                639 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  MCS004G12_161218 Ice plant Lambda Uni-Zap XR expression library, 5
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
            AM). Mesembryanthemum crystallinum cDNA clone MCS004G12 5, mRNA
            sequence.
ACCESSION   CA835855
VERSION     CA835855.1  GI:26563620
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 004  row: G  column: 12
            Seq primer: T3 20mer
            High quality sequence stop: 639.
FEATURES             Location/Qualifiers
     source          1. .639
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCS004G12"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase I (2 AM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.:              4.38e-07        Length:         639
Score:                  131.50          Matches:        32
Percent Similarity:     62.3%           Conservative:   6
Best Local Similarity:  52.5%           Mismatches:     22
Query Match:            17.1%           Indels:         1
DB:                     6               Gaps:           1

US-10-758-902-9 (1-149) x CA835855 (1-639)

Qy         86 PheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArg 105
              ||||||            |||||||||         ||||||   |||   |||   |||
Db          6 TTCCTTCAAGATGCATCTACGGTTGCGAAGGAGAATCTCTTTCATGGAGCAACAGTTCGG 65

Qy        106 ValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
                 |||   |||   |||:::|||      |||   |||||||||              |||
Db         66 ---AACCTTGCGTTCAAAGGGACTTACACATCCTTAGAGAATGCTGCAAACCAACGACGA 122

Qy        126 LysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGlyLys 145
              :::   :::||||||||||||   ||||||||||:::||||||:::   :::||||||
Db        123 GAAGCCATAGAGTTAGGGGTGGATAAACTAGAGTTTGCGATCGAGTCGGGTTATGGTAAG 182

Qy        146 Thr 146
              |||
Db        183 ACA 185

RESULT 30
CN846973
LOCUS       CN846973                671 bp    mRNA    linear   EST 02-JUN-2004
DEFINITION  PG07022B02 Ginseng cDNA library from MeJA treated hairy root Panax
            ginseng cDNA clone PG07022B02 5', mRNA sequence.
ACCESSION   CN846973
VERSION     CN846973.1  GI:47964264
KEYWORDS    EST.
SOURCE      Panax ginseng
  ORGANISM  Panax ginseng
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Apiales; Araliaceae; Panax.
REFERENCE   1  (bases 1 to 671)
  AUTHORS   Choi,D.W., Jung,J.D., Ha,Y.I., Park,H.W., In,D.S., Chung,H.J. and
            Liu,J.R.
  TITLE     Analysis of transcripts in methyl jasmonate-treated ginseng hairy
            roots to identify genes involved in the biosynthesis of
            ginsenosides and other secondary metabolites
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Dong-Woog Choi
            Eugentech / KRIBB
            52 Oun-Dong, Yusong-Gu, Daejen 305-333, Korea
            Tel: 82 42 863 2051
            Fax: 82 42 863 2049
            Email: dwchoi@eugentech.com
            PCR PRimers
            FORWARD: T3
            BACKWARD: T7
            Seq primer: T3
            High quality sequence stop: 671
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .671
                     /organism="Panax ginseng"
                     /mol_type="mRNA"
                     /db_xref="taxon:4054"
                     /clone="PG07022B02"
                     /tissue_type="MeJA treated hairy root"
                     /clone_lib="Ginseng cDNA library from MeJA treated hairy
                     root"
                     /note="Vector: lambda ZAP XR; cDNAs from MeJA treated
                     ginseng hairy root were cloned into lambda ZAP XR vector"
ORIGIN

Alignment Scores:
Pred. No.:              1.21e-06        Length:         671
Score:                  128.50          Matches:        42
Percent Similarity:     54.6%           Conservative:   29
Best Local Similarity:  32.3%           Mismatches:     48
Query Match:            16.7%           Indels:         11
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x CN846973 (1-671)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGln 33
              :::      |||:::      :::|||:::   :::      |||   ||||||
Db        192 TTCAACAATTTCGTGGATGCTGTGCGAGATCTCGTGGTAAGCGGACCTCCTGTCCATGGA 251

Qy         34 LeuProValThrLeuGln---------ThrIleAlaAspAspLysArgPheValLeuVal 50
              |||   :::   |||:::         |||:::         :::||||||:::||||||
Db        252 TTA---TTGAGATTGCGCGACCGCTCCACGGTGCCAATTTCTCAACGGTTTATTCTGGTG 308

Qy         51 AspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyr 70
              ::::::                      :::   :::|||||||||||||||:::::|||
Db        309 GAACTTTATAATTATGAAGCGACACCTATTACTTTGGCAATAGATGTCACAAATTTATAC 368

Qy         71 ValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysVal 90
              ||||||||||:::            |||                 ||||||||
Db        369 GTGGTGGGTTATCGT---------ACCGGAGACCTGTTTTACTACTTTCTTGATTCT--- 416
```

```
Qy          91 ProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPhe 110
               |||   |||      :::|||      :::   :::   :::   |||   |||
Db         417 ---GCTGTTGACACACCAGGTATTTTCAGAGAATTGCCACAT---ATTGAGCTCCCATTT 470

Qy         111 AspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeu 130
               :::   ||||||      |||   :::   |||      ||||||   ::::::   |||
Db         471 AACAGTAGTTATCCAGCTCTCCAGCATGAGGCAGGT---GATAGAGTTAATATTCCCTTG 527

Qy         131 GlyValTyrLysLeuGluPheSerIleGlu 140
               |||:::   :::|||:::   ||||||:::
Db         528 GGGATAACTGAACTAGATCAATCCATCCAA 557

RESULT 31
CF227084
LOCUS       CF227084                 665 bp    mRNA    linear   EST 04-AUG-2003
DEFINITION  IHSLP22 subtracted Iris tepal cDNA library Iris hollandica cDNA
            clone IHSLP22, mRNA sequence.
ACCESSION   CF227084
VERSION     CF227084.1  GI:33438122
KEYWORDS    EST.
SOURCE      Iris hollandica
  ORGANISM  Iris hollandica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
            Iris.
REFERENCE   1  (bases 1 to 665)
  AUTHORS   van Doorn,W.G., Balk,P.A., van Houwelingen,A.M., Hoeberichts,F.A.,
            Hall,R.D., Vorst,O., van der Schoot,C. and van Wordragen,M.F.
  TITLE     Gene expression during anthesis and senescence in Iris flowers
  JOURNAL   Plant Mol. Biol. 53 (6), 845-863 (2003)
   PUBMED   15082930
COMMENT     Contact: Wouter G. van Doorn
            Institute for Agrotechnological Research (ATO)
            Wageningen University and Research Centre
            P.O. Box 17, 6700 AA, Wageningen, The Netherlands
            Tel: 0031 317 475105
            Fax: 0031 317 475347
            Email: wouter.vandoorn@wur.nl.
FEATURES             Location/Qualifiers
     source          1. .665
                     /organism="Iris hollandica"
                     /mol_type="mRNA"
                     /cultivar="Blue Magic"
                     /db_xref="taxon:35876"
                     /clone="IHSLP22"
                     /tissue_type="sepals"
                     /clone_lib="subtracted Iris tepal cDNA library"
                     /note="Vector: pGEMT-Easy; mRNA isolated from Iris sepals
                     was subtracted using pedicel material as the driver. Equal
                     amounts of mRNA from each developmental stage were pooled
                     for cDNA synthesis. The pGEM-T Easy Vector System
                     (Promega) was used to construct the cDNA library."
ORIGIN

Alignment Scores:
Pred. No.:              1.4e-06       Length:          665
Score:                  128.00        Matches:         34
Percent Similarity:     48.1%         Conservative:    28
Best Local Similarity:  26.4%         Mismatches:      59
Query Match:            16.7%         Indels:          8
DB:                     6             Gaps:            3

US-10-758-902-9 (1-149) x CF227084 (1-665)

Qy          14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGln 33
               |||      |||:::|||   ||||||      |||:::   |||::   |||
Db           9 TATAGTGCTTTCCTACAGACCCTACGAACGCGCTTAAGCAGTGGAAGTAGCGTGCATGAT 68

Qy          34 LeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr 53
               :::|||:::                        :::      :::   |||   :::
Db          69 ATTCCTTTGCTTCCTGCGCAATCCGGTTCTCAGCAGGATTTGCTCTTTGTGCGACTCTTT 128

Qy          54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73
```

```
                   :::   :::   :::   :::   ::::::      :::   |||||||||
Db         129 GACTGGGCCAACAGGCCGATCACGCTAGTGTTAAATCGCGTCAATGCTTATGTGGTGGCT 188

Qy          74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93
               ||||||               ::::::|||          |||          |||
Db         189 TATCAA------------GCTCAAAATCGTTTTTACTTGCTTTCCGGCACTCCC------ 230

Qy          94 AlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
               |||      :::::::::            :::|||      |||||||||   ||||||
Db         231 GCCAATCCTCAGGTTTATGGAAACAACCCACACCGC------CTTACTTTTACAGGTAGC 284

Qy         114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
               |||      |||   |||   ||||||      |||::::::::::::   |||:::
Db         285 TATGGTGCACTTCAAAATGTTGCGAAAACAAGTAGAGAAAATATTGATTGGGGAATCAAT 344

Qy         134 LysLeuGluPheSerIleGluAlaIle 142
               |||      :::|||      :::
Db         345 CCACTTGCAACGGCAATCTCGACACTC 371

RESULT 32
CN848288
LOCUS       CN848288                 669 bp    mRNA    linear   EST 02-JUN-2004
DEFINITION  PG07019B04 Ginseng cDNA library from MeJA treated hairy root Panax
            ginseng cDNA clone PG07019B04 5', mRNA sequence.
ACCESSION   CN848288
VERSION     CN848288.1  GI:47965579
KEYWORDS    EST.
SOURCE      Panax ginseng
  ORGANISM  Panax ginseng
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Apiales; Araliaceae; Panax.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Choi,D.W., Jung,J.D., Ha,Y.I., Park,H.W., In,D.S., Chung,H.J. and
            Liu,J.R.
  TITLE     Analysis of transcripts in methyl jasmonate-treated ginseng hairy
            roots to identify genes involved in the biosynthesis of
            ginsenosides and other secondary metabolites
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Dong-Woog Choi
            Eugentech / KRIBB
            52 Oun-Dong, Yusong-Gu, Daejen 305-333, Korea
            Tel: 82 42 863 2051
            Fax: 82 42 863 2049
            Email: dwchoi@eugentech.com
            PCR PRimers
            FORWARD: T3
            BACKWARD: T7
            Seq primer: T3
            High quality sequence stop: 669
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Panax ginseng"
                     /mol_type="mRNA"
                     /db_xref="taxon:4054"
                     /clone="PG07019B04"
                     /tissue_type="MeJA treated hairy root"
                     /clone_lib="Ginseng cDNA library from MeJA treated hairy
                     root"
                     /note="Vector: lambda ZAP XR; cDNAs from MeJA treated
                     ginseng hairy root were cloned into lambda ZAP XR vector"
ORIGIN

Alignment Scores:
Pred. No.:              4.26e-06      Length:          669
Score:                  124.50        Matches:         41
Percent Similarity:     53.8%         Conservative:    29
Best Local Similarity:  31.5%         Mismatches:      49
Query Match:            16.2%         Indels:          11
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x CN848288 (1-669)
```

```
Qy          14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGln 33
               :::       |||:::      :::|||:::   :::      |||   ||||||
Db         138 TTCAACAATTTCGTGGATGCTGTGCGAGATCTCGTGGTAAGCGGACCTCCTGTCCATGGA 197

Qy          34 LeuProValThrLeuGln---------ThrIleAlaAspAspLysArgPheValLeuVal 50
               |||   :::   |||:::         |||:::         :::||||||:::||||||
Db         198 TTA---TTGAGATTGCGCGACCGCTCCACGGTGCCAATTTCTCAACGGTTTATTCTGGTG 254

Qy          51 AspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyr 70
               ::::::                    :::   :::|||||||||||||||:::::|||
Db         255 GAACTTTATAATTATGAAGCGACACCTATTACTTTGGCAATAGATGTCACAAATTTATAC 314
                    ↓
Qy          71 ValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysVal 90
               ||||||||||||:::           |||              |||||||||
Db         315 GTGGTGGGTTATCGT---------ACCGGAGACCTGTTTTACTACTTTCTTGATTCT--- 362

Qy          91 ProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPhe 110
                  |||   |||      :::|||      :::   :::   :::   |||   |||
Db         363 ---GCTGTTGACACACCAGGTATTTTCAGAGAATTGCCACAT---ATTGAGCTCCCATTT 416

Qy         111 AspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeu 130
               :::   ||||||      |||   :::             ||||||   ::::::   |||
Db         417 AACAGTAGTTATCCAGCTCTCCAGCATGAGGGAGGT---GATAGAGTTAATATTCCCTTG 473

Qy         131 GlyValTyrLysLeuGluPheSerIleGlu 140
               |||:::   :::|||:::   ||||||:::
Db         474 GGGATAACTGAACTAGATCAATCCATCCAA 503
```

RESULT 33
CA838757

```
LOCUS       CA838757                649 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  MCT020B02_167445 Ice plant Lambda Uni-Zap XR expression library, 5
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
            (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT020B02 5,
            mRNA sequence.
ACCESSION   CA838757
VERSION     CA838757.1  GI:26566522
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 020  row: B  column: 02
            Seq primer: T3 20mer
            High quality sequence stop: 649.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCT020B02"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase IV (5:30 PM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN
```

Alignment Scores:

Pred. No.:	2.71e-05	Length:	649
Score:	118.50	Matches:	27
Percent Similarity:	69.4%	Conservative:	7
Best Local Similarity:	55.1%	Mismatches:	14
Query Match:	15.4%	Indels:	1
DB:	6	Gaps:	1

US-10-758-902-9 (1-149) x CA838757 (1-649)

```
Qy          98 LeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
               ||||||   |||   |||   |||       |||   |||   |||:::|||       |||
Db          31 CTCTTTCATGGAGCAACAGTTCGG---AACCTTGCGTTCAAAGGGACTTACACATCCTTA 87

Qy         118 ValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPhe 137
               |||||||||          |||:::   :::||||||||||||   ||||||||||||
Db          88 GAGAATGCTGCAAACCAACGACGAGAAGCCATAGAGTTAGGGGTGGATAAACTAGAGTTT 147

Qy         138 SerIleGluAlaIleTrpGlyLysThr 146
               :::||||||::::::::::|||||||||
Db         148 GCGATCGAGTCGGTTTATGGTAAGACA 174
```

RESULT 34
CA839330

```
LOCUS       CA839330                649 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  MCT026C11_171755 Ice plant Lambda Uni-Zap XR expression library, 5
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
            (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11 5,
            mRNA sequence.
ACCESSION   CA839330
VERSION     CA839330.1  GI:26567095
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 026  row: C  column: 11
            Seq primer: T3 20mer
            High quality sequence stop: 649.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCT026C11"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase IV (5:30 PM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
```

EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.:	2.71e-05	Length:	649
Score:	118.50	Matches:	27
Percent Similarity:	69.4%	Conservative:	7
Best Local Similarity:	55.1%	Mismatches:	14
Query Match:	15.4%	Indels:	1
DB:	6	Gaps:	1

US-10-758-902-9 (1-149) x CA839330 (1-649)

```
Qy         98 LeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
              ||||||   |||   |||   |||       |||   |||   |||:::|||       |||
Db         31 CTCTTTCATGGAGCAACAGTTCGG---AACCTTGCGTTCAAAGGGACTTACACATCCTTA 87

Qy        118 ValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPhe 137
              |||||||||         |||:::   :::||||||||||||   ||||||||||||
Db         88 GAGAATGCTGCAAACCAACGACGAGAAGCCATAGAGTTAGGGGTGGATAAACTAGAGTTT 147

Qy        138 SerIleGluAlaIleTrpGlyLysThr 146
              :::||||||:::::::::|||||||||
Db        148 GCGATCGAGTCGGTTTATGGTAAGACA 174
```

RESULT 35
CA839511
LOCUS CA839511 671 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT028D04_172117 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT028D04 5, mRNA sequence.
ACCESSION CA839511
VERSION CA839511.1 GI:26567276
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 671)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 028 row: D column: 04
Seq primer: T3 20mer
High quality sequence stop: 671.
FEATURES Location/Qualifiers
source 1. .671
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT028D04"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.:	2.84e-05	Length:	671
Score:	118.50	Matches:	27
Percent Similarity:	69.4%	Conservative:	7
Best Local Similarity:	55.1%	Mismatches:	14
Query Match:	15.4%	Indels:	1
DB:	6	Gaps:	1

US-10-758-902-9 (1-149) x CA839511 (1-671)

```
Qy         98 LeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
              ||||||   |||   |||   |||       |||   |||   |||:::|||       |||
Db         31 CTCTTTCATGGAGCAACAGTTCGG---AACCTTGCGTTCAAAGGGACTTACACATCCTTA 87

Qy        118 ValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPhe 137
              |||||||||         |||:::   :::||||||||||||   ||||||||||||
Db         88 GAGAATGCTGCAAACCAACGACGAGAAGCCATAGAGTTAGGGGTGGATAAACTAGAGTTT 147

Qy        138 SerIleGluAlaIleTrpGlyLysThr 146
              :::||||||:::::::::|||||||||
Db        148 GCGATCGAGTCGGTTTATGGTAAGACA 174
```

RESULT 36
CX175757
LOCUS CX175757 672 bp mRNA linear EST 28-DEC-2004
DEFINITION G06_69-68_14.ab1 leaf inoculated with Marssonia pathogen of Populus deltoides Populus deltoides cDNA, mRNA sequence.
ACCESSION CX175757
VERSION CX175757.1 GI:56823181
KEYWORDS EST.
SOURCE Populus deltoides
ORGANISM Populus deltoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
REFERENCE 1 (bases 1 to 672)
AUTHORS Huang,M., Zhang,X., Zhuge,Q., Zhou,Y., Zhou,H., Zhang,L., Guan,Y., Zhang,B. and Wang,M.
TITLE Identification and Expression Analysis of EST-based Genes in the Leaf of poplar
JOURNAL Unpublished (2004)
COMMENT Contact: Minren Huang
Key Laboratory Tree Genetic Engineering of Nanjing Forestry University
Nanjing Forestry University
Longpan road 9#, Nanjing, Jiangsu, P.R.China
Tel: 086-025-85427412
Fax: 086-025-85427412
Email: mrhuang@njfu.edu.cn
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .672
/organism="Populus deltoides"
/mol_type="mRNA"
/db_xref="taxon:3696"
/clone_lib="leaf inoculated with Marssonia pathogen of Populus deltoides"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	5.36e-05	Length:	672
Score:	116.50	Matches:	39
Percent Similarity:	46.4%	Conservative:	26
Best Local Similarity:	27.9%	Mismatches:	48
Query Match:	15.2%	Indels:	27
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x CX175757 (1-672)

```
Qy          14 TyrProThrPheIleGlnAspLeuArgAsnGluLeu-----------AlaLysGlyThr 29
               |||      ||||||::::::||||||      |||            :::
Db         188 TATCGAGCTTTCATTGAGAATCTACGTGTTCGATTGGGAGTGAGATTTTCCCACAATCTT 247

Qy          30 ProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeu 49
               |||              :::   :::|||             :::   |||   |||
Db         248 CCTGCA-----------CTTGCTGTTCAAGAGGAGCCACCCACTCGATTCTTCAATTTG 295

Qy          50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
               |||          |||:::     :::|||:::     :::   :::   ::::::
Db         296 GTA------ATACGAACCAACGATCACTCTGTGAGGTTCAGGTTGCGAATGGATAACCTG 349

Qy          70 TyrValValGlyTyrGln---------AspLysTrp-----------AspGlyLysAsp 82
               ||||||:::|||||||||           ||||||           :::     |||
Db         350 TACGTGATTGGCTACCAGATGGAAAACGGAAAGTGGTTAGAGTTCGGCAACGAGAACGAC 409

Qy          83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
               |||   :::    :::|||          |||
Db         410 ACCCCTGTCCCTGTGCATCTAATTCCAGAACAAGGAACCGAA----------------- 451

Qy         103 ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLys 122
                   |||   ||||||||||||||   ||||||:::||||||||||
Db         452 -----------TTCCTAGGCTTCGATGGTAGCTACGGTAAGCTACTCAATGCTGCTGGC 499

Qy         123 ValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
               ::::::   :::::::::   :::|||   |||   |||   :::   |||      :::
Db         500 CTGAATATGGAGGAAGTAAGAGTTGGCTTCTACAACCTAGGGTACGGTATAAATCAGCTT 559

RESULT 37
CF974701
LOCUS       CF974701               502 bp    mRNA    linear   EST 24-NOV-2003
DEFINITION  PSU_weup3.2A03 Defense-related ESTs from Cacao Leaves Theobroma
            cacao cDNA, mRNA sequence.
ACCESSION   CF974701
VERSION     CF974701.1  GI:38500461
KEYWORDS    EST.
SOURCE      Theobroma cacao (cacao)
  ORGANISM  Theobroma cacao
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
            Theobroma.
REFERENCE   1  (bases 1 to 502)
  AUTHORS   Verica,J.A., Maximova,S.N., Strem,M., Carlson,J., Bailey,B. and
            Guiltinan,M.J.
  TITLE     Isolation of Defense-related ESTs from Subtracted-Normalized cDNA
            Libraries of Elicited Cacao (Theobroma cacao L.) Leaves
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Guiltinan MJ
            Department of Horticulture
            Penn State University
            306 Wartik Lab, Universtiy Park, PA 16801, USA
            Tel: 814 863 7957
            Fax: 814 863 6139
            Email: mjg9@psu.edu.
FEATURES             Location/Qualifiers
     source          1. .502
                     /organism="Theobroma cacao"
                     /mol_type="mRNA"
                     /cultivar="Commun"
                     /db_xref="taxon:3641"
                     /lab_host="E. coli"
                     /clone_lib="Defense-related ESTs from Cacao Leaves"
                     /note="Organ: Leaves; Vector: pCR4-TOPO; Subtracted
                     Normalized EST library from cacao leaves sprayed with the
                     defense elicitors: benzothiadiazole, methyl jasmonate,
                     ethylene, and Nep1"
ORIGIN

Alignment Scores:
Pred. No.:              5.7e-05        Length:        502
Score:                  115.00         Matches:       45
Percent Similarity:     41.1%          Conservative:  24
Best Local Similarity:  26.8%          Mismatches:    43
Query Match:            15.0%          Indels:        56
DB:                     7              Gaps:          9

US-10-758-902-9 (1-149) x CF974701 (1-502)

Qy           3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
               :::::::::||||||:::   |||      :::|||   ||||||||||||:::||||||
Db          55 TCAATTGCTTTCAATGTTGATGAAGAN---GATTACCAGACATTTATCCAAAACCTAAGA 111

Qy          23 AsnGluLeuAlaLysGlyThr-----------------------------------Pro 30
               :::   |||:::                                           |||
Db         112 TCCATACTCTCCTCCTCCATGTCACATGATATCCATGTGCTCATGCCACAGACAGGGCCT 171

Qy          31 ValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuVal 50
               ||||||   |||   :::   |||
Db         172 GTATGCTGGTTAGATATTCGCCTA---------------------------------- 195

Qy          51 AspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyr 70
                  |||:::         |||:::   :::   |||||      ::::::|||
Db         196 ---------ACTTCTGGCGATTCCACCATCATCTTGAGAATCGACCAGAGAAATCTATAC 246

Qy          71 ValValGlyTyr------------GlnAspLys------TrpAspGlyLysAspArgAla 84
               |||   ||||||           :::|||:::      |||:::      |||
Db         247 GTGCGTGGATATTCAAGAGATATTGAAGACGAACCATTTTGGGAGTTTTCAGAT------ 300

Qy          85 ValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyValThrAsn 104
                                                  |||   |||   ||||||      :::
Db         301 --------------------------------TCATCTCTGATTCCTGGATCGAGACAT 327

Qy         105 ArgValThrLeuThrPheAspGlySerTyr---------GlnLysLeuValAsnAlaAla 121
                  |||   :::   ||||||||                     :::   ||||||
Db         328 ---------CTCGCATATGGNGGAAGCTATGTAGATGGTTACAATTTTATTGTTGCAGCC 378

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||   ::::::   ||||||:::      |||                  |||
Db         379 GGCACTACCCGCTTAAATGTTCATCTGGGNTTACCTAANTTGCGA---------AATGCC 429

Qy         142 IleTrpGlyLysThrGlnAsnGly 149
               |||         :::   ||||||
Db         430 ATTGCTAATCCTAGCAACAACGGA 453

RESULT 38
CF974192
LOCUS       CF974192               560 bp    mRNA    linear   EST 24-NOV-2003
DEFINITION  PSU_meup2.1\H06 Defense-related ESTs from Cacao Leaves Theobroma
            cacao cDNA, mRNA sequence.
ACCESSION   CF974192
VERSION     CF974192.1  GI:38499952
KEYWORDS    EST.
SOURCE      Theobroma cacao (cacao)
  ORGANISM  Theobroma cacao
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
            Theobroma.
REFERENCE   1  (bases 1 to 560)
  AUTHORS   Verica,J.A., Maximova,S.N., Strem,M., Carlson,J., Bailey,B. and
            Guiltinan,M.J.
  TITLE     Isolation of Defense-related ESTs from Subtracted-Normalized cDNA
            Libraries of Elicited Cacao (Theobroma cacao L.) Leaves
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Guiltinan MJ
            Department of Horticulture
            Penn State University
            306 Wartik Lab, Universtiy Park, PA 16801, USA
            Tel: 814 863 7957
            Fax: 814 863 6139
            Email: mjg9@psu.edu.
FEATURES             Location/Qualifiers
     source          1. .560
                     /organism="Theobroma cacao"
```

/mol_type="mRNA"
/cultivar="Commun"
/db_xref="taxon:3641"
/lab_host="E. coli"
/clone_lib="Defense-related ESTs from Cacao Leaves"
/note="Organ: Leaves; Vector: pCR4-TOPO; Subtracted Normalized EST library from cacao leaves sprayed with the defense elicitors: benzothiadiazole, methyl jasmonate, ethylene, and Nep1"

ORIGIN

Alignment Scores:

Pred. No.:	9.12e-05	Length:	560
Score:	114.00	Matches:	45
Percent Similarity:	41.1%	Conservative:	24
Best Local Similarity:	26.8%	Mismatches:	43
Query Match:	14.8%	Indels:	56
DB:	7	Gaps:	9

US-10-758-902-9 (1-149) x CF974192 (1-560)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              :::::::::||||||:::   |||      :::|||   ||||||||||||::||||||
Db         55 TCAATTGCTTTCAATGTTGATGAAGAT---GATTACCAGACATTTATCCAAAACCTAAGA 111

Qy         23 AsnGluLeuAlaLysGlyThr-----------------------------------Pro 30
              :::   |||:::                                            |||
Db        112 TCCATACTCTCCTCCTCCATGTCACATGATATCCATGTGCTCATGCCACAGACAGGGCCT 171

Qy         31 ValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuVal 50
              ||||||  |||   :::   |||
Db        172 GTATGCTGGTTAGATATTCGCCTA---------------------------------- 195

Qy         51 AspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyr 70
                     |||:::         |||:::   :::   ||||||      ::::::|||
Db        196 ---------ACTTCTGGCGATTCCACCATCATCTTGAGAATCGACCAGAGAAATCTATAC 246

Qy         71 ValValGlyTyr------------GlnAspLys------TrpAspGlyLysAspArgAla 84
              |||   ||||||            :::|||:::      |||:::       |||
Db        247 GTGCGTGGATATTCAAGAGATATTGAAGACGAACCATTTTGGGAGTTTTCAGAT------ 300

Qy         85 ValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThrAsn 104
                                          |||   |||   ||||||      :::
Db        301 --------------------------------TCATCTCTGATTCCTGGATCGAGACAT 327

Qy        105 ArgValThrLeuThrPheAspGlySerTyr---------GlnLysLeuValAsnAlaAla 121
                  |||   ::   |||||||||                  :::   ||||||
Db        328 ---------CTCGCATATGGTGGAAGCTATGTAGATGGTTACAATTTTATTGTTGCAGCC 378

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||   ::::::   ||||||:::      |||                  |||
Db        379 GGCACTACCCGCTTAAATGTTCATCTGGGTTTACCTAATTTGCGA---------AATGCC 429

Qy        142 IleTrpGlyLysThrGlnAsnGly 149
              |||         :::   ||||||
Db        430 ATTGCTAATCCTAGCAACAACGGA 453
```

RESULT 39
DN501509
LOCUS DN501509 644 bp mRNA linear EST 10-MAR-2005
DEFINITION UR108TF08.5pR Populus root cDNA library Populus tremula x Populus tremuloides cDNA clone UR108TF08 5', mRNA sequence.
ACCESSION DN501509
VERSION DN501509.1 GI:60711699
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
REFERENCE 1 (bases 1 to 644)
AUTHORS Sterky,F., Bhalerao,R.R., Unneberg,P., Segerman,B., Nilsson,P., Brunner,A.M., Charbonnel-Campaa,L., Lindvall,J.J., Tandre,K., Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P., Nilsson,O., Sandberg,G., Karlsson,J., Lundeberg,J. and Jansson,S.
TITLE A Populus EST resource for plant functional genomics
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
PUBMED 15353603
COMMENT Other_ESTs: UR108TF08, UR108TF08.3pR
Contact: Bo Segerman
Umea Plant Science Center, Department of Plant Physiology
Umea University
901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: bo.segerman@plantphys.umu.se.
FEATURES Location/Qualifiers
source 1. .644
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/clone="UR108TF08"
/tissue_type="root"
/clone_lib="Populus root cDNA library"

ORIGIN

Alignment Scores:

Pred. No.:	0.000244	Length:	644
Score:	111.50	Matches:	39
Percent Similarity:	47.1%	Conservative:	25
Best Local Similarity:	28.7%	Mismatches:	53
Query Match:	14.5%	Indels:	19
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x DN501509 (1-644)

```
Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeu------------AlaLysGlyThr 29
              |||      ||||||:::::::||||||      |||            :::
Db        137 TATCGAGCTTTCATTGAGAATCTACGTGTTCGATTGGGAGTGAGATTTTCCCACAATCTT 196

Qy         30 ProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeu 49
              |||                  :::   :::|||            :::   |||   |||
Db        197 CCTGCA------------CTTGCTGTTCAAGAGGAGCCACCCACTCGATTCTTCAATTTG 244

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||            |||:::         |||:::      :::   :::   ::::::
Db        245 GTA------ATACGAACCAACGATCACTTTGTGAGGTTCAGGTTGCGAATGGATAACCTG 298

Qy         70 TyrValValGlyTyrGln---------AspLysTrpAspGlyLysAspArgAlaValPhe 86
              ||||||:::|||||||||           :::|||                   |||
Db        299 TACGTGATTGGCTACCAGATGGAAAACGGACAGTGG--------------TTAGAGTTC 343

Qy         87 LeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgVal 106
                  ::::::      |||            |||   |||            |||
Db        344 GGCAACGAGAACGACACCCCTGTCCCTGAGCATCTAATTCCAGAACAAGGAACCAGATTC 403

Qy        107 ThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLys 126
              |||   ||||||||||||||   ||||||:::|||||||||   ::::::   :::
Db        404 ---CTAGGCTTCGATGGCAGCTACGGTAAGTTACTCAATGCTGCTGGCCTGAATATGGAG 460

Qy        127 AspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ::::::   :::|||   |||   |||   :::   |||      :::
Db        461 GAAGTAAGAGTTGGCTTCTACAACCTAAGGTACGGTATAAATCAGCTT 508
```

RESULT 40
DN142823
LOCUS DN142823 491 bp mRNA linear EST 16-FEB-2005
DEFINITION 5054_D09_G17 Switchgrass crown cDNA library Panicum virgatum cDNA clone 5054_D09_G17 5', mRNA sequence.
ACCESSION DN142823
VERSION DN142823.1 GI:59863680
KEYWORDS EST.
SOURCE Panicum virgatum (switchgrass)
ORGANISM Panicum virgatum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

```
            clade; Panicoideae; Paniceae; Panicum.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Tobias,C.M., Twigg,P., Hayden,D.M., Fladseth,M.R., Vivian,L.A.,
            Chow,E.K. and Sarath,G.
  TITLE     An EST survey of Switchgrass: a C4 perennial grass
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Tobias CM
            Genomics and Gene Discovery Unit
            USDA, Agricultural Research Service, Western Regional Research
            Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 510 559-6172
            Fax: 510 559-5818
            Email: ctobias@pw.usda.gov
            The phred basecalling program was used to call bases and identify
            the high scoring region using the -trim_alt '' and trim_cutoff 0.01
            options. Vector sequences have been removed using the program
            cross_match.
            Seq primer: M13 reverse.
FEATURES             Location/Qualifiers
     source          1. .491
                     /organism="Panicum virgatum"
                     /mol_type="mRNA"
                     /cultivar="Kanlow"
                     /db_xref="taxon:38727"
                     /clone="5054_D09_G17"
                     /dev_stage="6-8 week old plants"
                     /lab_host="E. coli DH5alpha"
                     /clone_lib="Switchgrass crown cDNA library"
                     /note="Organ: Crown; Vector: pSPORT1; Site_1: Sal1;
                     Site_2: Not1; Switchgrass cv. Kanlow plants were grown
                     from seed. Young crowns collected from approx 6-8 week old
                     glasshouse grown plants that were starting to tiller.
                     Crowns were cleaned of roots and tillers and flash frozen
                     in liquid nitrogen. The tissue was prepared by Gautam
                     Sarath, USDA, ARS, Wheat Forage and Sorghum Research Unit,
                     U. Nebraska, Lincoln. Total RNA and poly(A) RNA were
                     prepared, cDNA synthesized, and directionally ligated into
                     pSPORT1 by Paul Twigg, Biology Department, U. Nebraska
                     Kearney, Kearney, NE. Plasmid DNA preparations and DNA
                     sequencing were performed in the laboratory of CM Tobias."
ORIGIN

Alignment Scores:
Pred. No.:              0.000314        Length:         491
Score:                  109.50          Matches:        43
Percent Similarity:     44.7%           Conservative:   25
Best Local Similarity:  28.3%           Mismatches:     73
Query Match:            14.3%           Indels:         11
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x DN142823 (1-491)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||:::      :::      |||   |||||||||      ||||||
Db         37 ACGGTGACATTCAATGTC---AGGTCGGACTCGTACACGACGTTCATATCCACTCTCCGG 93

Qy         23 AsnGluLeuAlaLysGlyThrPro------ValCysGlnLeuProValThrLeuGlnThr 40
                 ||||||       |||      |||         ||||||      :::
Db         94 GGCGCACTAGCGGGCAGCAAACCCGACAAGGTGAAGGACCGCCCCGTGTTGGCCAAGCAG 153

Qy         41 IleAlaAspAspLys---------ArgPheValLeuValAspIleThrThrThrSerLys 57
                  :::               |||::::::   |||   :::|||
Db        154 ACCGGCGAGACCTCCCAGCCGCCGCGGTGGATCCACGTCGTGCTCACCGGCGACGACGGC 213

Qy         58 LysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLys 77
                    ||||||||||||         :::   |||:::   |||:::   ::::::
Db        214 GCCGCACCCAAGGTGGCCATCCGCAGCGACAACGCCTACATCGCTGGCTTCGCCAACCGG 273

Qy         78 TrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys 97
                 |||          |||:::      ::::::          :::::::::
Db        274 CCCAAGGGCAGCACTGAAGACGTGTGGTAC---CAGCTGAGCGCTAGGAACAGCACCCAG 330

Qy         98 LeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
              ||||||   |||                  |||   |||:::|||   |||      |||
Db        331 CTCTTCAAGGGCGCCAAG---------ATGCTCGGCTTCAATGGCCACTACTCGACGCTG 381

Qy        118 ValAsnAlaAlaLysVal---AspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              |||           |||   |||         |||:::||||||      :::
Db        382 GTCGGCGGCCAGGGCGTCAAAGACCTGCCGACCCTGAAGCTCGGCAAGGAGAGGACGTTG 441

Qy        137 PheSerIleGluAlaIleTrpGlyLysThrGlnAsn 148
                 :::       :::|||         |||:::
Db        442 GAGGCCGCCACCGTCCTCTGGAGCTACAAGCAGGAC 477


Search completed: February 20, 2006, 02:07:47
Job time : 5253.3 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:54:27 ; Search time 6017.44 Seconds
(without alignments)
1407.522 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 149
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 1

Total number of hits satisfying chosen parameters: 11757775

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160833_4016/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10758902_@CGN_1_1_5142_@runat_17022006_160833_4016 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	142	95.3	1387	15	AF445416	AF445416 Bougainvi
2	120	80.5	363	6	A82773	A82773 Sequence 8
3	120	80.5	363	6	AR454123	AR454123 Sequence
4	98	65.8	1085	15	AY437531	AY437531 Bougainvi
5	21	14.1	65	6	A82770	A82770 Sequence 5
6	21	14.1	65	6	AR454120	AR454120 Sequence
7	10	6.7	242506	14	AC094821	AC094821 Rattus no
c 8	9	6.0	1637	5	BC086634	BC086634 Xenopus l
c 9	9	6.0	110000	14	TANN2_02	Continuation (3 of
c 10	9	6.0	140020	14	AC046162	AC046162 Homo sapi
11	9	6.0	172555	14	AC150461	AC150461 Callithri
12	9	6.0	179641	8	AC098591	AC098591 Homo sapi
c 13	9	6.0	191191	8	AC000119	AC000119 Homo sapi
14	9	6.0	198134	14	AC024117	AC024117 Homo sapi
15	9	6.0	208404	9	AC102364	AC102364 Mus muscu
16	9	6.0	241803	14	AC096458	AC096458 Rattus no
17	9	6.0	242531	9	AC108805	AC108805 Mus muscu
18	9	6.0	244273	14	AC106167	AC106167 Rattus no
19	8	5.4	324	1	BCCSPCGEN	X93041 B.cereus cs
c 20	8	5.4	549	10	BV363497	BV363497 S231P6376
21	8	5.4	610	9	BC048651	BC048651 Mus muscu
22	8	5.4	720	15	CNS018XO	AL110931 Botrytis
23	8	5.4	724	10	BV631147	BV631147 S215P6346
24	8	5.4	752	10	BV512710	BV512710 rag91f07.
25	8	5.4	937	1	AY744941	AY744941 Mycoplasm
c 26	8	5.4	979	6	AR353769	AR353769 Sequence
c 27	8	5.4	979	6	AX082393	AX082393 Sequence
28	8	5.4	1104	13	AY444911	AY444911 Avian ort
29	8	5.4	1104	13	AY444913	AY444913 Avian ort
30	8	5.4	1228	15	AB050491	AB050491 Vitreochl
31	8	5.4	1238	6	AX069004	AX069004 Sequence
32	8	5.4	1320	15	AY612682	AY612682 Saccoloma
33	8	5.4	1320	15	OKU18644	U18644 Orthiopteri
34	8	5.4	1364	15	DQ013264	DQ013264 Bougainvi
c 35	8	5.4	1449	15	S76264	S76264 NR1=nitrate
36	8	5.4	1676	15	AK069521	AK069521 Oryza sat
37	8	5.4	1702	5	CR848128	CR848128 Xenopus t
c 38	8	5.4	1905	6	CQ797957	CQ797957 Sequence
c 39	8	5.4	2000	6	AX510374	AX510374 Sequence
c 40	8	5.4	2000	6	AX652416	AX652416 Sequence
41	8	5.4	2108	8	BC069192	BC069192 Homo sapi
42	8	5.4	2134	8	AF374416	AF374416 Homo sapi
c 43	8	5.4	2199	15	BT018755	BT018755 Zea mays
44	8	5.4	2291	6	CQ845798	CQ845798 Sequence
45	8	5.4	2291	8	AK131393	AK131393 Homo sapi
46	8	5.4	2437	5	AF522297	AF522297 Ictalurus
47	8	5.4	2454	5	AF522298	AF522298 Ictalurus
c 48	8	5.4	5413	2	DSU289802	AJ289802 Drosophil
c 49	8	5.4	5448	2	DSU289798	AJ289798 Drosophil
c 50	8	5.4	5467	2	DSU289800	AJ289800 Drosophil
c 51	8	5.4	6413	6	AX251116	AX251116 Sequence
c 52	8	5.4	6413	6	AX458484	AX458484 Sequence
c 53	8	5.4	7046	5	BC084217	BC084217 Xenopus l
c 54	8	5.4	7900	15	AY277723	AY277723 Botryotin
55	8	5.4	9903	1	AE009761	AE009761 Pyrobacul
56	8	5.4	15626	2	AF507073	AF507073 Trypanoso
57	8	5.4	17981	14	AC153364_5	Continuation (6 of
c 58	8	5.4	36372	14	AC019920	AC019920 Drosophil
59	8	5.4	41984	2	CBRG42E09	AC084593 Caenorhab
c 60	8	5.4	42282	2	CEC08H9	Z54342 Caenorhabdi
61	8	5.4	47872	14	AC106844	AC106844 Mus muscu
62	8	5.4	55266	8	AY192161	AY192161 Homo sapi
c 63	8	5.4	62536	8	AC005692	AC005692 Homo sapi
c 64	8	5.4	63032	14	AC025363	AC025363 Homo sapi
c 65	8	5.4	67778	14	AC101009	AC101009 Mus muscu
c 66	8	5.4	75586	14	AC021444	AC021444 Mus muscu
c 67	8	5.4	76351	5	BX957329	BX957329 Zebrafish
c 68	8	5.4	78680	8	AC010228	AC010228 Homo sapi
69	8	5.4	82454	15	AC012193	AC012193 Arabidops
c 70	8	5.4	84371	14	AP001963	AP001963 Homo sapi
c 71	8	5.4	84540	8	AC107031	AC107031 Homo sapi
72	8	5.4	85813	15	AP006644	AP006644 Lotus cor
c 73	8	5.4	88733	14	AC132855	AC132855 Homo sapi
74	8	5.4	91219	8	AL162719	AL162719 Human DNA
c 75	8	5.4	91573	8	AC012372	AC012372 Homo sapi
76	8	5.4	91587	1	AE016970	AE016970 Mycoplasm

	77	8	5.4	91863	15	AC004667 AC004667 Arabidops
c	78	8	5.4	93244	14	CT009621 CT009621 Danio rer
c	79	8	5.4	96334	14	AC021343 AC021343 Homo sapi
c	80	8	5.4	97191	15	AP004499 AP004499 Lotus cor
c	81	8	5.4	106267	14	AP000749 AP000749 Homo sapi
c	82	8	5.4	107641	9	AF125313 AF125313 Mus muscu
	83	8	5.4	110000	1	AE017180_35 Continuation (36 o
	84	8	5.4	110000	1	AP006840_00 AP006840 Symbiobac
	85	8	5.4	110000	1	AP006840_02 Continuation (3 of
	86	8	5.4	110000	1	AP006840_08 Continuation (9 of
c	87	8	5.4	110000	1	AP006840_29 Continuation (30 o
c	88	8	5.4	110000	1	AP006840_34 Continuation (35 o
	89	8	5.4	110000	1	BA000019_60 Continuation (61 o
	90	8	5.4	110000	1	BX897700_04 Continuation (5 of
c	91	8	5.4	110000	14	AC098193_4 Continuation (5 of
c	92	8	5.4	110000	14	AC108609_2 Continuation (3 of
	93	8	5.4	110000	14	AC153364_4 Continuation (5 of
c	94	8	5.4	110000	14	BX276116_02 Continuation (3 of
	95	8	5.4	110000	14	CR954205_5 Continuation (6 of
c	96	8	5.4	110000	14	CR954206_3 Continuation (4 of
c	97	8	5.4	110000	14	TANN3_10 Continuation (11 o
	98	8	5.4	110000	15	AP008217_191 Continuation (192
	99	8	5.4	110000	15	CR380954_08 Continuation (9 of
	100	8	5.4	110000	15	CR382132_30 Continuation (31 o
c	101	8	5.4	110000	15	CR382136_11 Continuation (12 o
c	102	8	5.4	110000	15	CR382136_12 Continuation (13 o
	103	8	5.4	110000	15	AP008208_151 Continuation (152
	104	8	5.4	110000	15	AP008208_152 Continuation (153
c	105	8	5.4	110000	15	AP008210_172 Continuation (173
c	106	8	5.4	110000	15	AP008211_012 Continuation (13 o
c	107	8	5.4	110000	15	AP008212_021 Continuation (22 o
	108	8	5.4	111130	15	AC144516 AC144516 Medicago
	109	8	5.4	114337	9	AC122019 AC122019 Mus muscu
	110	8	5.4	119095	15	AC144515 AC144515 Medicago
	111	8	5.4	123323	8	AP001816 AP001816 Homo sapi
	112	8	5.4	124133	5	BX649630 BX649630 Zebrafish
	113	8	5.4	126042	5	CR735103 CR735103 Zebrafish
	114	8	5.4	127549	14	AC155384 AC155384 Zea mays
c	115	8	5.4	128990	8	AC113344 AC113344 Homo sapi
c	116	8	5.4	131366	8	AL354701 AL354701 Human DNA
	117	8	5.4	133621	9	AC132585 AC132585 Mus muscu
	118	8	5.4	134006	14	AC124166 AC124166 Felis cat
c	119	8	5.4	135809	15	AC079021 AC079021 Oryza sat
c	120	8	5.4	138187	2	AC159438 AC159438 Trypanoso
c	121	8	5.4	140055	14	AP005013 AP005013 Homo sapi
c	122	8	5.4	140572	8	AL354743 AL354743 Human DNA
	123	8	5.4	142422	9	AL844588 AL844588 Mouse DNA
c	124	8	5.4	143900	5	AL929400 AL929400 Zebrafish
	125	8	5.4	146008	15	AP005608 AP005608 Oryza sat
	126	8	5.4	146059	5	AL929549 AL929549 Zebrafish
c	127	8	5.4	148008	14	AC130471 AC130471 Homo sapi
c	128	8	5.4	148142	8	AC011421 AC011421 Homo sapi
c	129	8	5.4	148423	8	HSJ875J14 AL109753 Human DNA
	130	8	5.4	150755	9	AC154274 AC154274 Mus muscu
c	131	8	5.4	151208	9	AC132306 AC132306 Mus muscu
	132	8	5.4	151492	8	CR376864 CR376864 Pan trogl
c	133	8	5.4	152220	15	OSJN00166 AL662967 Oryza sat
c	134	8	5.4	152336	8	AP004714 AP004714 Homo sapi
	135	8	5.4	154918	14	AC166157 AC166157 Mus muscu
c	136	8	5.4	155629	14	AC108196 AC108196 Felis cat
	137	8	5.4	156840	14	AC146810 AC146810 Zea mays
	138	8	5.4	157158	2	AC159411 AC159411 Trypanoso
	139	8	5.4	158792	15	AP005696 AP005696 Oryza sat
	140	8	5.4	158807	14	AC011771 AC011771 Homo sapi
	141	8	5.4	161280	8	AP000676 AP000676 Homo sapi
c	142	8	5.4	161451	8	AL355989 AL355989 Human DNA
	143	8	5.4	161485	9	AC159100 AC159100 Mus muscu
c	144	8	5.4	162489	8	AP001572 AP001572 Homo sapi
c	145	8	5.4	163209	14	AC007949 AC007949 Homo sapi
c	146	8	5.4	163230	15	AP003708 AP003708 Oryza sat
	147	8	5.4	163387	8	AC146920 AC146920 Otolemur
	148	8	5.4	163403	2	AC007765 AC007765 Drosophil
	149	8	5.4	163599	8	HSDJ81D8 AL109933 Human DNA
	150	8	5.4	164920	2	AC092187 AC092187 Drosophil
c	151	8	5.4	165507	14	AC155537 AC155537 Zea mays
c	152	8	5.4	165575	14	AC007994 AC007994 Mus muscu
	153	8	5.4	165720	9	AL732475 AL732475 Mouse DNA
	154	8	5.4	165802	8	AL135914 AL135914 Human DNA
c	155	8	5.4	166194	14	AC139647 AC139647 Rattus no
	156	8	5.4	166428	8	AC146879 AC146879 Otolemur
	157	8	5.4	166860	9	AC115924 AC115924 Mus muscu
	158	8	5.4	169225	8	AC146208 AC146208 Pan trogl
c	159	8	5.4	169841	8	AC099793 AC099793 Homo sapi
c	160	8	5.4	170388	14	AC027750 AC027750 Homo sapi
	161	8	5.4	170404	8	AC012493 AC012493 Homo sapi
c	162	8	5.4	170429	9	AC142146 AC142146 Mus muscu
c	163	8	5.4	170533	8	AP003356 AP003356 Homo sapi
	164	8	5.4	171713	9	AC154587 AC154587 Mus muscu
c	165	8	5.4	172210	9	AC122562 AC122562 Mus muscu
c	166	8	5.4	172714	9	AC112269 AC112269 Mus muscu
c	167	8	5.4	173882	5	BX640462 BX640462 Zebrafish
	168	8	5.4	175178	14	AC011783 AC011783 Homo sapi
	169	8	5.4	175425	15	AC108223 AC108223 Oryza sat
	170	8	5.4	176753	5	CR391999 CR391999 Zebrafish
	171	8	5.4	177087	14	AC093687 AC093687 Homo sapi
c	172	8	5.4	177623	9	AC138667 AC138667 Mus muscu
c	173	8	5.4	177734	8	AC073569 AC073569 Homo sapi
c	174	8	5.4	177878	14	AC010893 AC010893 Homo sapi
c	175	8	5.4	179681	14	AC013785 AC013785 Homo sapi
	176	8	5.4	180590	5	AL954656 AL954656 Zebrafish
	177	8	5.4	181050	14	AC141642 AC141642 Mus muscu
	178	8	5.4	182150	9	AC044807 AC044807 Mus muscu
c	179	8	5.4	182926	9	AC118620 AC118620 Mus muscu
	180	8	5.4	184736	14	CT025568 CT025568 Mus muscu
	181	8	5.4	185830	14	AC146924 AC146924 Otolemur
	182	8	5.4	187245	14	CT025543 CT025543 Danio rer
c	183	8	5.4	187816	9	AL606919 AL606919 Mouse DNA
	184	8	5.4	188148	14	AC152016 AC152016 Callithri
c	185	8	5.4	188408	14	AC155541 AC155541 Zea mays
c	186	8	5.4	189341	14	AC147190 AC147190 Otolemur
	187	8	5.4	189941	14	AC128854 AC128854 Rattus no
	188	8	5.4	190041	14	AC163680 AC163680 Mus muscu
c	189	8	5.4	190653	9	AC118022 AC118022 Mus muscu
c	190	8	5.4	191541	4	AC144399 AC144399 Oryctolag
	191	8	5.4	191713	14	CR925834 CR925834 Danio rer
c	192	8	5.4	191908	14	AC155594 AC155594 Zea mays
	193	8	5.4	192000	1	AE001438 AE001438 Clostridi
	194	8	5.4	193211	9	AC130823 AC130823 Mus muscu
c	195	8	5.4	193870	9	AL731674 AL731674 Mouse DNA
	196	8	5.4	194209	5	BX248318 BX248318 Zebrafish
c	197	8	5.4	194376	14	CR933558 CR933558 Danio rer
	198	8	5.4	194520	9	AL691424 AL691424 Mouse DNA
c	199	8	5.4	196162	9	AC108508 AC108508 Genomic s
c	200	8	5.4	196404	14	AC150221 AC150221 Callithri
	201	8	5.4	197426	9	AC153892 AC153892 Mus muscu
	202	8	5.4	199854	9	AL591208 AL591208 Mouse DNA
	203	8	5.4	200107	14	AC150008 AC150008 Callithri
c	204	8	5.4	200465	14	AC161416 AC161416 Mus muscu
	205	8	5.4	201868	14	AC149841 AC149841 Papio anu
	206	8	5.4	203138	5	BX640539 BX640539 Zebrafish
	207	8	5.4	203414	9	AL845296 AL845296 Mouse DNA
c	208	8	5.4	203718	8	AC009486 AC009486 Homo sapi
	209	8	5.4	204328	14	AL591119 AL591119 Homo sapi
c	210	8	5.4	205015	9	AC007937 AC007937 Mus muscu
	211	8	5.4	205508	9	AC079243 AC079243 Mus muscu
	212	8	5.4	205734	9	AC125065 AC125065 Mus muscu
c	213	8	5.4	205949	14	AC134940 AC134940 Rattus no
c	214	8	5.4	206094	9	AC129583 AC129583 Mus muscu
c	215	8	5.4	206383	14	AC166604 AC166604 Oryctolag
	216	8	5.4	206806	14	AC147189 AC147189 Otolemur
c	217	8	5.4	207365	14	AC093653 AC093653 Homo sapi
c	218	8	5.4	207845	14	AC108507 AC108507 Mus muscu
	219	8	5.4	208341	8	AC107933 AC107933 Homo sapi
	220	8	5.4	209119	14	AC083818 AC083818 Mus muscu
	221	8	5.4	215381	9	CR382328 CR382328 Mouse DNA
c	222	8	5.4	215756	9	AC087889 AC087889 Mus Muscu

	223	8	5.4	216998	14	AC109936 AC109936 Rattus no
c	224	8	5.4	217229	14	AC161656 AC161656 Bos tauru
	225	8	5.4	218249	14	AC097425 AC097425 Rattus no
	226	8	5.4	219903	14	AC098309 AC098309 Rattus no
c	227	8	5.4	222180	9	AC161058 AC161058 Mus muscu
	228	8	5.4	222808	14	AC130053 AC130053 Rattus no
c	229	8	5.4	223267	9	AC123662 AC123662 Mus muscu
c	230	8	5.4	223820	14	AC161463 AC161463 Gallus ga
c	231	8	5.4	224028	14	AC111276 AC111276 Rattus no
c	232	8	5.4	226657	9	AL731843 AL731843 Mouse DNA
c	233	8	5.4	227646	14	AC125687 AC125687 Rattus no
	234	8	5.4	228200	14	AC138253 AC138253 Mus muscu
c	235	8	5.4	228743	14	AC161992 AC161992 Bos tauru
	236	8	5.4	228995	14	AC136961 AC136961 Rattus no
	237	8	5.4	230706	14	AC134261 AC134261 Rattus no
c	238	8	5.4	230783	14	AC118913 AC118913 Rattus no
c	239	8	5.4	232473	9	AC122896 AC122896 Mus muscu
	240	8	5.4	233010	14	AC096368 AC096368 Rattus no
	241	8	5.4	236157	14	AC111356 AC111356 Rattus no
	242	8	5.4	236333	14	AC162989 AC162989 Bos tauru
	243	8	5.4	237096	14	AC131974 AC131974 Mus muscu
	244	8	5.4	240105	14	AC115207 AC115207 Rattus no
	245	8	5.4	240787	14	AC107683 AC107683 Mus muscu
c	246	8	5.4	242558	5	BX088589 BX088589 Zebrafish
c	247	8	5.4	243563	14	AC098187 AC098187 Rattus no
c	248	8	5.4	244604	14	AC120277 AC120277 Rattus no
	249	8	5.4	244962	14	AC098272 AC098272 Rattus no
c	250	8	5.4	245468	14	AC109534 AC109534 Rattus no
c	251	8	5.4	249701	14	AC106525 AC106525 Rattus no
c	252	8	5.4	250770	14	AC140246 AC140246 Mus muscu
c	253	8	5.4	253389	14	AC151293 AC151293 Mus muscu
	254	8	5.4	258088	14	AC131516 AC131516 Rattus no
c	255	8	5.4	258658	2	AE014832 AE014832 Plasmodiu
	256	8	5.4	258907	14	AC115190 AC115190 Rattus no
	257	8	5.4	265438	14	AC129451 AC129451 Rattus no
c	258	8	5.4	269153	5	BX571947 BX571947 Zebrafish
	259	8	5.4	270856	14	AC164034 AC164034 Bos tauru
	260	8	5.4	271105	14	AC163917 AC163917 Bos tauru
c	261	8	5.4	271229	14	AC107649 AC107649 Mus muscu
	262	8	5.4	283054	14	AC160292 AC160292 Bos tauru
c	263	8	5.4	284337	14	AC119016 AC119016 Rattus no
c	264	8	5.4	289751	9	AC091458 AC091458 Mus muscu
c	265	8	5.4	292533	14	AC107260 AC107260 Rattus no
	266	8	5.4	295001	14	AC118175 AC118175 Rattus no
c	267	8	5.4	296171	14	AC153296 AC153296 Bos tauru
c	268	8	5.4	300363	1	AE016781 AE016781 Pseudomon
c	269	8	5.4	302529	1	AE016851 AE016851 Tropherym
c	270	8	5.4	307462	14	AC112828 AC112828 Rattus no
c	271	8	5.4	314957	2	AE003581 AE003581 Drosophil
	272	8	5.4	318044	14	AC163505 AC163505 Bos tauru
	273	8	5.4	324050	1	BX251410 BX251410 Tropherym
	274	8	5.4	335638	14	AC135235 AC135235 Mus muscu
c	275	8	5.4	336678	14	AL355363 AL355363 Homo sapi
c	276	8	5.4	344954	14	AC163141 AC163141 Bos tauru
	277	8	5.4	349980	6	AX344559 AX344559 Sequence
	278	7	4.7	23	6	A82768 A82768 Sequence 3
c	279	7	4.7	23	6	A82769 A82769 Sequence 4
	280	7	4.7	23	6	AR454118 AR454118 Sequence
c	281	7	4.7	23	6	AR454119 AR454119 Sequence
	282	7	4.7	25	6	A82771 A82771 Sequence 6
	283	7	4.7	25	6	AR454121 AR454121 Sequence
c	284	7	4.7	51	9	U92119 U92119 Mus musculu
	285	7	4.7	90	6	AX451463 AX451463 Sequence
c	286	7	4.7	117	6	CQ658591 CQ658591 Sequence
	287	7	4.7	150	6	CQ706583 CQ706583 Sequence
	288	7	4.7	156	15	PSITS2156 Y15832 Phoma sp. H
c	289	7	4.7	166	6	CQ081185 CQ081185 Sequence
c	290	7	4.7	166	6	CQ115713 CQ115713 Sequence
c	291	7	4.7	166	6	CQ312329 CQ312329 Sequence
c	292	7	4.7	166	6	CQ349773 CQ349773 Sequence
	293	7	4.7	177	8	AY523800S1 AY523800 Homo sapi
	294	7	4.7	177	8	AY523802S1 AY523802 Homo sapi
c	295	7	4.7	179	13	HEC406073 AJ406073 Hepatitis
c	296	7	4.7	179	13	HEC406074 AJ406074 Hepatitis
c	297	7	4.7	179	13	HEC406075 AJ406075 Hepatitis
c	298	7	4.7	179	13	HEC406077 AJ406077 Hepatitis
	299	7	4.7	180	8	AY523790S1 AY523790 Homo sapi
	300	7	4.7	180	8	AY523792S1 AY523792 Homo sapi
	301	7	4.7	180	8	AY523794S1 AY523794 Homo sapi
	302	7	4.7	180	8	AY523796S1 AY523796 Homo sapi
	303	7	4.7	194	1	AF500162 AF500162 Salmonell
	304	7	4.7	201	10	BV180934 BV180934 sqnm11290
	305	7	4.7	201	10	BV180940 BV180940 sqnm11292
	306	7	4.7	201	10	BV203725 BV203725 sqnm21287
	307	7	4.7	201	10	BV203760 BV203760 sqnm21296
	308	7	4.7	201	10	BV203761 BV203761 sqnm21296
	309	7	4.7	201	10	BV203762 BV203762 sqnm21296
	310	7	4.7	201	10	BV203763 BV203763 sqnm21296
c	311	7	4.7	213	13	AY936049 AY936049 Hepatitis
c	312	7	4.7	215	13	AY536076 AY536076 Hepatitis
	313	7	4.7	217	8	AY523798S1 AY523798 Homo sapi
	314	7	4.7	222	6	BD032920 BD032920 Sequence
	315	7	4.7	222	6	AX897387 AX897387 Sequence
	316	7	4.7	230	15	AY023499 AY023499 Oryza sat
	317	7	4.7	231	2	S58549 S58549 (microsatel
	318	7	4.7	236	6	BD023689 BD023689 Protein s
	319	7	4.7	241	2	AME509239 AJ509239 Apis mell
	320	7	4.7	263	6	BD023685 BD023685 Protein s
	321	7	4.7	264	1	AJ781001 AJ781001 Mycoplasm
	322	7	4.7	264	6	CQ112454 CQ112454 Sequence
	323	7	4.7	264	6	CQ113370 CQ113370 Sequence
	324	7	4.7	264	6	CQ114909 CQ114909 Sequence
	325	7	4.7	264	6	CQ151323 CQ151323 Sequence
	326	7	4.7	264	6	CQ152245 CQ152245 Sequence
	327	7	4.7	264	6	CQ153781 CQ153781 Sequence
	328	7	4.7	264	6	CQ185658 CQ185658 Sequence
	329	7	4.7	264	6	CQ234711 CQ234711 Sequence
	330	7	4.7	264	6	CQ235593 CQ235593 Sequence
	331	7	4.7	264	6	CQ237041 CQ237041 Sequence
	332	7	4.7	264	6	CQ272266 CQ272266 Sequence
	333	7	4.7	264	6	CQ273157 CQ273157 Sequence
	334	7	4.7	264	6	CQ274643 CQ274643 Sequence
	335	7	4.7	264	6	CQ310634 CQ310634 Sequence
	336	7	4.7	264	6	CQ347446 CQ347446 Sequence
	337	7	4.7	274	15	PHEXRRNA2 AF079895 Phoma exi
	338	7	4.7	274	15	PHFORRNA2 AF079893 Phoma fov
c	339	7	4.7	278	13	AY793080 AY793080 Hepatitis
c	340	7	4.7	278	13	AY793081 AY793081 Hepatitis
c	341	7	4.7	278	13	AY793082 AY793082 Hepatitis
c	342	7	4.7	278	13	AY793084 AY793084 Hepatitis
c	343	7	4.7	278	13	AY793085 AY793085 Hepatitis
c	344	7	4.7	278	13	AY793086 AY793086 Hepatitis
c	345	7	4.7	278	13	AY793087 AY793087 Hepatitis
c	346	7	4.7	278	13	AY793088 AY793088 Hepatitis
c	347	7	4.7	278	13	AY793089 AY793089 Hepatitis
c	348	7	4.7	278	13	AY793090 AY793090 Hepatitis
c	349	7	4.7	278	13	AY793091 AY793091 Hepatitis
c	350	7	4.7	278	13	AY793092 AY793092 Hepatitis
c	351	7	4.7	278	13	AY793093 AY793093 Hepatitis
c	352	7	4.7	278	13	AY793094 AY793094 Hepatitis
c	353	7	4.7	278	13	AY793109 AY793109 Hepatitis
c	354	7	4.7	278	13	AY793111 AY793111 Hepatitis
c	355	7	4.7	278	13	AY793112 AY793112 Hepatitis
c	356	7	4.7	278	13	AY793113 AY793113 Hepatitis
	357	7	4.7	279	6	BD265831 BD265831 Schizophr
	358	7	4.7	279	6	BD265854 BD265854 Schizophr
	359	7	4.7	279	6	AR244361 AR244361 Sequence
	360	7	4.7	279	6	AR244384 AR244384 Sequence
	361	7	4.7	279	8	HS68A6F Z62372 H.sapiens C
c	362	7	4.7	279	13	AY338835 AY338835 Hepatitis
c	363	7	4.7	279	13	AY338840 AY338840 Hepatitis
	364	7	4.7	280	6	BD265843 BD265843 Schizophr
	365	7	4.7	280	6	BD265866 BD265866 Schizophr
	366	7	4.7	280	6	BD265878 BD265878 Schizophr
	367	7	4.7	280	6	AR244373 AR244373 Sequence
	368	7	4.7	280	6	AR244396 AR244396 Sequence

	369	7	4.7	280	6	AR244408 AR244408 Sequence
	370	7	4.7	282	1	AJ780988 AJ780988 Mycoplasm
	371	7	4.7	291	8	F314931S11 AF314941 Homo sapi
	372	7	4.7	297	6	AX237347 AX237347 Sequence
	373	7	4.7	300	6	CQ753071 CQ753071 Sequence
	374	7	4.7	304	8	HSACO2G13 AF093092 Homo sapi
	375	7	4.7	306	8	AF303899 AF303899 Homo sapi
	376	7	4.7	308	1	AJ781002 AJ781002 Mycoplasm
	377	7	4.7	312	10	BV120882 BV120882 PZA00916
	378	7	4.7	312	10	BV120883 BV120883 PZA00916
	379	7	4.7	318	10	AB135065 AB135065 Homo sapi
	380	7	4.7	322	1	AY566216 AY566216 Mycoplasm
	381	7	4.7	322	10	BV100274 BV100274 RPAMMSEQ0
	382	7	4.7	322	10	BV162632 BV162632 RPAMMSEQ0
	383	7	4.7	331	8	HSKIRP2 AF133897 Homo sapi
c	384	7	4.7	331	9	AF232726 AF232726 Marmota m
	385	7	4.7	341	15	AF509876 AF509876 Petunia x
	386	7	4.7	342	10	BV179333 BV179333 sqnm10490
	387	7	4.7	349	2	DQ018879 DQ018879 Baliochil
	388	7	4.7	350	2	AF233548 AF233548 Baliochil
c	389	7	4.7	353	2	AF233385 AF233385 Poecilimo
c	390	7	4.7	356	6	BD026300 BD026300 Sequence
c	391	7	4.7	356	6	AX886690 AX886690 Sequence
	392	7	4.7	356	6	BD023680 BD023680 Protein s
	393	7	4.7	357	6	CQ946566 CQ946566 Sequence
	394	7	4.7	357	6	AX606845 AX606845 Sequence
	395	7	4.7	360	6	CQ645042 CQ645042 Sequence
	396	7	4.7	368	6	CQ476872 CQ476872 Sequence
	397	7	4.7	382	8	AB062031 AB062031 Pan trogl
	398	7	4.7	382	8	AB062032 AB062032 Pan trogl
	399	7	4.7	387	6	CQ506797 CQ506797 Sequence
	400	7	4.7	388	6	BD265829 BD265829 Schizophr
	401	7	4.7	388	6	BD265852 BD265852 Schizophr
	402	7	4.7	388	6	AR244359 AR244359 Sequence
	403	7	4.7	388	6	AR244382 AR244382 Sequence
	404	7	4.7	389	6	BD265841 BD265841 Schizophr
	405	7	4.7	389	6	BD265864 BD265864 Schizophr
	406	7	4.7	389	6	BD265876 BD265876 Schizophr
	407	7	4.7	389	6	AR244371 AR244371 Sequence
	408	7	4.7	389	6	AR244394 AR244394 Sequence
	409	7	4.7	389	6	AR244406 AR244406 Sequence
	410	7	4.7	401	8	HS2KIR6 AF134315 Homo sapi
c	411	7	4.7	401	10	BV195641 BV195641 sqnm18531
c	412	7	4.7	405	10	BV090638 BV090638 RPAMMSEQ0
	413	7	4.7	420	10	G46576 G46576 Z14306_1 Ze
	414	7	4.7	423	6	AX440403 AX440403 Sequence
	415	7	4.7	427	10	G75745 G75745 8-130 Perip
c	416	7	4.7	431	6	CQ486483 CQ486483 Sequence
c	417	7	4.7	432	6	BD267249 BD267249 Compositi
c	418	7	4.7	432	6	AR566770 AR566770 Sequence
	419	7	4.7	432	8	AY102624 AY102624 Homo sapi
	420	7	4.7	439	6	AR128236 AR128236 Sequence
	421	7	4.7	443	8	AF082949 AF082949 Homo sapi
	422	7	4.7	449	1	AF443613 AF443613 Mycoplasm
	423	7	4.7	450	1	AF443606 AF443606 Mycoplasm
	424	7	4.7	454	15	AY618247 AY618247 Phoma exi
c	425	7	4.7	455	15	AY805589 AY805589 Phoma her
	426	7	4.7	459	8	AF135566 AF135566 Homo sapi
	427	7	4.7	460	6	CQ662786 CQ662786 Sequence
c	428	7	4.7	461	6	AR264016 AR264016 Sequence
	429	7	4.7	463	6	CQ050585 CQ050585 Sequence
	430	7	4.7	463	6	CQ065633 CQ065633 Sequence
	431	7	4.7	463	6	CQ092603 CQ092603 Sequence
	432	7	4.7	463	6	CQ131405 CQ131405 Sequence
	433	7	4.7	463	6	CQ170016 CQ170016 Sequence
	434	7	4.7	463	6	CQ199163 CQ199163 Sequence
	435	7	4.7	463	6	CQ214612 CQ214612 Sequence
	436	7	4.7	463	6	CQ253216 CQ253216 Sequence
	437	7	4.7	463	6	CQ290356 CQ290356 Sequence
	438	7	4.7	463	6	CQ327316 CQ327316 Sequence
c	439	7	4.7	472	10	BV289128 BV289128 S232P6517
c	440	7	4.7	472	13	AJ866168 AJ866168 Hepatitis
	441	7	4.7	473	6	CQ697103 CQ697103 Sequence
c	442	7	4.7	475	6	CQ069897 CQ069897 Sequence
c	443	7	4.7	475	6	CQ097335 CQ097335 Sequence
c	444	7	4.7	475	6	CQ136165 CQ136165 Sequence
c	445	7	4.7	475	6	CQ174302 CQ174302 Sequence
c	446	7	4.7	475	6	CQ219465 CQ219465 Sequence
c	447	7	4.7	475	6	CQ257958 CQ257958 Sequence
c	448	7	4.7	475	6	CQ295270 CQ295270 Sequence
c	449	7	4.7	475	6	CQ331884 CQ331884 Sequence
c	450	7	4.7	475	15	AY787726 AY787726 Phoma exi
	451	7	4.7	476	1	AF443607 AF443607 Mycoplasm
	452	7	4.7	476	6	AX741668 AX741668 Sequence
	453	7	4.7	476	6	AX776491 AX776491 Sequence
	454	7	4.7	476	15	AF268186 AF268186 Phoma exi
c	455	7	4.7	478	6	CQ431554 CQ431554 Sequence
	456	7	4.7	480	15	AF268192 AF268192 Phoma exi
c	457	7	4.7	484	6	CQ892691 CQ892691 Sequence
	458	7	4.7	484	6	AX284224 AX284224 Sequence
	459	7	4.7	484	8	HSNKAT2A4 U97176 Homo sapien
c	460	7	4.7	484	15	NTA538552 AJ538552 Nicotiana
	461	7	4.7	484	15	AF268189 AF268189 Phoma exi
	462	7	4.7	485	15	AF268191 AF268191 Phoma des
	463	7	4.7	486	15	AF268182 AF268182 Phoma exi
	464	7	4.7	486	15	AF268185 AF268185 Phoma exi
	465	7	4.7	487	15	AF268183 AF268183 Phoma exi
c	466	7	4.7	488	10	BV007485 BV007485 MASC_STS1
	467	7	4.7	488	15	AF268187 AF268187 Phoma exi
	468	7	4.7	489	15	AF268190 AF268190 Phoma exi
	469	7	4.7	491	6	AR508380 AR508380 Sequence
	470	7	4.7	492	15	AF268184 AF268184 Phoma exi
	471	7	4.7	493	15	AY210335 AY210335 Phoma sp.
	472	7	4.7	497	15	AY089978 AY089978 Phoma exi
c	473	7	4.7	498	6	CQ516297 CQ516297 Sequence
	474	7	4.7	502	15	AY305375 AY305375 Phoma sp.
	475	7	4.7	502	15	AY550992 AY550992 Phoma exi
	476	7	4.7	502	15	PSP493582 AJ493582 Phoma sp.
	477	7	4.7	504	15	AY207331 AY207331 Phoma sp.
c	478	7	4.7	506	15	AY207335 AY207335 Phoma sp.
	479	7	4.7	509	15	AY367351 AY367351 Phoma exi
c	480	7	4.7	510	1	AY004474 AY004474 Helicobac
c	481	7	4.7	511	10	BV009451 BV009451 MASC_STS1
c	482	7	4.7	511	10	BV366443 BV366443 S231P6131
	483	7	4.7	512	6	CQ101876 CQ101876 Sequence
	484	7	4.7	512	6	CQ140861 CQ140861 Sequence
	485	7	4.7	512	6	CQ224157 CQ224157 Sequence
	486	7	4.7	512	6	CQ262149 CQ262149 Sequence
c	487	7	4.7	512	8	HSA250855 AJ250855 Homo sapi
c	488	7	4.7	512	10	BV009453 BV009453 MASC_STS1
c	489	7	4.7	513	4	AF536282 AF536282 Equus cab
	490	7	4.7	513	6	AX284836 AX284836 Sequence
	491	7	4.7	513	8	AF135564 AF135564 Homo sapi
	492	7	4.7	513	10	BV009450 BV009450 MASC_STS1
	493	7	4.7	514	10	BV009448 BV009448 MASC_STS1
	494	7	4.7	522	5	AF069554 AF069554 Lampetra
	495	7	4.7	524	10	BV009444 BV009444 MASC_STS1
	496	7	4.7	525	10	BV009446 BV009446 MASC_STS1
	497	7	4.7	529	15	DQ093698 DQ093698 Phoma exi
c	498	7	4.7	531	10	BV009449 BV009449 MASC_STS1
	499	7	4.7	532	15	AY927784 AY927784 Phoma exi
	500	7	4.7	532	15	DQ093769 DQ093769 Phoma exi
c	501	7	4.7	533	10	BV009452 BV009452 MASC_STS1
	502	7	4.7	535	15	AY899262 AY899262 Phoma exi
c	503	7	4.7	536	10	BV009445 BV009445 MASC_STS1
	504	7	4.7	536	10	BV009447 BV009447 MASC_STS1
c	505	7	4.7	537	10	G79395 G79395 S209P6132RD
	506	7	4.7	538	15	AY131200 AY131200 Phoma exi
	507	7	4.7	541	15	AJ608976 AJ608976 Phoma exi
	508	7	4.7	542	10	BV240766 BV240766 S234P6502
c	509	7	4.7	543	6	CQ406899 CQ406899 Sequence
c	510	7	4.7	543	6	AX462317 AX462317 Sequence
	511	7	4.7	545	6	AX308734 AX308734 Sequence
	512	7	4.7	552	15	AF413038 AF413038 Fungal en
	513	7	4.7	553	15	AY514900 AY514900 Phoma sp.
	514	7	4.7	553	15	AF413036 AF413036 Fungal en

c	515	7	4.7	553	15	AJ839268 AJ839268 Arabidops
	516	7	4.7	554	10	BV155718 BV155718 RPAMMSEQ0
	517	7	4.7	555	10	BV091028 BV091028 RPAMMSEQ0
	518	7	4.7	557	6	CQ395589 CQ395589 Sequence
	519	7	4.7	557	6	CQ401922 CQ401922 Sequence
	520	7	4.7	557	6	BD023677 BD023677 Protein s
c	521	7	4.7	566	6	CQ071991 CQ071991 Sequence
c	522	7	4.7	566	6	CQ102656 CQ102656 Sequence
c	523	7	4.7	566	6	CQ299901 CQ299901 Sequence
c	524	7	4.7	566	6	CQ337109 CQ337109 Sequence
c	525	7	4.7	566	10	HS68E16S AL450193 H.sapiens
	526	7	4.7	570	10	BV237400 BV237400 S234P640F
	527	7	4.7	573	6	AX438951 AX438951 Sequence
c	528	7	4.7	574	6	CQ072816 CQ072816 Sequence
c	529	7	4.7	574	6	CQ103623 CQ103623 Sequence
c	530	7	4.7	574	6	CQ142457 CQ142457 Sequence
c	531	7	4.7	574	6	CQ177944 CQ177944 Sequence
c	532	7	4.7	574	6	CQ225695 CQ225695 Sequence
c	533	7	4.7	574	6	CQ263728 CQ263728 Sequence
c	534	7	4.7	574	6	CQ300804 CQ300804 Sequence
c	535	7	4.7	574	6	CQ338097 CQ338097 Sequence
c	536	7	4.7	574	10	BV350793 BV350793 S230P6166
c	537	7	4.7	574	15	PAB292701 AJ292701 Picea abi
c	538	7	4.7	576	10	BV266220 BV266220 S235P6179
	539	7	4.7	581	10	BV445893 BV445893 MARC 3634
c	540	7	4.7	585	6	AR385876 AR385876 Sequence
c	541	7	4.7	585	10	BV364577 BV364577 S231P6422
	542	7	4.7	586	6	CQ100292 CQ100292 Sequence
	543	7	4.7	586	6	CQ139280 CQ139280 Sequence
	544	7	4.7	586	6	CQ175781 CQ175781 Sequence
	545	7	4.7	586	6	CQ222666 CQ222666 Sequence
	546	7	4.7	586	6	CQ260619 CQ260619 Sequence
	547	7	4.7	586	6	CQ298202 CQ298202 Sequence
	548	7	4.7	586	6	CQ334755 CQ334755 Sequence
c	549	7	4.7	586	10	BV249192 BV249192 S234P6258
	550	7	4.7	587	10	BV063160 BV063160 S212P6016
	551	7	4.7	588	6	CQ523157 CQ523157 Sequence
	552	7	4.7	588	6	AX436488 AX436488 Sequence
c	553	7	4.7	589	10	BV291189 BV291189 S232P6206
	554	7	4.7	591	10	BV463108 BV463108 rqa87a10.
	555	7	4.7	596	8	AF082941 AF082941 Homo sapi
	556	7	4.7	596	8	AF177238 AF177238 Homo sapi
	557	7	4.7	596	8	AF177239 AF177239 Homo sapi
	558	7	4.7	596	10	BV004188 BV004188 S208P6407
	559	7	4.7	600	6	CQ099372 CQ099372 Sequence
	560	7	4.7	600	6	CQ138354 CQ138354 Sequence
	561	7	4.7	600	6	CQ221780 CQ221780 Sequence
	562	7	4.7	600	6	CQ259724 CQ259724 Sequence
	563	7	4.7	601	10	BV385967 BV385967 S244P6358
	564	7	4.7	602	10	G85266 G85266 S208P6440RG
	565	7	4.7	602	10	BV214767 BV214767 S233P638F
	566	7	4.7	602	10	BV313178 BV313178 S236P693F
	567	7	4.7	604	6	CQ738014 CQ738014 Sequence
c	568	7	4.7	605	10	BV258337 BV258337 S235P6343
c	569	7	4.7	607	10	BV390233 BV390233 S243P684F
c	570	7	4.7	608	10	G97019 G97019 S209P6029RA
	571	7	4.7	609	8	AF135554 AF135554 Homo sapi
	572	7	4.7	609	8	AF135555 AF135555 Homo sapi
	573	7	4.7	609	8	AF135556 AF135556 Homo sapi
	574	7	4.7	609	8	AF135557 AF135557 Homo sapi
	575	7	4.7	609	8	AF135559 AF135559 Homo sapi
	576	7	4.7	609	8	AF135560 AF135560 Homo sapi
	577	7	4.7	609	8	AF135561 AF135561 Homo sapi
	578	7	4.7	609	8	AF135562 AF135562 Homo sapi
	579	7	4.7	609	8	HSU96188 U96188 Homo sapien
	580	7	4.7	609	8	HSU96189 U96189 Homo sapien
	581	7	4.7	609	8	HSU96190 U96190 Homo sapien
	582	7	4.7	613	10	G96031 G96031 S208P6002RG
	583	7	4.7	615	6	CQ408306 CQ408306 Sequence
	584	7	4.7	617	10	BV003658 BV003658 S209P6128
c	585	7	4.7	618	10	BV244424 BV244424 S234P6330
	586	7	4.7	622	10	BV220886 BV220886 S233P6181
	587	7	4.7	633	10	G92545 G92545 S208P6695FH
c	588	7	4.7	635	10	BV347350 BV347350 S230P6170
	589	7	4.7	637	3	AY625577 AY625577 Unculture
c	590	7	4.7	638	10	BV265301 BV265301 S235P691R
c	591	7	4.7	644	10	BV429986 BV429986 S237P6264
c	592	7	4.7	648	10	BV305207 BV305207 S236P619F
	593	7	4.7	651	6	AR393990 AR393990 Sequence
c	594	7	4.7	654	10	BV295335 BV295335 S232P613F
c	595	7	4.7	654	15	BT005237 BT005237 Arabidops
c	596	7	4.7	657	10	BV360857 BV360857 S231P6504
	597	7	4.7	659	8	HSU87911 U87936 Human aconi
c	598	7	4.7	659	10	BV438678 BV438678 S237P6229
c	599	7	4.7	660	8	BT007398 BT007398 Homo sapi
c	600	7	4.7	661	10	BV069297 BV069297 S212P6779
	601	7	4.7	663	6	AR509265 AR509265 Sequence
c	602	7	4.7	663	10	BV631696 BV631696 S215P6121
	603	7	4.7	678	9	AH006793S2 U87615 Mus musculu
	604	7	4.7	678	10	G61747 G61747 SHGC-89059
	605	7	4.7	681	8	AY102623 AY102623 Homo sapi
	606	7	4.7	681	10	BV585498 BV585498 G591P6284
c	607	7	4.7	686	10	BV425456 BV425456 S237P6315
c	608	7	4.7	687	10	BV532574 BV532574 G591P6221
	609	7	4.7	690	10	BV455485 BV455485 pzr79d02.
	610	7	4.7	691	10	BV499878 BV499878 S222P643F
	611	7	4.7	693	6	AX436495 AX436495 Sequence
	612	7	4.7	693	10	BV072481 BV072481 S212P6604
	613	7	4.7	694	3	AY341333 AY341333 Unculture
c	614	7	4.7	695	15	AY174615 AY174615 Arabidops
c	615	7	4.7	696	15	AY174617 AY174617 Arabidops
c	616	7	4.7	697	10	BV032835 BV032835 S212P6050
c	617	7	4.7	697	15	AY174616 AY174616 Arabidops
c	618	7	4.7	697	15	AY174619 AY174619 Arabidops
c	619	7	4.7	697	15	AY174620 AY174620 Arabidops
c	620	7	4.7	697	15	AY174621 AY174621 Arabidops
c	621	7	4.7	697	15	AY174622 AY174622 Arabidops
c	622	7	4.7	697	15	AY174623 AY174623 Arabidops
c	623	7	4.7	698	15	AY174631 AY174631 Arabidops
c	624	7	4.7	699	15	AY174614 AY174614 Arabidops
c	625	7	4.7	699	15	AY174628 AY174628 Arabidops
c	626	7	4.7	700	15	AY174618 AY174618 Arabidops
c	627	7	4.7	700	15	AY174624 AY174624 Arabidops
c	628	7	4.7	700	15	AY174625 AY174625 Arabidops
c	629	7	4.7	700	15	AY174626 AY174626 Arabidops
c	630	7	4.7	700	15	AY174627 AY174627 Arabidops
c	631	7	4.7	700	15	AY174629 AY174629 Arabidops
c	632	7	4.7	700	15	AY174630 AY174630 Arabidops
c	633	7	4.7	703	13	HCVCR1E2 X72979 Hepatitis C
c	634	7	4.7	709	10	BV616484 BV616484 S215P6135
	635	7	4.7	711	10	BV133335 BV133335 PZA00648
	636	7	4.7	712	10	BV133323 BV133323 PZA00648
	637	7	4.7	715	4	BTVPAM92 Y15285 Bos taurus
c	638	7	4.7	720	10	BV576688 BV576688 G591P6083
	639	7	4.7	720	10	BV673647 BV673647 S215P6074
	640	7	4.7	723	6	AR544883 AR544883 Sequence
	641	7	4.7	727	6	CQ413456 CQ413456 Sequence
	642	7	4.7	727	6	CQ489569 CQ489569 Sequence
	643	7	4.7	727	6	CQ490567 CQ490567 Sequence
	644	7	4.7	727	6	CQ492860 CQ492860 Sequence
	645	7	4.7	727	6	CQ493739 CQ493739 Sequence
	646	7	4.7	727	6	CQ495410 CQ495410 Sequence
	647	7	4.7	727	6	CQ496401 CQ496401 Sequence
	648	7	4.7	727	6	AX284965 AX284965 Sequence
	649	7	4.7	731	6	AR655413 AR655413 Sequence
c	650	7	4.7	731	15	BT017562 BT017562 Zea mays
c	651	7	4.7	738	15	AY174656 AY174656 Arabidops
	652	7	4.7	739	10	BV676161 BV676161 S217P6069
	653	7	4.7	742	2	AY324135 AY324135 Babesia b
	654	7	4.7	742	6	BD265800 BD265800 Schizophr
	655	7	4.7	742	6	AR244330 AR244330 Sequence
	656	7	4.7	742	6	AX741666 AX741666 Sequence
	657	7	4.7	742	6	AX776489 AX776489 Sequence
	658	7	4.7	742	8	AY138546 AY138546 Homo sapi
c	659	7	4.7	745	10	BV591022 BV591022 G591P6420
c	660	7	4.7	745	15	AY174653 AY174653 Arabidops

c 661	7	4.7	745	15	AY174654	AY174654 Arabidops
c 662	7	4.7	746	5	BX933368	BX933368 Gallus ga
663	7	4.7	748	6	BD091088	BD091088 DNA chip
664	7	4.7	752	10	BV581324	BV581324 G591P6209
c 665	7	4.7	753	13	AY571864	AY571864 Vulture h
c 666	7	4.7	753	15	AY174655	AY174655 Arabidops
667	7	4.7	759	10	BV244570	BV244570 S234P6531
c 668	7	4.7	770	10	BV580379	BV580379 G591P6165
669	7	4.7	771	10	BV673569	BV673569 S215P6093
670	7	4.7	774	10	BV336969	BV336969 S230P6398
671	7	4.7	776	6	BD265806	BD265806 Schizophr
672	7	4.7	776	6	AR244336	AR244336 Sequence
c 673	7	4.7	776	15	AF494367	AF494367 Arabidops
674	7	4.7	777	6	BD265794	BD265794 Schizophr
675	7	4.7	777	6	AR244324	AR244324 Sequence
c 676	7	4.7	777	13	HEC507016	AJ507016 Hepatitis
677	7	4.7	778	10	BV591165	BV591165 G591P6414
678	7	4.7	778	10	BV495826	BV495826 S217P6165
c 679	7	4.7	781	10	BV612420	BV612420 S217P6115
c 680	7	4.7	781	10	BV488738	BV488738 S216P6147
681	7	4.7	783	6	I41255	I41255 Sequence 1
c 682	7	4.7	786	10	BV588228	BV588228 G591P6370
c 683	7	4.7	787	10	BV481469	BV481469 svu15c06.
684	7	4.7	790	6	BD145495	BD145495 Primer fo
685	7	4.7	790	6	AX865433	AX865433 Sequence
c 686	7	4.7	796	10	BV485960	BV485960 S215P6076
687	7	4.7	798	15	LAF532730	AJ532730 Limeum af
c 688	7	4.7	800	10	BV482823	BV482823 soq36h05.
c 689	7	4.7	802	10	BV580179	BV580179 G591P6165
690	7	4.7	803	10	BV525861	BV525861 G591P6071
c 691	7	4.7	805	10	BV582031	BV582031 G591P6189
c 692	7	4.7	806	10	BV564499	BV564499 qzh19d12.
693	7	4.7	807	6	AX283940	AX283940 Sequence
694	7	4.7	808	10	BV605139	BV605139 S217P6004
695	7	4.7	809	6	BD218494	BD218494 Diacylgly
696	7	4.7	809	6	AR608838	AR608838 Sequence
697	7	4.7	811	6	BD265802	BD265802 Schizophr
698	7	4.7	811	6	AR244332	AR244332 Sequence
699	7	4.7	813	6	AR003721	AR003721 Sequence
700	7	4.7	813	6	AR010057	AR010057 Sequence
701	7	4.7	813	6	AR055263	AR055263 Sequence
702	7	4.7	813	6	AR067747	AR067747 Sequence
703	7	4.7	813	6	AR141192	AR141192 Sequence
704	7	4.7	813	6	AR141429	AR141429 Sequence
705	7	4.7	813	6	AR164985	AR164985 Sequence
706	7	4.7	813	6	I11901	I11901 Sequence 11
707	7	4.7	813	6	I11947	I11947 Sequence 57
708	7	4.7	813	6	I40474	I40474 Sequence 11
709	7	4.7	813	6	AR367958	AR367958 Sequence
710	7	4.7	813	6	AR430939	AR430939 Sequence
711	7	4.7	816	10	BV020706	BV020706 S212P6007
712	7	4.7	822	6	BD265805	BD265805 Schizophr
713	7	4.7	822	6	AR244335	AR244335 Sequence
714	7	4.7	823	6	BD265795	BD265795 Schizophr
715	7	4.7	823	6	AR244325	AR244325 Sequence
716	7	4.7	823	10	BV660099	BV660099 S216P6188
c 717	7	4.7	824	10	BV210335	BV210335 UBE2L3_38
718	7	4.7	827	8	AY170469	AY170469 Homo sapi
c 719	7	4.7	833	15	AY087837	AY087837 Arabidops
c 720	7	4.7	834	10	BV658812	BV658812 S215P6148
721	7	4.7	836	6	BD265796	BD265796 Schizophr
722	7	4.7	836	6	AR244326	AR244326 Sequence
723	7	4.7	839	8	AJ620615	AJ620615 Homo sapi
724	7	4.7	839	8	AJ620616	AJ620616 Homo sapi
725	7	4.7	851	6	BD265799	BD265799 Schizophr
726	7	4.7	851	6	AR244329	AR244329 Sequence
727	7	4.7	853	10	BV571869	BV571869 G591P6539
c 728	7	4.7	855	6	AX505866	AX505866 Sequence
c 729	7	4.7	855	6	AX651599	AX651599 Sequence
c 730	7	4.7	855	15	AY081747	AY081747 Arabidops
731	7	4.7	860	15	ATH531004	AJ531004 Arabidops
c 732	7	4.7	861	15	BT004013	BT004013 Arabidops
733	7	4.7	863	6	BD265787	BD265787 Schizophr
734	7	4.7	863	6	AR244317	AR244317 Sequence
735	7	4.7	876	1	AY827869	AY827869 Xanthomon
736	7	4.7	878	8	AY366246	AY366246 Homo sapi
737	7	4.7	882	6	BD265797	BD265797 Schizophr
738	7	4.7	882	6	AR244327	AR244327 Sequence
739	7	4.7	889	4	AF140655	AF140655 Bos tauru
740	7	4.7	891	8	AY366244	AY366244 Homo sapi
741	7	4.7	892	4	AF140653	AF140653 Bos tauru
742	7	4.7	892	4	AF140654	AF140654 Bos tauru
743	7	4.7	892	8	AM050795	AM050795 Homo sapi
744	7	4.7	897	6	BD265793	BD265793 Schizophr
745	7	4.7	897	6	AR244323	AR244323 Sequence
746	7	4.7	902	1	AY827908	AY827908 Stenotrop
c 747	7	4.7	903	2	AF005904	AF005904 Trypanoso
748	7	4.7	903	10	BV446144	BV446144 MARC 4101
749	7	4.7	903	10	BV525838	BV525838 G591P6073
750	7	4.7	905	1	AY766090	AY766090 Mycoplasm
751	7	4.7	915	8	HSNKRECT2	X89893 H.sapiens m
752	7	4.7	916	1	AY729935	AY729935 Mycoplasm
753	7	4.7	920	6	BD265801	BD265801 Schizophr
754	7	4.7	920	6	AR244331	AR244331 Sequence
755	7	4.7	921	8	AY170470	AY170470 Homo sapi
c 756	7	4.7	921	15	BT020570	BT020570 Arabidops
757	7	4.7	923	1	AY796061	AY796061 Mycoplasm
c 758	7	4.7	924	2	AF005421	AF005421 Trypanoso
c 759	7	4.7	927	6	AR449656	AR449656 Sequence
760	7	4.7	930	1	AY762639	AY762639 Mycoplasm
761	7	4.7	930	1	AY816344	AY816344 Mycoplasm
762	7	4.7	930	1	AY816345	AY816345 Mycoplasm
763	7	4.7	932	8	HSNKREC	X98858 H.sapiens m
764	7	4.7	936	1	AY741675	AY741675 Mycoplasm
765	7	4.7	937	3	UAR294869	AJ294869 Unculture
766	7	4.7	940	1	AY973571	AY973571 Mycoplasm
767	7	4.7	942	1	AY781780	AY781780 Mycoplasm
768	7	4.7	943	1	AY768810	AY768810 Mycoplasm
769	7	4.7	946	10	BV573697	BV573697 G591P6055
770	7	4.7	947	1	AY755603	AY755603 Mycoplasm
771	7	4.7	947	6	BD265807	BD265807 Schizophr
772	7	4.7	947	6	AR244337	AR244337 Sequence
773	7	4.7	948	8	CR450351	CR450351 Homo sapi
774	7	4.7	951	8	BT019859	BT019859 Homo sapi
775	7	4.7	951	8	CR542203	CR542203 Homo sapi
776	7	4.7	951	11	AY888231	AY888231 Synthetic
777	7	4.7	951	11	AY888576	AY888576 Synthetic
778	7	4.7	951	11	AY888577	AY888577 Synthetic
779	7	4.7	951	11	AY889446	AY889446 Synthetic
780	7	4.7	951	11	AY890821	AY890821 Synthetic
781	7	4.7	951	11	AY890822	AY890822 Synthetic
782	7	4.7	951	11	AY891225	AY891225 Synthetic
783	7	4.7	951	11	AY891915	AY891915 Synthetic
784	7	4.7	951	11	AY893310	AY893310 Synthetic
785	7	4.7	951	11	AY893311	AY893311 Synthetic
786	7	4.7	951	11	AY893762	AY893762 Synthetic
787	7	4.7	951	11	BT019858	BT019858 Synthetic
788	7	4.7	952	8	HSNKRECT1	X89892 H.sapiens m
c 789	7	4.7	953	5	CR522998	CR522998 Gallus ga
790	7	4.7	953	8	AB070126	AB070126 Macaca fa
791	7	4.7	955	6	AR067753	AR067753 Sequence
792	7	4.7	955	6	AR164991	AR164991 Sequence
793	7	4.7	955	6	BD265798	BD265798 Schizophr
794	7	4.7	955	6	AR244328	AR244328 Sequence
795	7	4.7	960	6	AR483977	AR483977 Sequence
796	7	4.7	960	6	AR484585	AR484585 Sequence
797	7	4.7	960	6	AX142069	AX142069 Sequence
798	7	4.7	960	6	AX143285	AX143285 Sequence
799	7	4.7	966	15	AF321101	AF321101 Pseudodic
800	7	4.7	973	8	AY170471	AY170471 Homo sapi
801	7	4.7	978	6	BD265803	BD265803 Schizophr
802	7	4.7	978	6	AR244333	AR244333 Sequence
c 803	7	4.7	984	5	CR523899	CR523899 Gallus ga
804	7	4.7	987	8	HSANKRMR	X94609 H.sapiens m
805	7	4.7	993	6	BD265804	BD265804 Schizophr
806	7	4.7	993	6	AR244334	AR244334 Sequence

	807	7	4.7	995	6	BD265783 BD265783 Schizophr
	808	7	4.7	995	6	AR244313 AR244313 Sequence
	809	7	4.7	998	10	CNS06ITR AL400741 T3 end of
	810	7	4.7	1003	6	AR067750 AR067750 Sequence
	811	7	4.7	1003	6	AR164988 AR164988 Sequence
	812	7	4.7	1003	10	CNS06K1G AL402314 T7 end of
	813	7	4.7	1008	15	AK109072 AK109072 Oryza sat
	814	7	4.7	1009	6	BD265792 BD265792 Schizophr
	815	7	4.7	1009	6	AR244322 AR244322 Sequence
	816	7	4.7	1009	8	AY138547 AY138547 Homo sapi
	817	7	4.7	1015	8	BC096694 BC096694 Homo sapi
c	818	7	4.7	1018	15	AK118583 AK118583 Arabidops
	819	7	4.7	1020	8	HSZ83679 Z83679 Homo sapien
c	820	7	4.7	1022	10	CNS06JTN AL402033 T3 end of
	821	7	4.7	1026	11	AY890543 AY890543 Synthetic
	822	7	4.7	1026	11	AY893010 AY893010 Synthetic
	823	7	4.7	1027	8	AY223901 AY223901 Homo sapi
c	824	7	4.7	1030	2	AB038503 AB038503 Caenorhab
	825	7	4.7	1039	8	AF258806 AF258806 Pan trogl
c	826	7	4.7	1040	8	BC008390 BC008390 Homo sapi
	827	7	4.7	1043	8	AF470360 AF470360 Pongo pyg
	828	7	4.7	1043	8	AF470361 AF470361 Pongo pyg
	829	7	4.7	1045	8	AF285432 AF285432 Homo sapi
	830	7	4.7	1045	8	AF285433 AF285433 Homo sapi
	831	7	4.7	1045	8	AF285434 AF285434 Homo sapi
	832	7	4.7	1048	8	AF285435 AF285435 Homo sapi
	833	7	4.7	1048	8	AF285437 AF285437 Homo sapi
	834	7	4.7	1048	8	AF285438 AF285438 Homo sapi
	835	7	4.7	1048	10	BV179291 BV179291 sqnm10472
	836	7	4.7	1050	6	BD093625 BD093625 Cell prol
	837	7	4.7	1053	6	BD229899 BD229899 Novel DKR
	838	7	4.7	1053	8	AY587550 AY587550 Homo sapi
	839	7	4.7	1057	8	HSAJ2105 AJ002105 Homo sapi
	840	7	4.7	1058	8	HSAJ2104 AJ002104 Homo sapi
	841	7	4.7	1059	13	ROB7 J02420 uk bovine r
c	842	7	4.7	1064	15	AY543067 AY543067 Pseudodic
c	843	7	4.7	1064	15	AY543068 AY543068 Pseudodic
c	844	7	4.7	1064	15	AY543069 AY543069 Pseudodic
	845	7	4.7	1068	8	HSA417554 AJ417554 Homo sapi
	846	7	4.7	1072	6	AR067749 AR067749 Sequence
	847	7	4.7	1072	6	AR164987 AR164987 Sequence
	848	7	4.7	1073	8	AY122874 AY122874 Gorilla g
c	849	7	4.7	1074	6	AR074145 AR074145 Sequence
c	850	7	4.7	1074	6	BD224330 BD224330 Materials
c	851	7	4.7	1074	6	AR216380 AR216380 Sequence
c	852	7	4.7	1074	6	AR432782 AR432782 Sequence
c	853	7	4.7	1074	6	BD005693 BD005693 Materials
c	854	7	4.7	1075	6	AR074146 AR074146 Sequence
c	855	7	4.7	1075	6	BD224331 BD224331 Materials
c	856	7	4.7	1075	6	AR216381 AR216381 Sequence
c	857	7	4.7	1075	6	AR432783 AR432783 Sequence
c	858	7	4.7	1075	6	BD005694 BD005694 Materials
c	859	7	4.7	1076	15	AF375453 AF375453 Arabidops
	860	7	4.7	1086	15	AY070291 AY070291 Stewartia
	861	7	4.7	1087	8	AY366245 AY366245 Homo sapi
	862	7	4.7	1087	15	AY070290 AY070290 Stewartia
	863	7	4.7	1087	15	AY070293 AY070293 Stewartia
	864	7	4.7	1088	8	AF022048 AF022048 Homo sapi
	865	7	4.7	1088	15	AY070292 AY070292 Stewartia
	866	7	4.7	1090	8	HSA417555 AJ417555 Homo sapi
	867	7	4.7	1092	8	AF022045 AF022045 Homo sapi
	868	7	4.7	1101	8	AF022046 AF022046 Homo sapi
	869	7	4.7	1106	8	HSAJ2102 AJ002102 Homo sapi
c	870	7	4.7	1107	15	AK101386 AK101386 Oryza sat
	871	7	4.7	1109	8	HSAJ2103 AJ002103 Homo sapi
c	872	7	4.7	1117	15	AY222859 AY222859 Saccharum
	873	7	4.7	1128	5	CR387462 CR387462 Gallus ga
	874	7	4.7	1128	15	AB044164 AB044164 Pandorina
	875	7	4.7	1128	15	AB044167 AB044167 Pandorina
	876	7	4.7	1128	15	AB084332 AB084332 Scenedesm
	877	7	4.7	1134	8	HUMNKAT2BA L76663 Homo sapien
	878	7	4.7	1134	8	HUMNKAT8AA L76671 Homo sapien
c	879	7	4.7	1139	15	BT020239 BT020239 Arabidops
c	880	7	4.7	1140	15	ATATHB2 X68145 A.thaliana
c	881	7	4.7	1141	6	AX720415 AX720415 Sequence
c	882	7	4.7	1143	6	BD062321 BD062321 Solution-
	883	7	4.7	1143	8	AF272389 AF272389 Homo sapi
	884	7	4.7	1145	15	AY507353 AY507353 Fossombro
c	885	7	4.7	1146	8	CR542268 CR542268 Homo sapi
c	886	7	4.7	1146	11	AY335755 AY335755 Synthetic
c	887	7	4.7	1146	15	AK060409 AK060409 Oryza sat
c	888	7	4.7	1155	6	AR376620 AR376620 Sequence
c	889	7	4.7	1176	15	ATHHOMEOA M90394 Arabidopsis
	890	7	4.7	1176	15	GLNGELONIN L12243 Gelonium mu
	891	7	4.7	1178	2	AY037767 AY037767 Scolymia
c	892	7	4.7	1182	6	CQ594882 CQ594882 Sequence
c	893	7	4.7	1182	11	AY774028 AY774028 Synthetic
c	894	7	4.7	1185	6	AR149829 AR149829 Sequence
c	895	7	4.7	1185	6	BD235333 BD235333 Enzyme fo
c	896	7	4.7	1195	15	AK101702 AK101702 Oryza sat
	897	7	4.7	1225	5	CR760858 CR760858 Xenopus t
	898	7	4.7	1233	8	BC069344 BC069344 Homo sapi
	899	7	4.7	1245	6	AR377469 AR377469 Sequence
c	900	7	4.7	1252	8	AB074031 AB074031 Homo sapi
	901	7	4.7	1255	9	AF135598 AF135598 Rattus no
c	902	7	4.7	1261	15	AY138800 AY138800 Nowakowsk
	903	7	4.7	1269	8	AB033421 AB033421 Homo sapi
	904	7	4.7	1274	9	RNO132718 AJ132718 Rattus no
	905	7	4.7	1274	15	DQ073045 DQ073045 Gossypium
	906	7	4.7	1280	5	BC079808 BC079808 Xenopus l
	907	7	4.7	1280	5	XTR512377 AJ512377 Silurana
c	908	7	4.7	1281	10	BV180340 BV180340 sqnm10900
c	909	7	4.7	1282	15	AK103054 AK103054 Oryza sat
c	910	7	4.7	1290	6	AX653607 AX653607 Sequence
c	911	7	4.7	1291	5	BX930027 BX930027 Gallus ga
	912	7	4.7	1294	8	AJ630586 AJ630586 Homo sapi
	913	7	4.7	1307	15	AF072404 AF072404 Gossypium
	914	7	4.7	1308	15	AF072406 AF072406 Gossypium
	915	7	4.7	1310	5	BC053793 BC053793 Xenopus l
	916	7	4.7	1312	8	AY366238 AY366238 Homo sapi
	917	7	4.7	1317	8	AF002255 AF002255 Homo sapi
	918	7	4.7	1322	8	AF258800 AF258800 Pan trogl
	919	7	4.7	1322	8	AF266731 AF266731 Pan panis
c	920	7	4.7	1323	6	AX010801 AX010801 Sequence
c	921	7	4.7	1323	6	AX010803 AX010803 Sequence
c	922	7	4.7	1323	6	AX010805 AX010805 Sequence
c	923	7	4.7	1323	6	AX010807 AX010807 Sequence
	924	7	4.7	1330	8	HSU24078 U24078 Human p58 n
	925	7	4.7	1331	8	HUMALRM J04795 Human aldos
	926	7	4.7	1332	8	AF204915S2 AF204916 Homo sapi
	927	7	4.7	1332	8	AF204918S2 AF204919 Homo sapi
	928	7	4.7	1333	8	AF258802 AF258802 Pan trogl
	929	7	4.7	1333	8	AF258803 AF258803 Pan trogl
c	930	7	4.7	1334	3	AB089054 AB089054 Unculture
	931	7	4.7	1335	6	AR380465 AR380465 Sequence
	932	7	4.7	1335	8	HUMARXA M34720 Human aldos
c	933	7	4.7	1339	6	AX416071 AX416071 Sequence
	934	7	4.7	1341	8	AY122871 AY122871 Gorilla g
c	935	7	4.7	1352	15	ATHAT4A Z19602 A.thaliana
	936	7	4.7	1354	8	HUMALRMB J05474 Human aldos
	937	7	4.7	1355	8	AF328729 AF328729 Homo sapi
c	938	7	4.7	1357	6	CQ722265 CQ722265 Sequence
c	939	7	4.7	1360	6	AX330198 AX330198 Sequence
c	940	7	4.7	1360	6	AX409622 AX409622 Sequence
c	941	7	4.7	1360	8	HUMCKB M16364 Human creat
	942	7	4.7	1366	8	HUMALRMA J05017 Human aldos
	943	7	4.7	1367	6	CQ716379 CQ716379 Sequence
	944	7	4.7	1367	6	AX440479 AX440479 Sequence
	945	7	4.7	1367	8	HSALRE X15414 Human mRNA
	946	7	4.7	1368	6	AX451813 AX451813 Sequence
	947	7	4.7	1371	6	E03157 E03157 cDNA sequen
	948	7	4.7	1371	8	AY366242 AY366242 Homo sapi
	949	7	4.7	1372	8	AY388471 AY388471 Homo sapi
c	950	7	4.7	1372	8	HUMCKBBA M16451 Human creat
	951	7	4.7	1374	8	AF285431 AF285431 Homo sapi
	952	7	4.7	1374	8	AY366240 AY366240 Homo sapi

953	7	4.7	1376	8	AY366239	AY366239 Homo sapi
954	7	4.7	1377	8	AF285440	AF285440 Homo sapi
c 955	7	4.7	1378	15	AB090877	AB090877 Monascus
956	7	4.7	1381	8	AY366243	AY366243 Homo sapi
c 957	7	4.7	1385	15	AK106262	AK106262 Oryza sat
958	7	4.7	1386	8	BC005387	BC005387 Homo sapi
c 959	7	4.7	1386	8	HUMCKBR	L47647 Homo sapien
c 960	7	4.7	1390	6	CQ613470	CQ613470 Sequence
961	7	4.7	1391	8	AF266732	AF266732 Pan panis
962	7	4.7	1391	8	BC010391	BC010391 Homo sapi
963	7	4.7	1392	8	AF258799	AF258799 Pan trogl
964	7	4.7	1394	6	A07588	A07588 Synthetic H
965	7	4.7	1394	8	HSNKR4M	X97230 H.sapiens m
c 966	7	4.7	1400	15	CSRIO1GEN	X96739 S.cerevisia
967	7	4.7	1405	8	AY366237	AY366237 Homo sapi
968	7	4.7	1406	8	AY366241	AY366241 Homo sapi
969	7	4.7	1407	8	AF204906S2	AF204907 Homo sapi
970	7	4.7	1409	8	AY388472	AY388472 Homo sapi
971	7	4.7	1416	8	BC000260	BC000260 Homo sapi
c 972	7	4.7	1418	8	BC004914	BC004914 Homo sapi
c 973	7	4.7	1420	1	AF152595	AF152595 Orenia si
974	7	4.7	1421	2	AK115127	AK115127 Ciona int
c 975	7	4.7	1424	8	BC008323	BC008323 Homo sapi
c 976	7	4.7	1426	8	BC001190	BC001190 Homo sapi
c 977	7	4.7	1426	8	BC019259	BC019259 Homo sapi
c 978	7	4.7	1431	6	CS115048	CS115048 Sequence
c 979	7	4.7	1431	6	CS119660	CS119660 Sequence
c 980	7	4.7	1432	6	CS080610	CS080610 Sequence
c 981	7	4.7	1432	6	CS119176	CS119176 Sequence
c 982	7	4.7	1438	2	AY071431	AY071431 Drosophil
c 983	7	4.7	1440	8	BC010002	BC010002 Homo sapi
c 984	7	4.7	1447	8	BC019281	BC019281 Homo sapi
985	7	4.7	1454	8	HUMNKAT6AA	L76669 Homo sapien
986	7	4.7	1457	8	HUMNKAT2AB	L76662 Homo sapien
c 987	7	4.7	1468	15	AY091183	AY091183 Arabidops
c 988	7	4.7	1487	6	AR361029	AR361029 Sequence
989	7	4.7	1530	2	AK113020	AK113020 Ciona int
990	7	4.7	1532	8	HSU24077	U24077 Human p58 n
991	7	4.7	1532	10	G28600	G28600 human STS S
992	7	4.7	1535	8	HSU24079	U24079 Human p58 n
c 993	7	4.7	1545	5	AY427786	AY427786 Salmo tru
994	7	4.7	1554	6	AX416290	AX416290 Sequence
995	7	4.7	1556	15	AF272710	AF272710 Solanum c
996	7	4.7	1557	8	HUMNKAT5M	L41347 Homo sapien
997	7	4.7	1562	2	AF526296	AF526296 Manduca s
998	7	4.7	1572	8	HSU24075	U24075 Human p58 n
999	7	4.7	1579	8	HSU24074	U24074 Human p58 n
1000	7	4.7	1587	8	HSU73395	U73395 Human NK-re

ALIGNMENTS

RESULT 1
AF445416
LOCUS AF445416 1387 bp mRNA linear PLN 29-NOV-2001
DEFINITION Bougainvillea spectabilis bouganin mRNA, complete cds.
ACCESSION AF445416
VERSION AF445416.1 GI:17149253
KEYWORDS .
SOURCE Bougainvillea spectabilis
ORGANISM Bougainvillea spectabilis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE 1 (bases 1 to 1387)
AUTHORS den Hartog,M.T., Lubelli,C., Boon,L., Heerkens,S., Ortiz Buijsse,A.P., de Boer,M. and Stirpe,F.
TITLE Cloning and expression of cDNA coding for bouganin: A type I ribosome-inactivating protein from Bougainvillea spectabilis Willd
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1387)
AUTHORS den Hartog,M.T.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Meibergdreef 45, Amsterdam 1105 BA, The Netherlands
FEATURES Location/Qualifiers
source 1. .1387
/organism="Bougainvillea spectabilis"
/mol_type="mRNA"
/db_xref="taxon:146096"
/note="authority: Bougainvillea spectabilis Willd"
CDS 238. .1155
/note="ribosome-inactivating protein"
/codon_start=1
/product="bouganin"
/protein_id="AAL35962.1"
/db_xref="GI:17149254"
/translation="MGWWAIIVEPMLVMPSIVNKETTSLGYNTVSFNLGEAYEYPTFI
QDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQD
KWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYK
LEFSIEAIHGKTINGQEIAKFFLIVIQMVSEAARFKYIETEVVDRGLYGSFKPNFKVL
NLENNWGDISDAIHKSSPQCTTINPALQLISPSNDPWVVNKVSQISPDMGILKFKSSK
LTQFATMIRSAIVEDLDGDELEILEPNIA"
ORIGIN

Alignment Scores:

Pred. No.:	1.02e-150	Length:	1387
Score:	142.00	Matches:	142
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	95.3%	Indels:	0
DB:	15	Gaps:	0

US-10-758-902-9 (1-149) x AF445416 (1-1387)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 375

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 435

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 495

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 555

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 615

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 675

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 GCCAAAGTGGATAGAAAGGATCTCGAACTGGGGGTTTACAAATTGGAATTTTCCATTGAA 735

Qy        141 AlaIle 142
              ||||||
Db        736 GCAATC 741
```

RESULT 2
A82773
LOCUS A82773 363 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 8 from Patent WO9855623.
ACCESSION A82773
VERSION A82773.1 GI:6732463
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified

```
            unclassified sequences.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     TYPE-1 RIBOSOME-INACTIVATING PROTEIN
  JOURNAL   Patent: WO 9855623-A 8 10-DEC-1998;
            STIRPE FIORENZO (IT); BOLOGNESI ANDREA (IT)
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:                2.6e-126      Length:          363
Score:                    120.00        Matches:         120
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              80.5%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-9 (1-149) x A82773 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361

RESULT 3
AR454123
LOCUS       AR454123                363 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 8 from patent US 6680296.
ACCESSION   AR454123
VERSION     AR454123.1  GI:42687052
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     Type-1 ribosome-inactivating protein
  JOURNAL   Patent: US 6680296-A 8 20-JAN-2004;
            Tanox Pharma B.V.; Amsterdam;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.6e-126      Length:          363
Score:                    120.00        Matches:         120
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              80.5%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-9 (1-149) x AR454123 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361

RESULT 4
AY437531
LOCUS       AY437531                1085 bp    mRNA    linear   PLN 20-JAN-2005
DEFINITION  Bougainvillea spectabilis antiviral protein (Ap1) mRNA, complete
            cds.
ACCESSION   AY437531
VERSION     AY437531.1  GI:40890052
KEYWORDS    .
SOURCE      Bougainvillea spectabilis
  ORGANISM  Bougainvillea spectabilis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE   1  (bases 1 to 1085)
  AUTHORS   Balasaraswathi,R., Suguna Rani,K. and Bansal,V.
  TITLE     A full length antiviral cDNA sequence from Bougainvillea
            spectabilis Willd.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1085)
  AUTHORS   Balasaraswathi,R., Suguna Rani,K. and Bansal,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-OCT-2003) Centre For Plant Molecular Biology, Tamil
            Nadu Agricultural University, Lawley Road, Coimbatore, Tamil Nadu
            641003, India
FEATURES             Location/Qualifiers
     source          1. .1085
                     /organism="Bougainvillea spectabilis"
                     /mol_type="mRNA"
                     /db_xref="taxon:146096"
                     /ecotype="Coimbatore region"
                     /country="India"
                     /note="biotype: red flower trait; authority: Bougainvillea
                     spectabilis Willd."
     gene            1. .1085
                     /gene="Ap1"
     5'UTR           1. .25
                     /gene="Ap1"
     CDS             26. .943
                     /gene="Ap1"
                     /note="crop antiviral and ribosome-inactivating protein;
                     BAP; BAP1; antiviral activity against tospo group of crop
                     viruses"
                     /codon_start=1
```

```
                     /product="antiviral protein"
                     /protein_id="AAR97371.1"
                     /db_xref="GI:40890053"
                     /translation="MGWWAIIVEPMLVMPSIVNKETTSLGYNTVSFNLGEAYEYPTFI
                     QDLRNELAKGTPVCQLPVTLQTIADAKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQD
                     KWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYK
                     LEPSIEAIHGKTINGQEIAKFFLITIQMVSEAARFKYIETEVVDRGLYGSFKPNFKVL
                     NLENNWGDISDAIHKSSPQCTTINPALQLISPSNDPWVVNKVSQISPDMGILKFKSSK
                     LTQFATMIRSAIAEDLDGDELEILEPNIA"
     3'UTR           944. .1085
                     /gene="Ap1"
     polyA_signal    984. .989
                     /gene="Ap1"
ORIGIN

Alignment Scores:
Pred. No.:                6.65e-101      Length:         1085
Score:                    98.00          Matches:        141
Percent Similarity:       98.6%          Conservative:   0
Best Local Similarity:    98.6%          Mismatches:     1
Query Match:              65.8%          Indels:         2
DB:                       15             Gaps:           0

US-10-758-902-9 (1-149) x AY437531 (1-1085)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 TACAACACTGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 163

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 223

Qy         41 IleAlaAspAsp-LysArgPheValLeuValAspIleThrThrThrSerLysLysThrVa 60
              |||||||||    ||||||||||||||||||||||||||||||||||||||||||||||
Db        224 ATAGCCGATGC-CAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGT 282

Qy         60 lLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGl 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 TAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGG 342

Qy         80 yLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 CAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCC 402

Qy        100 oGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAl 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 AGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGC 462

Qy        120 aAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGl 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 TGCCAAAGTGGATAGAAAGGATCTCGAACTGGGGGTTTACAAATTGGAATTTTCCATTGA 522

Qy        140 uAlaIle 142
              |||||||
Db        523 AGCAATC 529

RESULT 5
A82770
LOCUS       A82770                    65 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 5 from Patent WO9855623.
ACCESSION   A82770
VERSION     A82770.1  GI:6732460
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     TYPE-1 RIBOSOME-INACTIVATING PROTEIN
  JOURNAL   Patent: WO 9855623-A 5 10-DEC-1998;
            STIRPE FIORENZO (IT); BOLOGNESI ANDREA (IT)
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:                1.04e-14       Length:         65
Score:                    21.00          Matches:        21
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              14.1%          Indels:         0
DB:                       6              Gaps:           0

US-10-758-902-9 (1-149) x A82770 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 6
AR454120
LOCUS       AR454120                  65 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 5 from patent US 6680296.
ACCESSION   AR454120
VERSION     AR454120.1  GI:42687049
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Stirpe,F. and Bolognesi,A.
  TITLE     Type-1 ribosome-inactivating protein
  JOURNAL   Patent: US 6680296-A 5 20-JAN-2004;
            Tanox Pharma B.V.; Amsterdam;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.04e-14       Length:         65
Score:                    21.00          Matches:        21
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              14.1%          Indels:         0
DB:                       6              Gaps:           0

US-10-758-902-9 (1-149) x AR454120 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 7
AC094821
LOCUS       AC094821              242506 bp    DNA     linear   HTG 09-MAY-2003
DEFINITION  Rattus norvegicus clone CH230-5J15, WORKING DRAFT SEQUENCE, 2
            unordered pieces.
ACCESSION   AC094821
VERSION     AC094821.4  GI:30466519
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
```

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 242506)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 242506)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 242506)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On May 9, 2003 this sequence version replaced gi:22771158.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
---------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
---------- Project Information
Center project name: GBLP
Center clone name: CH230-5J15
---------- Summary Statistics
Assembly program: Atlas;
Consensus quality: 225401 bases at least Q40
Consensus quality: 228343 bases at least Q30
Consensus quality: 229973 bases at least Q20
Estimated insert size: 238404; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 241329: contig of 241329 bp in length
* 241330 241429: gap of unknown length
* 241430 242506: contig of 1077 bp in length.

FEATURES Location/Qualifiers
source 1. .242506
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-5J15"
misc_feature 1. .3779
/note="wgs_end_extension
clone_end:T7"
misc_feature complement(4623. .5437)
/note="clone_boundary
clone_end:T7
site:EcoRI
end_sequence:BH362066"
misc_feature 205296. .207179
/note="wgs_contig"
misc_feature complement(239399. .240181)
/note="clone_boundary
clone_end:Sp6
site:EcoRI
end_sequence:BH362067"
gap 241330. .241429
/estimated_length=unknown
ORIGIN

Alignment Scores:

Pred. No.:	75.1	Length:	242506
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	6.7%	Indels:	0
DB:	14	Gaps:	0

US-10-758-902-9 (1-149) x AC094821 (1-242506)

Qy 85 ValPheLeuAspLysValProThrValAla 94

```
                    ||||||||||||||||||||||||||||||
Db      83702 GTTTTTCTGGATAAGGTGCCCACTGTGGCT 83731

RESULT 8
BC086634/c
LOCUS       BC086634               1637 bp    mRNA    linear   VRT 01-FEB-2005
DEFINITION  Xenopus laevis hypothetical LOC495842, mRNA (cDNA clone MGC:98789
            IMAGE:3396392), complete cds.
ACCESSION   BC086634
VERSION     BC086634.1  GI:55991536
KEYWORDS    MGC.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 1637)
  AUTHORS   Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W.
            and Richardson,P.
  TITLE     Genetic and genomic tools for Xenopus research: The NIH Xenopus
            initiative
  JOURNAL   Dev. Dyn. 225 (4), 384-391 (2002)
   PUBMED   12454917
REFERENCE   2  (bases 1 to 1637)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   3  (bases 1 to 1637)
  AUTHORS   Klein,S. and Gerhard,D.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-NOV-2004) National Institutes of Health, Xenopus Gene
            Collection (XGC), National Institute of Child Health and Human
            Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
            20892-7510, USA
  REMARK    NIH-MGC Project
COMMENT     Contact: XGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 187 Row: a Column: 4
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis.
FEATURES             Location/Qualifiers
     source          1. .1637
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="MGC:98789 IMAGE:3396392"
                     /tissue_type="Liver"
                     /clone_lib="NICHD_XGC_Lil"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     gene            1. .1637
                     /gene="LOC495842"
                     /db_xref="GeneID:495842"
     CDS             306. .590
                     /gene="LOC495842"
                     /codon_start=1
                     /product="LOC495842 protein"
                     /protein_id="AAH86634.1"
                     /db_xref="GI:55991537"
                     /db_xref="GeneID:495842"
                     /translation="MVVQENENVVFCLECALRHVEKQKSSRGLKLMYRYDEEQIKSLV
                     NQICGKASFKNSNENCPMNCTPKRGPRKRATLEMPSSRVSSSTLSKSASS"
ORIGIN

Alignment Scores:
Pred. No.:              9.03          Length:         1637
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            6.0%          Indels:         0
DB:                     5             Gaps:           0

US-10-758-902-9 (1-149) x BC086634 (1-1637)

Qy          18 IleGlnAspLeuArgAsnGluLeuAla 26
               ||||||||||||||||||||||||||
Db         620 ATTCAGGATTTGAGAAATGAGTTGGCA 594

RESULT 9
TANN2_02/c
WPCOMMENT
  Sequence split into 20 fragments  LOCUS TANN2 Accession CR940348
     Fragment Name      Begin     End
     TANN2_00               1    110000
     TANN2_01          100001    210000
     TANN2_02          200001    310000
     TANN2_03          300001    410000
     TANN2_04          400001    510000
     TANN2_05          500001    610000
     TANN2_06          600001    710000
     TANN2_07          700001    810000
     TANN2_08          800001    910000
     TANN2_09          900001   1010000
     TANN2_10         1000001   1110000
     TANN2_11         1100001   1210000
     TANN2_12         1200001   1310000
     TANN2_13         1300001   1410000
     TANN2_14         1400001   1510000
     TANN2_15         1500001   1610000
     TANN2_16         1600001   1710000
     TANN2_17         1700001   1810000
     TANN2_18         1800001   1910000
     TANN2_19         1900001   1979170
Continuation (3 of 20) of TANN2 from base 200001 (CR940348 Theileria annulata strain An

Alignment Scores:
Pred. No.:              485           Length:         110000
```

```
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            6.0%          Indels:        0
DB:                     14            Gaps:          0

US-10-758-902-9 (1-149) x TANN2_02 (1-110000)

Qy         56 SerLysLysThrValLysValAlaIle 64
              |||||||||||||||||||||||||
Db      80607 AGCAAAAAAACTGTTAAAGTAGCGATT 80581

RESULT 10
AC046162/c
LOCUS       AC046162              140020 bp    DNA     linear   HTG 03-MAY-2000
DEFINITION  Homo sapiens clone RP11-22K13, WORKING DRAFT SEQUENCE, 31 unordered
            pieces.
ACCESSION   AC046162
VERSION     AC046162.2  GI:7684441
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 140020)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-22K13
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 140020)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
            Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
            McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
            Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
            Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
            Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
            Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-APR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On May 3, 2000 this sequence version replaced gi:7547139.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L4135
                Center clone name: 22_K_13
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 125984 bases at least Q40
                Consensus quality: 132935 bases at least Q30
                Consensus quality: 135506 bases at least Q20
                Insert size: 182000; agarose-fp
                Insert size: 137020; sum-of-contigs
                Quality coverage: 3.3 in Q20 bases; agarose-fp
                Quality coverage: 4.4 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 31 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1004: contig of 1004 bp in length
            *     1005     1104: gap of 100 bp
            *     1105     2449: contig of 1345 bp in length
            *     2450     2549: gap of 100 bp
            *     2550     4378: contig of 1829 bp in length
            *     4379     4478: gap of 100 bp
            *     4479     5708: contig of 1230 bp in length
            *     5709     5808: gap of 100 bp
            *     5809     7705: contig of 1897 bp in length
            *     7706     7805: gap of 100 bp
            *     7806     9726: contig of 1921 bp in length
            *     9727     9826: gap of 100 bp
            *     9827    11656: contig of 1830 bp in length
            *    11657    11756: gap of 100 bp
            *    11757    14319: contig of 2563 bp in length
            *    14320    14419: gap of 100 bp
            *    14420    16468: contig of 2049 bp in length
            *    16469    16568: gap of 100 bp
            *    16569    19787: contig of 3219 bp in length
            *    19788    19887: gap of 100 bp
            *    19888    23005: contig of 3118 bp in length
            *    23006    23105: gap of 100 bp
            *    23106    25986: contig of 2881 bp in length
            *    25987    26086: gap of 100 bp
            *    26087    28828: contig of 2742 bp in length
            *    28829    28928: gap of 100 bp
            *    28929    29816: contig of 888 bp in length
            *    29817    29916: gap of 100 bp
            *    29917    32448: contig of 2532 bp in length
            *    32449    32548: gap of 100 bp
            *    32549    37102: contig of 4554 bp in length
            *    37103    37202: gap of 100 bp
            *    37203    40190: contig of 2988 bp in length
            *    40191    40290: gap of 100 bp
            *    40291    44029: contig of 3739 bp in length
            *    44030    44129: gap of 100 bp
            *    44130    47944: contig of 3815 bp in length
            *    47945    48044: gap of 100 bp
            *    48045    51368: contig of 3324 bp in length
            *    51369    51468: gap of 100 bp
            *    51469    57694: contig of 6226 bp in length
            *    57695    57794: gap of 100 bp
            *    57795    64254: contig of 6460 bp in length
            *    64255    64354: gap of 100 bp
            *    64355    70197: contig of 5843 bp in length
            *    70198    70297: gap of 100 bp
            *    70298    71861: contig of 1564 bp in length
            *    71862    71961: gap of 100 bp
            *    71962    76274: contig of 4313 bp in length
            *    76275    76374: gap of 100 bp
            *    76375    82337: contig of 5963 bp in length
            *    82338    82437: gap of 100 bp
            *    82438    89527: contig of 7090 bp in length
            *    89528    89627: gap of 100 bp
            *    89628    98935: contig of 9308 bp in length
            *    98936    99035: gap of 100 bp
            *    99036   110508: contig of 11473 bp in length
            *   110509   110608: gap of 100 bp
            *   110609   120586: contig of 9978 bp in length
            *   120587   120686: gap of 100 bp
```

```
          *   120687   140020: contig of 19334 bp in length.
FEATURES             Location/Qualifiers
     source          1. .140020
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="RP11-22K13"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .1004
                     /note="assembly_fragment"
     gap             1005. .1104
                     /estimated_length=100
     misc_feature    1105. .2449
                     /note="assembly_fragment"
     gap             2450. .2549
                     /estimated_length=100
     misc_feature    2550. .4378
                     /note="assembly_fragment"
     gap             4379. .4478
                     /estimated_length=100
     misc_feature    4479. .5708
                     /note="assembly_fragment"
     gap             5709. .5808
                     /estimated_length=100
     misc_feature    5809. .7705
                     /note="assembly_fragment"
     gap             7706. .7805
                     /estimated_length=100
     misc_feature    7806. .9726
                     /note="assembly_fragment"
     gap             9727. .9826
                     /estimated_length=100
     misc_feature    9827. .11656
                     /note="assembly_fragment"
     gap             11657. .11756
                     /estimated_length=100
     misc_feature    11757. .14319
                     /note="assembly_fragment"
     gap             14320. .14419
                     /estimated_length=100
     misc_feature    14420. .16468
                     /note="assembly_fragment"
     gap             16469. .16568
                     /estimated_length=100
     misc_feature    16569. .19787
                     /note="assembly_fragment"
     gap             19788. .19887
                     /estimated_length=100
     misc_feature    19888. .23005
                     /note="assembly_fragment"
     gap             23006. .23105
                     /estimated_length=100
     misc_feature    23106. .25986
                     /note="assembly_fragment"
     gap             25987. .26086
                     /estimated_length=100
     misc_feature    26087. .28828
                     /note="assembly_fragment"
     gap             28829. .28928
                     /estimated_length=100
     misc_feature    28929. .29816
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
     gap             29817. .29916
                     /estimated_length=100
     misc_feature    29917. .32448
                     /note="assembly_fragment"

Alignment Scores:
Pred. No.:              609          Length:         140020
Score:                  9.00         Matches:        9
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            6.0%         Indels:         0
DB:                     14           Gaps:           0

US-10-758-902-9 (1-149) x AC046162 (1-140020)

Qy        135 LeuGluPheSerIleGluAlaIleTrp 143
              ||||||||||||||||||||||||||||
Db      64129 TTAGAATTTTCCATTGAAGCTATTTGG 64103

RESULT 11
AC150461
LOCUS       AC150461              172555 bp    DNA     linear   HTG 06-AUG-2004
DEFINITION  Callithrix jacchus clone CH259-451B5, WORKING DRAFT SEQUENCE, 8
            ordered pieces.
ACCESSION   AC150461
VERSION     AC150461.2  GI:51011160
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Callithrix jacchus (white-tufted-ear marmoset)
  ORGANISM  Callithrix jacchus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
            Callitrichidae; Callithrix.
REFERENCE   1  (bases 1 to 172555)
  AUTHORS   Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W.,
            Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,B.,
            Coleman,H., Daki,N., Engle,J., Guan,X., Gupta,J., Haghighi,P.,
            Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Jones,C.,
            Karlins,E., Kim,H., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,
            Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H.,
            Masiello,C., Maskeri,B., McDowell,J., Mullikin,J.C., Paguirigan,C.,
            Park,M., Portnoy,M.E., Prasad,A., Puri,O., Reddix-Dugue,N.,
            Schandler,K., Schueler,M.G., Shah,K., Sison,C., Stantripop,S.,
            Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D.,
            Young,A. and Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 172555)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-2004) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
REFERENCE   3  (bases 1 to 172555)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-AUG-2004) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     On Aug 6, 2004 this sequence version replaced gi:50428603.
            -------------- Genome Center
                 Center: NIH Intramural Sequencing Center
                 Center code: NISC
                 Web site: http://www.nisc.nih.gov
                 Contact: nisc_zoo@nhgri.nih.gov
            -------------- Project Information
                 Center project name: fst
                 Center clone name: 451B05

            The sequence data in this record represents an 'enhanced'
            version of a Phase 2 submission. Specifically, the indicated
            order and orientation of each sequence contig has been
            established using one or more of the following: read-pair
            data from individual subclones, overlaps with neighboring
            clones, alignment with available reference sequence (e.g.,
            human), and/or confirmation by PCR testing. In addition,
            the sequence assembly is based on at least 8X average
            coverage in Q20 bases and has been reviewed to rule out
            gross misassemblies, the low-quality ends of sequence
            contigs have been trimmed away, and each base is associated
            with a Phrap-derived quality score.
            -------------- Summary Statistics
                 Sequencing vector: plasmid; n/a; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990319
```

```
            Consensus quality: 170979 bases at least Q40
            Consensus quality: 171489 bases at least Q30
            Consensus quality: 171682 bases at least Q20
            Insert size: 175000; agarose-fp
            Insert size: 171855; sum-of-contigs
            Quality coverage: 10.31x in Q20 bases; agarose-fp
            Quality coverage: 10.50x in Q20 bases; sum-of-contigs
          --------------.
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 8 contigs. Gaps between the contigs
          * are represented as runs of N. The order of the pieces
          * is believed to be correct as given, however the sizes
          * of the gaps between them are based on estimates that have
          * provided by the submittor.
          * This sequence will be replaced
          * by the finished sequence as soon as it is available and
          * the accession number will be preserved.
          *        1     3962: contig of 3962 bp in length
          *     3963     4062: gap of unknown length
          *     4063    18752: contig of 14690 bp in length
          *    18753    18852: gap of unknown length
          *    18853    57213: contig of 38361 bp in length
          *    57214    57313: gap of unknown length
          *    57314    75206: contig of 17893 bp in length
          *    75207    75306: gap of unknown length
          *    75307   116747: contig of 41441 bp in length
          *   116748   116847: gap of unknown length
          *   116848   120274: contig of 3427 bp in length
          *   120275   120374: gap of unknown length
          *   120375   156727: contig of 36353 bp in length
          *   156728   156827: gap of unknown length
          *   156828   172555: contig of 15728 bp in length.
FEATURES             Location/Qualifiers
     source          1. .172555
                     /organism="Callithrix jacchus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9483"
                     /clone="CH259-451B5"
                     /clone_lib="CH259"
                     /note="BAC resource: http://bacpac.chori.org/"
     misc_feature    1. .3962
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:left"
     gap             3963. .4062
                     /estimated_length=unknown
     misc_feature    4063. .18752
                     /note="assembly_fragment"
     gap             18753. .18852
                     /estimated_length=unknown
     misc_feature    18853. .57213
                     /note="assembly_fragment"
     gap             57214. .57313
                     /estimated_length=unknown
     misc_feature    57314. .75206
                     /note="assembly_fragment"
     gap             75207. .75306
                     /estimated_length=unknown
     misc_feature    75307. .116747
                     /note="assembly_fragment"
     gap             116748. .116847
                     /estimated_length=unknown
     misc_feature    116848. .120274
                     /note="assembly_fragment"
     gap             120275. .120374
                     /estimated_length=unknown
     misc_feature    120375. .156727
                     /note="assembly_fragment"
     gap             156728. .156827
                     /estimated_length=unknown
     misc_feature    156828. .172555
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:right"
ORIGIN

Alignment Scores:
Pred. No.:              742             Length:         172555
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.0%            Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-9 (1-149) x AC150461 (1-172555)

Qy          27 LysGlyThrProValCysGlnLeuPro 35
               |||||||||||||||||||||||||||
Db      133662 AAGGGCACTCCGGTCTGTCAGCTCCCT 133688

RESULT 12
AC098591
LOCUS       AC098591               179641 bp    DNA     linear   PRI 07-SEP-2002
DEFINITION  Homo sapiens BAC clone RP11-333E13 from 4, complete sequence.
ACCESSION   AC098591 AC037439
VERSION     AC098591.4  GI:21956631
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 179641)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
   PUBMED   9847074
REFERENCE   2  (bases 1 to 179641)
  AUTHORS   Pearman,C., Haglund,K. and Spalding,L.
  TITLE     The sequence of Homo sapiens BAC clone RP11-333E13
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 179641)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 179641)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAR-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 179641)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6  (bases 1 to 179641)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-SEP-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On or before Jul 26, 2002 this sequence version replaced
            gi:8705163, gi:19697518.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0333E13
                Drafting Center: WIBR
            --------------.
```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP13-339P19; the clone sequenced to the right is RP11-395I6, 2000 bp overlap. Actual start of this clone is at base position 96857 of RP13-339P19; actual end is at base position 46946 of RP11-395I6.

Polymorphisms exist between AC098591, AC113150, AC068352 and AC046162. Data from AC113150, AC068352 and AC046162 was used to finish AC098591.

The sequence of AC037439 has been incorporated into AC098591.

FEATURES Location/Qualifiers

```
     source          1. .179641
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="4"
                     /map="4"
                     /clone="RP11-333E13"
                     /clone_lib="RPCI-11"
     repeat_region   1. .59
                     /rpt_family="Alu"
     repeat_region   65. .362
                     /rpt_family="Alu"
     repeat_region   371. .668
                     /rpt_family="Alu"
     repeat_region   855. .956
                     /rpt_family="Tc2"
     repeat_region   960. .1095
                     /rpt_family="Tc2"
     repeat_region   1096. .1396
                     /rpt_family="Alu"
     repeat_region   1397. .1525
                     /rpt_family="Tc2"
     repeat_region   1526. .1821
                     /rpt_family="Alu"
     repeat_region   1822. .1984
                     /rpt_family="Tc2"
     repeat_region   1989. .2201
                     /rpt_family="ERVL"
     repeat_region   2202. .2499
                     /rpt_family="Alu"
     repeat_region   2500. .2859
                     /rpt_family="ERVL"
     repeat_region   2864. .2922
                     /rpt_family="MER1_type"
     repeat_region   2927. .3212
                     /rpt_family="Alu"
     repeat_region   3295. .3356
                     /rpt_family="MER1_type"
     repeat_region   3535. .3849
                     /rpt_family="Alu"
     repeat_region   3852. .4096
                     /rpt_family="Alu"
     repeat_region   4147. .4173
                     /rpt_family="(A)n"
     repeat_region   4234. .4547
                     /rpt_family="Alu"
     repeat_region   4796. .5102
                     /rpt_family="Alu"
     repeat_region   5203. .5296
                     /rpt_family="L1"
     repeat_region   5310. .5608
                     /rpt_family="Alu"
     repeat_region   5685. .5985
                     /rpt_family="Alu"
     repeat_region   6145. .6448
                     /rpt_family="Alu"
     repeat_region   6746. .6815
                     /rpt_family="Alu"
     repeat_region   6986. .7286
                     /rpt_family="Alu"
     repeat_region   7351. .7456
                     /rpt_family="Alu"
     repeat_region   7457. .7667
                     /rpt_family="Alu"
     repeat_region   7701. .7999
                     /rpt_family="Alu"
     repeat_region   8082. .8384
                     /rpt_family="Alu"
     repeat_region   8398. .8532
                     /rpt_family="L2"
     repeat_region   8774. .8796
                     /rpt_family="AT_rich"
     repeat_region   8830. .9112
                     /rpt_family="Alu"
     repeat_region   9149. .9284
                     /rpt_family="Alu"
     repeat_region   9285. .9587
                     /rpt_family="Alu"
     repeat_region   9588. .9771
                     /rpt_family="Alu"
     repeat_region   10027. .10171
                     /rpt_family="Alu"
     repeat_region   10172. .10463
                     /rpt_family="Alu"
     repeat_region   10464. .10576
                     /rpt_family="Alu"
     repeat_region   10642. .10681
                     /rpt_family="U3"
     repeat_region   10765. .11036
                     /rpt_family="Alu"
     repeat_region   11045. .11168
                     /rpt_family="Alu"
     repeat_region   11534. .11831
                     /rpt_family="Alu"
     repeat_region   12000. .12270
                     /rpt_family="Alu"
     repeat_region   12287. .12460
                     /rpt_family="Alu"
     repeat_region   12461. .12504
                     /rpt_family="L1"
     repeat_region   12523. .12649
                     /rpt_family="Alu"
     repeat_region   12650. .12946
                     /rpt_family="Alu"
     repeat_region   12947. .12982
```

```
Alignment Scores:
Pred. No.:              771           Length:         179641
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            6.0%          Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-9 (1-149) x AC098591 (1-179641)

Qy        135 LeuGluPheSerIleGluAlaIleTrp 143
              |||||||||||||||||||||||||||
Db     141725 TTAGAATTTTCCATTGAAGCTATTTGG 141751

RESULT 13
AC000119/c
LOCUS       AC000119               191191 bp    DNA     linear   PRI 15-OCT-2003
DEFINITION  Homo sapiens BAC clone CTB-104I4 from 7, complete sequence.
ACCESSION   AC000119
VERSION     AC000119.1  GI:1809226
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 191191)
  AUTHORS   Sulston,J.E. and Wilson,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
   PUBMED   9847074
REFERENCE   2  (bases 1 to 191191)
  AUTHORS   Gibson,A. and Wamsley,P.
  TITLE     The sequence of Homo sapiens BAC clone CTB-104I4
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 191191)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-1997)
REFERENCE   4  (bases 1 to 191191)
  AUTHORS   Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-OCT-2003) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     -------------- Genome Center
              Center: Washington University Genome Sequencing Center
              Center code: WUGSC
              Web site: http://genome.wustl.edu
              Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
              Center project name: H_RG104I04
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            The sequence of this clone was established as part of a mapping and
            sequencing collaboration between the NHGRI Chromosome 7 Mapping
            Project and the Washington University Genome Sequencing Center. For
            additional information about the map position of this sequence, see
            http://www.nhgri.nih.gov/DIR/GTB/CHR7 or
            mailto:egreen@nhgri.nih.gov

            SOURCE INFORMATION:
            Clone CTB-104I4 is from the first release of the human BAC library
            CITB-978SK-B. The library contains cloned DNA from the male
            fibroblast cell line 978SK. See:  Shizuya et al., Proc. Natl. Acad.
            Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8
            (1996). This clone is available from Research Genetics, Inc.
            (http://www.resgen.com).
            VECTOR:  pBeloBAC11
            Selection:  chloramphenicol

            NEIGHBORING SEQUENCE INFORMATION:
            The actual start of this clone is at base position 1 of CTB-104I4
            actual end is at 191191 of CTB-104I4. The orientation of this clone
            is unknown.
FEATURES                Location/Qualifiers
     source             1. .191191
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /chromosome="7"
                        /map="7"
                        /clone="CTB-104I4"
                        /clone_lib="CITB-978SK-B"
     repeat_region      1655. .1726
                        /rpt_family="AcHobo"
     repeat_region      1752. .1870
                        /rpt_family="Alu"
     repeat_region      1872. .1960
                        /rpt_family="AcHobo"
     repeat_region      4418. .4465
                        /rpt_family="CT-rich"
     repeat_region      5384. .5471
                        /rpt_family="MIR"
     repeat_region      6010. .6439
                        /rpt_family="MaLR"
     repeat_region      7812. .7895
                        /rpt_family="MER1_type"
     repeat_region      7931. .9288
                        /rpt_family="L1"
     repeat_region      11003. .11945
                        /rpt_family="ERV1"
     repeat_region      12538. .12710
                        /rpt_family="MIR"
     repeat_region      13031. .13142
                        /rpt_family="L2"
     repeat_region      13982. .14096
                        /rpt_family="MIR"
     repeat_region      14993. .15226
                        /rpt_family="MIR"
     repeat_region      16169. .16205
                        /rpt_family="AT_rich"
     repeat_region      16229. .16266
                        /rpt_family="AT_rich"
     repeat_region      16354. .16452
                        /rpt_family="L2"
     repeat_region      16509. .16797
                        /rpt_family="Alu"
     repeat_region      16798. .16870
                        /rpt_family="(TA)n"
     repeat_region      16901. .17789
                        /rpt_family="L1"
     repeat_region      17802. .18188
                        /rpt_family="ERVL"
     repeat_region      18189. .18219
                        /rpt_family="(TCTG)n"
     repeat_region      19807. .20062
                        /rpt_family="Alu"
     repeat_region      24317. .24420
                        /rpt_family="(TA)n"
     repeat_region      26099. .26146
                        /rpt_family="L2"
```

```
  repeat_region   26468. .26588
                  /rpt_family="T2_type"
  repeat_region   26589. .26784
                  /rpt_family="Alu"
  repeat_region   26792. .26841
                  /rpt_family="T2_type"
  repeat_region   26845. .27684
                  /rpt_family="T2_type"
  repeat_region   27689. .29178
                  /rpt_family="ERV1"
  repeat_region   29183. .29603
                  /rpt_family="T2_type"
  repeat_region   30200. .30243
                  /rpt_family="(CAAAAA)n"
  repeat_region   30249. .30273
                  /rpt_family="AT_rich"
  repeat_region   30274. .30416
                  /rpt_family="L1"
  repeat_region   30521. .30622
                  /rpt_family="(TATATG)n"
  repeat_region   30840. .30970
                  /rpt_family="Alu"
  repeat_region   31658. .31711
                  /rpt_family="(CA)n"
  misc_feature    31884. .32110
                  /note="CpG_island (%GC=72.2, o/e=0.56, #CpGs=22)"
  repeat_region   34694. .34782
                  /rpt_family="MIR"
  repeat_region   35891. .36437
                  /rpt_family="L1"
  repeat_region   36645. .37229
                  /rpt_family="L1"
  repeat_region   37230. .37275
                  /rpt_family="(CAAAA)n"
  repeat_region   37276. .38427
                  /rpt_family="L1"
  repeat_region   38428. .38699
                  /rpt_family="Alu"
  repeat_region   38700. .39084
                  /rpt_family="L1"
  repeat_region   39085. .39362
                  /rpt_family="Alu"
  repeat_region   39363. .39600
                  /rpt_family="L1"
  repeat_region   39601. .39885
                  /rpt_family="L1"
  repeat_region   39886. .40005
                  /rpt_family="L1"
  repeat_region   40006. .40343
                  /rpt_family="MER1_type"
  repeat_region   40344. .40364
                  /rpt_family="L1"
  repeat_region   40381. .40537
                  /rpt_family="L1"
  repeat_region   40564. .40976
                  /rpt_family="L1"
  repeat_region   41007. .41120
                  /rpt_family="L1"
  repeat_region   41355. .41630
                  /rpt_family="L1"
  repeat_region   41965. .42126
                  /rpt_family="Alu"
  repeat_region   42148. .42293
                  /rpt_family="GA-rich"
  repeat_region   42425. .42532
                  /rpt_family="CR1"
  repeat_region   42669. .42699
                  /rpt_family="AT_rich"
  repeat_region   42751. .42939
                  /rpt_family="MIR"
  repeat_region   42979. .43272

Alignment Scores:

Pred. No.:              818             Length:         191191
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.0%            Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-9 (1-149) x AC000119 (1-191191)

Qy          1 TyrAsnThrValSerPheAsnLeuGly 9
              |||||||||||||||||||||||||||
Db     186265 TACAACACAGTCAGTTTTAACTTGGGC 186239

RESULT 14
AC024117
LOCUS       AC024117              198134 bp    DNA     linear   HTG 03-MAR-2000
DEFINITION  Homo sapiens chromosome 3p clone RP11-327i12, WORKING DRAFT
            SEQUENCE, 30 unordered pieces.
ACCESSION   AC024117
VERSION     AC024117.1  GI:7025690
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 198134)
  AUTHORS   Tu,Y., Zhao,Y., Lin,W., Dong,H., Wan,M., Xu,S., Gu,W., Zhang,C.,
            Jia,J., Wu,C., Lu,G., Zhong,M., Zhou,Y., Ren,S., Fu,G., Chen,Z. and
            Huang,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-2000) Genomic Dept., Chinese National Human
            Genome Center at Shanghai, 315 Guo Shou Jing Road, Shanghai,
            Shanghai 201203, P. R. China
COMMENT     ----------------Genome Center Informations-----------------
            Center: Chinese National Human Genome Center at Shanghai
            Center Code: CHGC
            Web site: http://www.chgc.sh.cn
            Email: mhuang@chgc.sh.cn or fugang@chgc.sh.cn
             ----------------End Genome Center Informations---------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 30 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2466: contig of 2466 bp in length
            *                   gap of unknown length
            *     2467     5597: contig of 3131 bp in length
            *                   gap of unknown length
            *     5598     7794: contig of 2197 bp in length
            *                   gap of unknown length
            *     7795    10770: contig of 2976 bp in length
            *                   gap of unknown length
            *    10771    14382: contig of 3612 bp in length
            *                   gap of unknown length
            *    14383    17264: contig of 2882 bp in length
            *                   gap of unknown length
            *    17265    22426: contig of 5162 bp in length
            *                   gap of unknown length
            *    22427    24914: contig of 2488 bp in length
            *                   gap of unknown length
            *    24915    27774: contig of 2860 bp in length
            *                   gap of unknown length
            *    27775    33263: contig of 5489 bp in length
            *                   gap of unknown length
            *    33264    38487: contig of 5224 bp in length
            *                   gap of unknown length
            *    38488    43890: contig of 5403 bp in length
            *                   gap of unknown length
            *    43891    49788: contig of 5898 bp in length
```

```
            *                    gap of unknown length
            *    49789    55574: contig of 5786 bp in length
            *                    gap of unknown length
            *    55575    60049: contig of 4475 bp in length
            *                    gap of unknown length
            *    60050    65641: contig of 5592 bp in length
            *                    gap of unknown length
            *    65642    72478: contig of 6837 bp in length
            *                    gap of unknown length
            *    72479    78441: contig of 5963 bp in length
            *                    gap of unknown length
            *    78442    85088: contig of 6647 bp in length
            *                    gap of unknown length
            *    85089    93621: contig of 8533 bp in length
            *                    gap of unknown length
            *    93622   102041: contig of 8420 bp in length
            *                    gap of unknown length
            *   102042   109859: contig of 7818 bp in length
            *                    gap of unknown length
            *   109860   119036: contig of 9177 bp in length
            *                    gap of unknown length
            *   119037   126228: contig of 7192 bp in length
            *                    gap of unknown length
            *   126229   134394: contig of 8166 bp in length
            *                    gap of unknown length
            *   134395   141786: contig of 7392 bp in length
            *                    gap of unknown length
            *   141787   151483: contig of 9697 bp in length
            *                    gap of unknown length
            *   151484   160283: contig of 8800 bp in length
            *                    gap of unknown length
            *   160284   173523: contig of 13240 bp in length
            *                    gap of unknown length
            *   173524   198134: contig of 24611 bp in length.
FEATURES             Location/Qualifiers
     source          1. .198134
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3p"
                     /clone="RP11-327i12"
ORIGIN

Alignment Scores:
Pred. No.:                846          Length:          198134
Score:                    9.00         Matches:         9
Percent Similarity:       100.0%       Conservative:    0
Best Local Similarity:    100.0%       Mismatches:      0
Query Match:              6.0%         Indels:          0
DB:                       14           Gaps:            0

US-10-758-902-9 (1-149) x AC024117 (1-198134)

Qy         17 PheIleGlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||||||
Db      17166 TTTATCCAAGACCTTCGAAATGAACTT 17192

RESULT 15
AC102364
LOCUS       AC102364               208404 bp    DNA     linear   ROD 30-SEP-2003
DEFINITION  Mus musculus chromosome 9, clone RP23-106P6, complete sequence.
ACCESSION   AC102364
VERSION     AC102364.5  GI:32813540
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 208404)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 9, clone RP23-106P6
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 208404)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
            Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
            Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 208404)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
            Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
            Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
            Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
            Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
            Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
            Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
            Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
            Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
            Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 208404)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
            Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
            Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
            Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
            Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C.,
            Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
            Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
            Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
            Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
            Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2003) Whitehead Institute/MIT Center for Genome
```

```
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   5  (bases 1 to 208404)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
            Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
            Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
            Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
            Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., MacLean,C.,
            Macdonal¢,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
            Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
            Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
            Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
            Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-SEP-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jul 16, 2003 this sequence version replaced gi:31249829.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L18579
                Center clone name: 106_P_6
            --------------.
FEATURES             Location/Qualifiers
     source          1. .208404
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="9"
                     /map="9"
                     /clone="RP23-106P6"
                     /clone_lib="RPCI-23 Female Mouse BAC"
     misc_feature    1. .651
                     /note="wgs_end_extension
                     clone_end:SP6"
     repeat_region   307. .367
                     /rpt_family="LTR33A"
     misc_feature    652. .657
                     /note="clone_boundary
                     clone_end:SP6
                     site:EcoRI"
     repeat_region   1125. .1176
                     /rpt_family="(TG)n"
     repeat_region   complement(1900. .1959)
                     /rpt_family="Lx8"
     repeat_region   complement(1960. .2281)
                     /rpt_family="ORR1A2"
     repeat_region   complement(2282. .2591)
                     /rpt_family="Lx8"
     repeat_region   3298. .3338
                     /rpt_family="(TA)n"
     repeat_region   3340. .3504
                     /rpt_family="L1MC3"
     repeat_region   3528. .4048
                     /rpt_family="L1MC3"
     repeat_region   4182. .4463
                     /rpt_family="L1MC3"
     repeat_region   4469. .4640
                     /rpt_family="B2_Mm2"
     repeat_region   4646. .5377
                     /rpt_family="Lx2"
     repeat_region   5404. .5445
                     /rpt_family="(GGAA)n"
     repeat_region   5447. .5559
                     /rpt_family="L1MC3"
     repeat_region   5560. .5588
                     /rpt_family="(CAAAA)n"
     repeat_region   5589. .5652
                     /rpt_family="L1MC3"
     repeat_region   complement(7766. .7834)
                     /rpt_family="L2"
     repeat_region   8379. .8519
                     /rpt_family="L2"
     repeat_region   8987. .9346
                     /rpt_family="MLT1D"
     repeat_region   9456. .9493
                     /rpt_family="(TC)n"
     repeat_region   9493. .9534
                     /rpt_family="(CA)n"
     repeat_region   9862. .9974
                     /rpt_family="Zaphod"
     repeat_region   10147. .10332
                     /rpt_family="MER31-int"
     repeat_region   complement(10702. .11632)
                     /rpt_family="L1_MM"
     unsure          10726. .10730
                     /note="<30 qual SNGL region"
     unsure          10749. .10753
                     /note="<30 qual SNGL region"
     repeat_region   14506. .14539
                     /rpt_family="AT_rich"
     repeat_region   15062. .15169
                     /rpt_family="LTR16A"
     repeat_region   15199. .15219
                     /rpt_family="AT_rich"
     repeat_region   17079. .17100
                     /rpt_family="AT_rich"
     repeat_region   17152. .17283

Alignment Scores:
Pred. No.:                887             Length:         208404
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              6.0%            Indels:         0
DB:                       9               Gaps:           0

US-10-758-902-9 (1-149) x AC102364 (1-208404)

Qy          56 SerLysLysThrValLysValAlaIle 64
               |||||||||||||||||||||||||||
Db       10429 AGCAAGAAAACTGTCAAGGTTGCCATC 10455

RESULT 16
AC096458
LOCUS       AC096458              241803 bp    DNA     linear   HTG 10-MAY-2003
DEFINITION  Rattus norvegicus clone CH230-104L19, WORKING DRAFT SEQUENCE.
ACCESSION   AC096458
VERSION     AC096458.5  GI:30521358
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 241803)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
```

```
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 241803)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 241803)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On May 10, 2003 this sequence version replaced gi:22855355.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GFWP
                Center clone name: CH230-104L19
            -------------- Summary Statistics
                Assembly program: Atlas 3.0;
                Consensus quality: 222004 bases at least Q40
                Consensus quality: 224169 bases at least Q30
                Consensus quality: 225734 bases at least Q20
                Estimated insert size: 233845; sum-of-contigs estimation
                Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *         1   241803: contig of 241803 bp in length.
FEATURES              Location/Qualifiers
     source           1. .241803
                      /organism="Rattus norvegicus"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:10116"
                      /clone="CH230-104L19"
     misc_feature     1. .1489
                      /note="wgs_contig"
     misc_feature     178459. .180250
                      /note="wgs_contig"
     misc_feature     240214. .241803
                      /note="wgs_contig"
ORIGIN

Alignment Scores:
Pred. No.:              1.02e+03        Length:         241803
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.0%            Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-9 (1-149) x AC096458 (1-241803)

Qy         28 GlyThrProValCysGlnLeuProVal 36
              |||||||||||||||||||||||||||
Db     230711 GGCACTCCAGTGTGCCAGCTGCCTGTT 230737

RESULT 17
AC108805
LOCUS       AC108805               242531 bp    DNA     linear   ROD 25-OCT-2003
DEFINITION  Mus musculus chromosome 9, clone RP23-226G13, complete sequence.
ACCESSION   AC108805
VERSION     AC108805.15  GI:37991999
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 242531)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 9, clone RP23-226G13
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 242531)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
```

```
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
            Landers,T., Lehoczky,J., Levine,R., Liu,G., MacLean,C.,
            Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
            McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
            Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
            Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
            Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
            Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
            Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 242531)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
            Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
            Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
            Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
            Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., MacLean,C.,
            Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
            Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
            Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
            Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
            Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-OCT-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 242531)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
            Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
            Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
            Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
            Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., MacLean,C.,
            Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
            Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
            Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
            Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
            Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Oct 25, 2003 this sequence version replaced gi:37361038.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L20787
                Center clone name: 226_G_13
            --------------.
FEATURES                Location/Qualifiers
     source             1. .242531
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:10090"
                        /chromosome="9"
                        /map="9"
                        /clone="RP23-226G13"
                        /clone_lib="RPCI-23 Female Mouse BAC"
     misc_feature       1. .9242
                        /note="wgs_end_extension
                        clone_end:SP6"
     repeat_region      complement(219. .465)
                        /rpt_family="MIR"
     repeat_region      1044. .1136
                        /rpt_family="(CA)n"
     repeat_region      1141. .1185
                        /rpt_family="(CAGAGA)n"
     repeat_region      8315. .8476
                        /rpt_family="MLT1F"
     repeat_region      8706. .8736
                        /rpt_family="(GA)n"
     misc_feature       9243. .9248
                        /note="clone_boundary
                        clone_end:SP6
                        site:EcoRI"
     repeat_region      complement(9374. .9598)
                        /rpt_family="URR1B"
     repeat_region      9883. .10003
                        /rpt_family="(TTTC)n"
     repeat_region      10706. .10773
                        /rpt_family="(TTCC)n"
     repeat_region      10774. .10957
                        /rpt_family="(TTCC)n"
     repeat_region      complement(11594. .11636)
                        /rpt_family="B3A"
     repeat_region      12397. .12444
                        /rpt_family="(CAAA)n"
     repeat_region      12702. .12735
                        /rpt_family="(TAAA)n"
     repeat_region      12853. .12882
                        /rpt_family="AT_rich"
     repeat_region      13022. .13064
                        /rpt_family="(TAGA)n"
     repeat_region      complement(13136. .13212)
                        /rpt_family="L1MC/D"
     repeat_region      14457. .14534
                        /rpt_family="ID4"
     repeat_region      14554. .14655
                        /rpt_family="B3"
     repeat_region      14701. .14831
                        /rpt_family="RSINE1"
     repeat_region      16425. .16447
                        /rpt_family="AT_rich"
     repeat_region      17011. .17069
                        /rpt_family="GA-rich"
     repeat_region      18242. .18338
                        /rpt_family="(TG)n"
     repeat_region      18486. .19543
                        /rpt_family="Lx8"
     repeat_region      20070. .20374
                        /rpt_family="MSTD"
```

```
     repeat_region   complement(20375. .20566)
                     /rpt_family="MTD"
     repeat_region   20590. .20651
                     /rpt_family="T-rich"
     repeat_region   complement(20653. .20842)
                     /rpt_family="MTC"
     repeat_region   complement(20885. .20960)
                     /rpt_family="L1M4"
     repeat_region   22360. .22713
                     /rpt_family="LTR69"
     repeat_region   22760. .22810
                     /rpt_family="(TAG)n"
     repeat_region   23679. .24126
                     /rpt_family="L1MB1"
     repeat_region   24265. .24519
                     /rpt_family="L1MB1"
     repeat_region   24522. .24621
                     /rpt_family="(GGA)n"
     repeat_region   24622. .24860
                     /rpt_family="L1MA6"
     repeat_region   24905. .25039
                     /rpt_family="B1F"
     repeat_region   25103. .25132
                     /rpt_family="(TTA)n"
     repeat_region   complement(25602. .25772)
                     /rpt_family="B2_Mm2"
     repeat_region   25959. .26243
                     /rpt_family="Lx4"
     repeat_region   28869. .29045
                     /rpt_family="MIR"
     repeat_region   29911. .29954
                     /rpt_family="(TG)n"
     repeat_region   30039. .30060
                     /rpt_family="(CAAA)n"
     repeat_region   30656. .30679
                     /rpt_family="(TTG)n"
     repeat_region   complement(31105. .31253)

Alignment Scores:
Pred. No.:                1.02e+03        Length:          242531
Score:                    9.00            Matches:         9
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              6.0%            Indels:          0
DB:                       9               Gaps:            0

US-10-758-902-9 (1-149) x AC108805 (1-242531)

Qy         56 SerLysLysThrValLysValAlaIle 64
              |||||||||||||||||||||||||||
Db     157363 AGCAAGAAAACTGTCAAGGTTGCCATC 157389

RESULT 18
AC106167
LOCUS       AC106167               244273 bp    DNA     linear   HTG 13-MAY-2003
DEFINITION  Rattus norvegicus clone CH230-103L19, WORKING DRAFT SEQUENCE, 2
            unordered pieces.
ACCESSION   AC106167
VERSION     AC106167.5  GI:30578530
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 244273)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 244273)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 244273)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On May 13, 2003 this sequence version replaced gi:24819227.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
```

```
            Contact: hgsc-help@bcm.tmc.edu
           ------------- Project Information
            Center project name: GJKN
            Center clone name: CH230-103L19
           ------------- Summary Statistics
            Assembly program: Atlas 3.0;
            Consensus quality: 226044 bases at least Q40
            Consensus quality: 228017 bases at least Q30
            Consensus quality: 229406 bases at least Q20
            Estimated insert size: 234362; sum-of-contigs estimation
            Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
           --------------
           * NOTE: Estimated insert size may differ from sequence length
           *   (see 'http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
           * NOTE: This is a 'working draft' sequence. It currently
           * consists of 2 contigs. The true order of the pieces
           * is not known and their order in this sequence record is
           * arbitrary. Gaps between the contigs are represented as
           * runs of N, but the exact sizes of the gaps are unknown.
           * This record will be updated with the finished sequence
           * as soon as it is available and the accession number will
           * be preserved.
           *       1   242778: contig of 242778 bp in length
           *  242779   242878: gap of unknown length
           *  242879   244273: contig of 1395 bp in length.
FEATURES             Location/Qualifiers
     source          1. .244273
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-103L19"
     misc_feature    1. .1456
                     /note="wgs_end_extension
                     clone_end:Sp6"
     misc_feature    complement(3505. .3979)
                     /note="clone_boundary
                     clone_end:Sp6
                     site:EcoRI
                     end_sequence:BH293524"
     misc_feature    complement(234627. .235549)
                     /note="clone_boundary
                     clone_end:T7
                     site:EcoRI
                     end_sequence:BH293522"
     misc_feature    238974. .241148
                     /note="wgs_end_extension
                     clone_end:T7"
     misc_feature    241577. .242778
                     /note="wgs_end_extension
                     clone_end:T7"
     gap             242779. .242878
                     /estimated_length=unknown
ORIGIN

Alignment Scores:
Pred. No.:              1.03e+03        Length:         244273
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.0%            Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-9 (1-149) x AC106167 (1-244273)

Qy         28 GlyThrProValCysGlnLeuProVal 36
              |||||||||||||||||||||||||||||
Db      97757 GGCACTCCAGTGTGCCAGCTGCCTGTT 97783

RESULT 19
BCCSPCGEN
LOCUS       BCCSPCGEN               324 bp    DNA     linear   BCT 26-SEP-1996
DEFINITION  B.cereus cspC gene.
ACCESSION   X93041
VERSION     X93041.1  GI:1565231
KEYWORDS    cspC gene; small nucleotide binding protein.
SOURCE      Bacillus cereus
  ORGANISM  Bacillus cereus
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
REFERENCE   1
  AUTHORS   Mayr,B., Kaplan,T., Lechner,S. and Scherer,S.
  TITLE     Identification and purification of a family of dimeric major cold
            shock protein homologs from the psychrotrophic Bacillus cereus WSBC
            10201
  JOURNAL   J. Bacteriol. 178 (10), 2916-2925 (1996)
   PUBMED   8631682
REFERENCE   2
  AUTHORS   Mayr,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-1995) B. Mayr, Institut fuer Mikrobiologie,
            Forschungszentrum f. Milch und Lebensmittel Weihenstephan,
            Technische Universitaet Muenchen, Voettinger Strasse. 45, 85350
            Freising, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 324)
  AUTHORS   Mayr,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-SEP-1996) B. Mayr, Institut fuer Mikrobiologie,
            Forschungszentrum f. Milch und Lebensmittel Weihenstephan,
            Technische Universitaet Muenchen, Voettinger Strasse. 45, 85350
            Freising, FRG
  REMARK    Information from journal
COMMENT     On Sep 27, 1996 this sequence version replaced gi:1405473.
FEATURES             Location/Qualifiers
     source          1. .324
                     /organism="Bacillus cereus"
                     /mol_type="genomic DNA"
                     /strain="WSBC10201"
                     /db_xref="taxon:1396"
                     /clone="E.coli K12 clone carrying the plasmid pCspC"
     RBS             27. .30
     gene            41. .238
                     /gene="cspC"
     CDS             41. .238
                     /gene="cspC"
                     /function="small nucleotide binding protein"
                     /codon_start=1
                     /transl_table=11
                     /product="CspC protein"
                     /protein_id="CAA63609.1"
                     /db_xref="GI:1405474"
                     /db_xref="GOA:Q45098"
                     /db_xref="UniProt/Swiss-Prot:Q45098"
                     /translation="MQGRVKWFNAEKGFGFIEREDGDDVFVHFSAIQQDGYKSLEEGQ
                     QVEFDIVDGARGPQAANVVKL"
ORIGIN

Alignment Scores:
Pred. No.:              26.6            Length:         324
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     1               Gaps:           0

US-10-758-902-9 (1-149) x BCCSPCGEN (1-324)

Qy         80 GlyLysAspArgAlaValPheLeu 87
              |||||||||||||||||||||||||
Db        252 GGAAAAGATAGAGCTGTGTTTTTA 275

RESULT 20
BV363497/c
LOCUS       BV363497                549 bp    DNA     linear   STS 28-JAN-2005
DEFINITION  S231P6376RD7.T0 BedlingtonTerrier Canis familiaris STS genomic,
            sequence tagged site.
```

```
ACCESSION   BV363497
VERSION     BV363497.1  GI:57617397
KEYWORDS    STS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 549)
  AUTHORS   Lindblad-Toh,K.
  TITLE     The genome sequence of Canis familiaris
  JOURNAL   Unpublished (2004)
COMMENT
            Contact: Kerstin Lindblad-Toh
            Whitehead Institute for Biomedical Research, Center for Genome
            Research
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172521477
            Fax: 6172580903
            Email: kersli@genome.wi.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 549
            Protocol:
            WGS-discovery (WGS):
            Paired-end low-coverage whole genome shotgun reads were generated
            from 9 breeds
            (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador
            Retriever, English
            Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese
            Water Dog -100,000 each)
            and five other canids (Chinese, Alaskan, Indian and Spanish Gray
            Wolf as well as the
            Californian Coyote).
            The WGS reads were placed uniquely on the CanFam1.0 boxer assembly
            and SNP detection was
            carried out by SSAHA-SNP. 863872 reads were annotated as STSs and
            485941 SNPs were
            annotated with alleles from the boxer and the breed or canid from
            which the particular
            read came. The validation rate for these SNPs was estimated at
            approximately 98%.
            WGA-discovery (WGA) of Boxer/Poodle SNPs:
            A second set of SNPs was generated using a similar methodology
            except that the contigs
            from the 1.5x poodle assembly (Kirkness 2003) were used instead of
            WGS reads. Since this
            sequence lacked base quality scores, arbitrary quality scores of
            phred 40 were assigned
            before the poddle segeunce was placed uniquely on the CanFam1.0
            boxer assembly and SNP
            detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated
            with alleles from the
            boxer and the poodle. The validation rate for these SNPs was
            estimated at approximately TBD%.
            Internal-WGA-discovery (I-WGA):
            A third set of SNPs were discovered by comparing reads in the WGA
            assembly. SNPs were
            defined as mismatch positions that had a base quality of >= 30 on
            both reads in a region
            that aligned without gaps, and with at most one additional mismatch
            in the ten flanking
            bases. For each allele, at least one additional read had to confirm
            it. 731476 SNPs were
            annotated with alleles between the two boxer alleles. The
            validation rate for these SNPs
            was estimated at approximately TBD%.
FEATURES            Location/Qualifiers
     source         1. .549
                    /organism="Canis familiaris"
                    /mol_type="genomic DNA"
                    /strain="BedlingtonTerrier"
                    /db_xref="taxon:9615"
                    /map="+ 6 22-501 35304374-35303895"
                    /clone_lib="BedlingtonTerrier"
     STS            <1. .>549
ORIGIN

Alignment Scores:
Pred. No.:              43.8          Length:         549
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     10            Gaps:           0

US-10-758-902-9 (1-149) x BV363497 (1-549)

Qy          94 AlaThrSerLysLeuPheProGly 101
               ||||||||||||||||||||||
Db         343 GCCACTTCGAAGTTGTTCCCTGGG 320

RESULT 21
BC048651
LOCUS       BC048651                610 bp    mRNA    linear   ROD 08-MAR-2005
DEFINITION  Mus musculus cDNA sequence BC048651, mRNA (cDNA clone MGC:58790
            IMAGE:6772735), complete cds.
ACCESSION   BC048651
VERSION     BC048651.1  GI:28913664
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
            Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
            B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
            Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
            GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
            Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
            Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
            SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
            Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
            Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
            Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
            Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
            Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
            Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
            Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 610)
  AUTHORS   Director MGC Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jonathan Kuo, NIMH
            cDNA Library Preparation: Michael Brownstein /  Ted Usdin
            Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
            Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
```

Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 46 Row: j Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 46402270.

```
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="MGC:58790 IMAGE:6772735"
                     /tissue_type="Testis, mouse"
                     /clone_lib="NIH_MGC_169"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-LIB"
     gene            1. .610
                     /gene="BC048651"
                     /note="synonyms: NYD-SP18, MGC58790"
                     /db_xref="GeneID:330277"
                     /db_xref="MGI:3032524"
     CDS             61. .453
                     /gene="BC048651"
                     /codon_start=1
                     /product="testes development-related NYD-SP18"
                     /protein_id="AAH48651.1"
                     /db_xref="GI:28913665"
                     /db_xref="GeneID:330277"
                     /db_xref="MGI:3032524"
                     /translation="MMTSVPPRKSWWTSKKTVKVIRSYPTFPSLNAWEKFRGLLPVDG
                     ETNPGVGLGVEEGLLCQMVHSPEFNLFPNSVVFESNFVQVRRSRNWKEIYKASNTMAL
                     GVHCPKVWSLEKSDAMRRGSWRRQAERK"
ORIGIN

Alignment Scores:
Pred. No.:                48.4          Length:          610
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              5.4%          Indels:          0
DB:                       9             Gaps:            0

US-10-758-902-9 (1-149) x BC048651 (1-610)

Qy          55 ThrSerLysLysThrValLysVal 62
               ||||||||||||||||||||||||
Db          97 ACATCGAAGAAGACAGTAAAAGTG 120

RESULT 22
CNS018XO
LOCUS       CNS018XO                  720 bp    mRNA    linear   PLN 20-MAR-2004
DEFINITION  Botrytis cinerea strain T4 cDNA library.
ACCESSION   AL110931
VERSION     AL110931.1  GI:5825218
KEYWORDS    cDNA library; EST, nitrate deprivation.
SOURCE      Botryotinia fuckeliana
  ORGANISM  Botryotinia fuckeliana
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
            78026 Versailles, France
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
            CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The cDNA library was made by using Botrytis cinerea T4 strain grown
            under nitrate deprivation conditions. The cDNA were cloned
            directionally in the pBSII vector.
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Botryotinia fuckeliana"
                     /mol_type="mRNA"
                     /strain="T4"
                     /db_xref="taxon:40559"
                     /note="Genoscope sequence ID : W52F081"
ORIGIN

Alignment Scores:
Pred. No.:                56.6          Length:          720
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              5.4%          Indels:          0
DB:                       15            Gaps:            0

US-10-758-902-9 (1-149) x CNS018XO (1-720)

Qy          125 ArgLysAspLeuGluLeuGlyVal 132
                ||||||||||||||||||||||||
Db          220 CGCAAAGACCTGGAGTTGGGCGTA 243

RESULT 23
BV631147
LOCUS       BV631147                  724 bp    DNA     linear   STS 15-APR-2005
DEFINITION  S215P6346RG8.T0 Clara Pan troglodytes troglodytes STS genomic,
            sequence tagged site.
ACCESSION   BV631147
VERSION     BV631147.1  GI:62621325
KEYWORDS    STS.
SOURCE      Pan troglodytes troglodytes
  ORGANISM  Pan troglodytes troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   Mikkelsen,T.S., Hillier,W.L., Eichler,E.E., Zody,M.C. and
            Jaffe,D.B.
  TITLE     Initial Sequence of the Chimpanzee Genome and Comparison with the
            Human Genome
  JOURNAL   Unpublished (2005)
COMMENT
            Contact: Michael C. Zody
            Broad Institute of MIT and Harvard
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172580933
            Fax: 6172580903
            Email: mczody@broad.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 724
            Protocol:
            23,021,928 chimpanzee whole genome shotgun reads were aligned to
            the Human genome NCBI
            Build 34 (hg16,July 2003). Chimp WGS reads were from 9 donors,
            including Clint (Pan
            troglodytes verus), 3 other Pan troglodytes verus chimps
            (Donald,Karlien,Yvonne), 3 Pan
            troglodytes troglodytes chimps (Noemie,Masuku,Clara) and 2 chimps
            of unknown origin
            (Gon,Unknown Chimp). Common names:  Pan troglodytes verus is the
            western chimp and Pan
            troglodytes troglodytes is the central chimp. To be included in
            chimpanzee SNP discovery, a
            read must be at least 500bp in length, at least 50% of its base
            calls must have Phred
            score >= 20, at least 30% of its base calls must satisfy
```

```
            SNQS(30,25)(single strand NQS, the
            base in question has Phred score >= 30, the surrounding 10 bases in
            the read have Phred
            score >= 25), and the read must have at least 200 bp SNQS(30,25)
            bases. Reads not uniquely
            placed in the genome and read pairs whose two ends were not
            consistently placed were
            discarded. After above filtering, NQS(30,25) standard was applied
            to all pairs of
            overlapping reads to call NQS bases and SNPs. Alignments (between
            two reads) with less
            than 100 NQS bases or with SNP rate > 0.01 were discarded. To
            exclude alignment between two
            copies of a single read, comparisons between two reads that share
            95% of their genome
            alignments (>=95% bases of read A and >=95% bases of read B were
            placed at the same locus
            of human genome) were discarded.
FEATURES              Location/Qualifiers
     source           1. .724
                      /organism="Pan troglodytes troglodytes"
                      /mol_type="genomic DNA"
                      /sub_species="troglodytes"
                      /db_xref="taxon:37011"
                      /clone_lib="Clara"
     STS              <1. .>724
ORIGIN

Alignment Scores:
Pred. No.:              56.9            Length:         724
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-9 (1-149) x BV631147 (1-724)

Qy        139 IleGluAlaIleTrpGlyLysThr 146
              ||||||||||||||||||||||||
Db         48 ATTGAGGCAATATGGGGGAAAACA 71

RESULT 24
BV512710
LOCUS       BV512710                752 bp    DNA     linear   STS 07-APR-2005
DEFINITION  rag91f07.g1 Clint Pan troglodytes verus STS genomic, sequence
            tagged site.
ACCESSION   BV512710
VERSION     BV512710.1  GI:62356452
KEYWORDS    STS.
SOURCE      Pan troglodytes verus
  ORGANISM  Pan troglodytes verus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Mikkelsen,T.S., Hillier,W.L., Eichler,E.E., Zody,M.C. and
            Jaffe,D.B.
  TITLE     Initial Sequence of the Chimpanzee Genome and Comparison with the
            Human Genome
  JOURNAL   Unpublished (2005)
COMMENT
            Contact: Michael C. Zody
            Broad Institute of MIT and Harvard
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172580933
            Fax: 6172580903
            Email: mczody@broad.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 752
            Protocol:
            23,021,928 chimpanzee whole genome shotgun reads were aligned to
            the Human genome NCBI
            Build 34 (hg16,July 2003). Chimp WGS reads were from 9 donors,
            including Clint (Pan
            troglodytes verus), 3 other Pan troglodytes verus chimps
            (Donald,Karlien,Yvonne), 3 Pan
            troglodytes troglodytes chimps (Noemie,Masuku,Clara) and 2 chimps
            of unknown origin
            (Gon,Unknown Chimp). Common names:  Pan troglodytes verus is the
            western chimp and Pan
            troglodytes troglodytes is the central chimp. To be included in
            chimpanzee SNP discovery, a
            read must be at least 500bp in length, at least 50% of its base
            calls must have Phred
            score >= 20, at least 30% of its base calls must satisfy
            SNQS(30,25)(single strand NQS, the
            base in question has Phred score >= 30, the surrounding 10 bases in
            the read have Phred
            score >= 25), and the read must have at least 200 bp SNQS(30,25)
            bases. Reads not uniquely
            placed in the genome and read pairs whose two ends were not
            consistently placed were
            discarded. After above filtering, NQS(30,25) standard was applied
            to all pairs of
            overlapping reads to call NQS bases and SNPs. Alignments (between
            two reads) with less
            than 100 NQS bases or with SNP rate > 0.01 were discarded. To
            exclude alignment between two
            copies of a single read, comparisons between two reads that share
            95% of their genome
            alignments (>=95% bases of read A and >=95% bases of read B were
            placed at the same locus
            of human genome) were discarded.
FEATURES              Location/Qualifiers
     source           1. .752
                      /organism="Pan troglodytes verus"
                      /mol_type="genomic DNA"
                      /sub_species="verus"
                      /db_xref="taxon:37012"
                      /clone_lib="Clint"
     STS              <1. .>752
ORIGIN

Alignment Scores:
Pred. No.:              59              Length:         752
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-9 (1-149) x BV512710 (1-752)

Qy         85 ValPheLeuAspLysValProThr 92
              ||||||||||||||||||||||||
Db         17 GTCTTCCTCGATAAAGTTCCCACT 40

RESULT 25
AY744941
LOCUS       AY744941                937 bp    DNA     linear   BCT 10-OCT-2004
DEFINITION  Mycoplasma cricetuli 16S ribosomal RNA gene, partial sequence;
            16S-23S intergenic spacer, complete sequence; and 23S ribosomal RNA
            gene, partial sequence.
ACCESSION   AY744941
VERSION     AY744941.1  GI:53828173
KEYWORDS    .
SOURCE      Mycoplasma cricetuli
  ORGANISM  Mycoplasma cricetuli
            Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
REFERENCE   1  (bases 1 to 937)
  AUTHORS   Volokhov,D.V., George,J., Liu,S.X. and Chizhikov,V.E.
  TITLE     Identification of Mollicutes species by microarray-based assay
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 937)
```

```
  AUTHORS   Volokhov,D.V. and George,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-2004) DHHS, CBER/FDA, 1401 Rockville Pike,
            Rockville, MD 20852, USA
FEATURES             Location/Qualifiers
     source          1. .937
                     /organism="Mycoplasma cricetuli"
                     /mol_type="genomic DNA"
                     /strain="ATCC 35279"
                     /db_xref="ATCC:35279"
                     /db_xref="taxon:171283"
     misc_RNA        <1. .>937
                     /note="contains 16S ribosomal RNA, 16S-23S intergenic
                     spacer and 23S ribosomal RNA"
ORIGIN

Alignment Scores:
Pred. No.:              72.6          Length:         937
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     1             Gaps:           0

US-10-758-902-9 (1-149) x AY744941 (1-937)

Qy         52 IleThrThrThrSerLysLysThr 59
              |||||||||||||||||||||||
Db        319 ATAACAACGACATCAAAAAAAACA 342

RESULT 26
AR353769/c
LOCUS       AR353769                979 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 71 from patent US 6593104.
ACCESSION   AR353769
VERSION     AR353769.1  GI:33759815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 979)
  AUTHORS   Stone,E.M. and Sheffield,V.C.
  TITLE     Macular degeneration diagnostics and therapeutics
  JOURNAL   Patent: US 6593104-A 71 15-JUL-2003;
            University of Iowa Research Foundation; Iowa City, IA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .979
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              75.7          Length:         979
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-9 (1-149) x AR353769 (1-979)

Qy         33 GlnLeuProValThrLeuGlnThr 40
              |||||||||||||||||||||||
Db        947 CAGTTACCGGTAACTCTGCAAACT 924

RESULT 27
AX082393/c
LOCUS       AX082393                979 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 71 from Patent WO0112823.
ACCESSION   AX082393
VERSION     AX082393.1  GI:13184569
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Stone,E.M. and Sheffield,V.C.
  TITLE     Macular degeneration diagnostics and therapeutics
  JOURNAL   Patent: WO 0112823-A 71 22-FEB-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .979
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="'n' bases at various positions throughout the
                     sequence may be a, t, c, g, other or unknown"
ORIGIN

Alignment Scores:
Pred. No.:              75.7          Length:         979
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-9 (1-149) x AX082393 (1-979)

Qy         33 GlnLeuProValThrLeuGlnThr 40
              |||||||||||||||||||||||
Db        947 CAGTTACCGGTAACTCTGCAAACT 924

RESULT 28
AY444911
LOCUS       AY444911                1104 bp    mRNA    linear   VRL 18-OCT-2004
DEFINITION  Avian orthoreovirus strain turkey reovirus TX98 sigma 2 protein
            (S3) mRNA, complete cds.
ACCESSION   AY444911
VERSION     AY444911.1  GI:38906024
KEYWORDS    .
SOURCE      Avian orthoreovirus
  ORGANISM  Avian orthoreovirus
            Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
REFERENCE   1  (bases 1 to 1104)
  AUTHORS   Sellers,H.S., Linnemann,E.G., Pereira,L. and Kapczynski,D.R.
  TITLE     Phylogenetic Analysis of the Sigma 2 Protein Gene of Turkey
            Reoviruses
  JOURNAL   Avian Dis. 48 (3), 651-657 (2004)
REFERENCE   2  (bases 1 to 1104)
  AUTHORS   Sellers,H.S., Linnemann,E., Pereira,L. and Kapczynski,D.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Department of Avian Medicine, University of
            Georgia, 953 College Station Road, Athens, GA 30602, USA
FEATURES             Location/Qualifiers
     source          1. .1104
                     /organism="Avian orthoreovirus"
                     /mol_type="mRNA"
                     /strain="turkey reovirus TX98"
                     /db_xref="taxon:38170"
                     /country="USA: Texas"
                     /note="isolated in 1998"
     gene            1. .1104
                     /gene="S3"
     CDS             1. .1104
                     /gene="S3"
                     /note="major outer capsid protein"
                     /codon_start=1
                     /product="sigma 2 protein"
                     /protein_id="AAR27797.1"
                     /db_xref="GI:38906025"
                     /translation="MEVRVPNFHSFVEGITSSYIRAPACWNAKTMWNIETFHLPDVIK
                     VGNAYCCSQCCGVLYYGAPPSDGNYFPHHKCHQQQYRSDTPLLRYVRIGRTTEHLLDQ
```

```
                     YAVTLQTIADYYDEASHRVADEPEEDTIAALDIVTRTESIRSDQAVDADFWTYPLERR
                     SDDSRRDIAASIWTMIDASARSFTLPDCLVSPSLHSRHIFDQMLTTTSIYDVAASGKT
                     ARFSPMVAALPQRAAGPITLSDADPLDGVATFWSPQFALSPMIGGVGITGQYARESYH
                     HVGHPVIGSGKKVSHYRNIFMDAWRGWSKSSFTCAAGLEPAECESRLRGHARTMLGRS
                     LPGVCDYGPEAQSRTAPSSLQKATKLTVVECGW"
ORIGIN

Alignment Scores:
Pred. No.:                84.8          Length:         1104
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              5.4%          Indels:         0
DB:                       13            Gaps:           0

US-10-758-902-9 (1-149) x AY444911 (1-1104)

Qy          36 ValThrLeuGlnThrIleAlaAsp 43
               |||||||||||||||||||||||
Db         313 GTCACCCTTCAGACTATCGCCGAT 336

RESULT 29
AY444913
LOCUS       AY444913                1104 bp    mRNA    linear   VRL 18-OCT-2004
DEFINITION  Avian orthoreovirus strain turkey reovirus PEMS 85 sigma 2 protein
            (S3) mRNA, complete cds.
ACCESSION   AY444913
VERSION     AY444913.1  GI:38906049
KEYWORDS    .
SOURCE      Avian orthoreovirus
  ORGANISM  Avian orthoreovirus
            Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
REFERENCE   1  (bases 1 to 1104)
  AUTHORS   Sellers,H.S., Linnemann,E.G., Pereira,L. and Kapczynski,D.R.
  TITLE     Phylogenetic Analysis of the Sigma 2 Protein Gene of Turkey
            Reoviruses
  JOURNAL   Avian Dis. 48 (3), 651-657 (2004)
REFERENCE   2  (bases 1 to 1104)
  AUTHORS   Sellers,H.S., Linnemann,E., Pereira,L. and Kapczynski,D.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Department of Avian Medicine, University of
            Georgia, 953 College Station Road, Athens, GA 30602, USA
FEATURES             Location/Qualifiers
     source          1. .1104
                     /organism="Avian orthoreovirus"
                     /mol_type="mRNA"
                     /strain="turkey reovirus PEMS 85"
                     /db_xref="taxon:38170"
     gene            1. .1104
                     /gene="S3"
     CDS             1. .1104
                     /gene="S3"
                     /note="major outer capsid protein"
                     /codon_start=1
                     /product="sigma 2 protein"
                     /protein_id="AAR27799.1"
                     /db_xref="GI:38906050"
                     /translation="MEVRVPNFHSFVEGITSSYIRAPACWNAKTMWNIETFHLPDVIK
                     VGNAYCCSQCCGVLYYGAPPSDGNYFPHHKCHQQQYRSDTPLLRYVRIGRTTEHLLDQ
                     YAVTLQTIADYYDEASHRVADEPEEDTIAALDIVTRTESIRSDQAVDADFWTYPLERR
                     SDDSRRDIAASIWTMIDASARSFTLPDCLVSPSLHSRHIFDQMLTTTSIYDVAASGKT
                     ARFSPMVAALPQRAAGPITLSDADPLDGVATFWSPQFALSPMIGGVGITGQYARESYH
                     HVGHPVIGSGKKVSHYRNIFMDAWRGWSKSSFTCAAGLEPAECESRLRGHARTMLGRS
                     LPGVCDYGPEAQSRTAPSSLQKATKLTVVECGW"
ORIGIN

Alignment Scores:
Pred. No.:                84.8          Length:         1104
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              5.4%          Indels:         0
DB:                       13            Gaps:           0

US-10-758-902-9 (1-149) x AY444913 (1-1104)

Qy          36 ValThrLeuGlnThrIleAlaAsp 43
               |||||||||||||||||||||||
Db         313 GTCACCCTTCAGACTATCGCCGAT 336

RESULT 30
AB050491
LOCUS       AB050491                1228 bp    DNA     linear   PLN 29-OCT-2004
DEFINITION  Vitreochlamys pinguis chloroplast rbcL gene for
            ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit,
            partial cds, strain:Spha-12/1998-7-16.
ACCESSION   AB050491 AB050490
VERSION     AB050491.2  GI:60391495
KEYWORDS    .
SOURCE      chloroplast Vitreochlamys pinguis
  ORGANISM  Vitreochlamys pinguis
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
            Chlamydomonadales; Chlamydomonadaceae; Vitreochlamys.
REFERENCE   1
  AUTHORS   Nakazawa,A., Krienitz,L. and Nozaki,H.
  TITLE     Taxonomy of the unicellular green algal genus Vitreochlamys
            (Volvocales), based on comparative morphology of cultured material
  JOURNAL   Eur. J. Phycol. 36, 113-128 (2001)
REFERENCE   2  (bases 1 to 1228)
  AUTHORS   Nakazawa,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-2000) Atsushi Nakazawa, Department of Biological
            Scienses, Guraduate School of Science, University of Tokyo; Hongo,
            Bunkyo-ku, Tokyo, 113-0033, Japan
            (E-mail:ss07202@mail.ecc.u-tokyo.ac.jp,
            Tel:81-3-5841-4047(ex.24047), Fax:81-3-5841-4047)
COMMENT     On or before Mar 1, 2005 this sequence version replaced
            gi:14715584, gi:14715585.
FEATURES             Location/Qualifiers
     source          1. .1228
                     /organism="Vitreochlamys pinguis"
                     /organelle="plastid:chloroplast"
                     /mol_type="genomic DNA"
                     /strain="Spha-12/1998-7-16"
                     /db_xref="taxon:140672"
     gene            <1. .>1228
                     /gene="rbcL"
     CDS             join(<1. .582,683. .>1228)
                     /gene="rbcL"
                     /codon_start=1
                     /transl_table=11
                     /product="ribulose-1,5-bisphosphate carboxylase/oxygenase
                     large subunit"
                     /protein_id="BAB62063.1"
                     /db_xref="GI:14715586"
                     /translation="AGFKAGVKDYRLTYYTPDYVVRDTDILAAFRMTPQPGVPPEECG
                     AAVAAESSTGTWTTVWTDGLTSLDRYKGRCYDIEPVPGEDNQYIAYVAYPIDLFEEGS
                     VTNMFTSIVGNVFGFKALRALRLEDLRIPPAYVKTFVGPPHGIQVERDKLNKYGRGLL
                     GCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFVAEAIYKA
                     QAETGEVKGHYLNATAGNCDEMMKRGQCAKDLGVPIIMHDYLTGGFTANTTLATFCRD
                     NGLLLHIHRAMHAVIDRQRNHGIHFRVLAKALRMSGGDHLHSGTVVGKLEGEREVTLG
                     FVDLMRDDYIEKDRSRGIYFTQDWCSMPGVMPVASGGIHVWH"
     exon            <1. .582
                     /gene="rbcL"
                     /product="ribulose-1,5-bisphosphate carboxylase/oxygenase
                     large subunit"
                     /note="exon proceeding to group I intron"
     gap             583. .682
                     /estimated_length=unknown
     exon            683. .>1228
                     /gene="rbcL"
                     /product="ribulose-1,5-bisphosphate carboxylase/oxygenase
                     large subunit"
                     /note="exon following to group I intron"
ORIGIN
```

```
Alignment Scores:
Pred. No.:              93.8          Length:        1228
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     15            Gaps:          0

US-10-758-902-9 (1-149) x AB050491 (1-1228)

Qy         53 ThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||
Db       1122 ACGACTACATCGAAAAAGACCGTA 1145

RESULT 31
AX069004
LOCUS       AX069004               1238 bp    DNA     linear   PAT 25-JAN-2001
DEFINITION  Sequence 12 from Patent WO0102569.
ACCESSION   AX069004
VERSION     AX069004.1  GI:12578824
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tang,Y.T., Yue,H., Yang,J., Azimzai,Y., Baughn,M.R. and Lu,D.A.
  TITLE     Human immune response molecules
  JOURNAL   Patent: WO 0102569-A 12 11-JAN-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1238
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              94.5          Length:        1238
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-9 (1-149) x AX069004 (1-1238)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        994 ACAGTGTCATTTAATTTGGGAGAG 1017

RESULT 32
AY612682
LOCUS       AY612682               1320 bp    DNA     linear   PLN 05-NOV-2004
DEFINITION  Saccoloma inaequale ribulose 1,5-bisphosphate carboxylase/oxygenase
            large subunit (rbcL) gene, partial cds; chloroplast.
ACCESSION   AY612682
VERSION     AY612682.1  GI:52632306
KEYWORDS    .
SOURCE      chloroplast Saccoloma inaequale
  ORGANISM  Saccoloma inaequale
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Moniliformopses; Filicophyta; Filicopsida; Filicales;
            Dennstaedtiaceae; Saccoloma.
REFERENCE   1  (bases 1 to 1320)
  AUTHORS   Pryer,K.M., Schuettpelz,E., Wolf,P.G., Schneider,H., Smith,A.R. and
            Cranfill,R.
  TITLE     Phylogeny and evolution of ferns (monilophytes) with a focus on the
            early leptosporangiate divergences
  JOURNAL   Am. J. Bot. 91 (10), 1582-1598 (2004)
REFERENCE   2  (bases 1 to 1320)
  AUTHORS   Pryer,K.M., Schuettpelz,E., Wolf,P.G., Schneider,H., Smith,A.R. and
            Cranfill,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) Department of Biology, Duke University,
            Durham, NC 27708, USA
FEATURES             Location/Qualifiers
     source          1. .1320
                     /organism="Saccoloma inaequale"
                     /organelle="plastid:chloroplast"
                     /mol_type="genomic DNA"
                     /specimen_voucher="D. Barrington s.n. (UTC)"
                     /db_xref="taxon:262953"
     gene            <1. .>1320
                     /gene="rbcL"
     CDS             <1. .>1320
                     /gene="rbcL"
                     /codon_start=1
                     /transl_table=11
                     /product="ribulose 1,5-bisphosphate carboxylase/oxygenase
                     large subunit"
                     /protein_id="AAU85514.1"
                     /db_xref="GI:52632307"
                     /translation="VGFKAGVKDYRLTYYTPEYPTKDTDILAAFRMTPQPGVPPEEAG
                     AAVAAESSTGTWTTVWTDGLTSLDRYKGRCYGIEPVPGEDNQYIAYVAYPLDLFEEGS
                     VTNMPTSIVGNVFGFKALRALRLEDLRIPPAYSKTFIGPPHGIQVERDKLNKYGRPLL
                     GCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFVAESLFKS
                     QAETGEIKGHYLNATAGTCEEMLKRAVFARELGAPIVMHDYLTGGFTANTTLAFYCRD
                     NGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRMSGGDHIHAGTVVGKLEGERDITLG
                     FVDLLRDDYIEKDRSRGIYFTQDWVSMPGVIPVASGGIHVWHMPALTEIFGDDSVLQF
                     GGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAREGNEIIREASK"
ORIGIN

Alignment Scores:
Pred. No.:              100           Length:        1320
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     15            Gaps:          0

US-10-758-902-9 (1-149) x AY612682 (1-1320)

Qy         53 ThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||
Db       1022 ACGACTACATCGAAAAAGACCGTA 1045

RESULT 33
OKU18644
LOCUS       OKU18644               1320 bp    DNA     linear   PLN 24-JAN-1996
DEFINITION  Orthiopteris kingii ribulose 1,5-bisphosphate carboxylase/oxygenase
            large subunit (rbcL) gene, chloroplast gene encoding chloroplast
            protein, partial cds.
ACCESSION   U18644
VERSION     U18644.1  GI:624659
KEYWORDS    .
SOURCE      chloroplast Orthiopteris kingii
  ORGANISM  Orthiopteris kingii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Moniliformopses; Filicophyta; Filicopsida; Filicales;
            Dennstaedtiaceae; Orthiopteris.
REFERENCE   1  (bases 1 to 1320)
  AUTHORS   Wolf,P.G.
  TITLE     Phylogenetic analyses of rbcL and nuclear ribosomal RNA gene
            sequences in Dennstaedtiaceae
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1320)
  AUTHORS   Wolf,P.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-DEC-1994) Paul G. Wolf, Biology, Utah State
            University, Logan, UT 84322-5305, USA
FEATURES             Location/Qualifiers
     source          1. .1320
                     /organism="Orthiopteris kingii"
                     /organelle="plastid:chloroplast"
```

```
                     /mol_type="genomic DNA"
                     /isolate="Wolf 684"
                     /db_xref="taxon:37220"
     gene            1. .1320
                     /gene="rbcL"
     CDS             <1. .>1320
                     /gene="rbcL"
                     /codon_start=1
                     /product="ribulose 1,5-bisphosphate carboxylase/oxygenase
                     large subunit"
                     /protein_id="AAA85537.1"
                     /db_xref="GI:624660"
                     /translation="VGFKAGVKDYRLTYYTPEYPTKDTDILAAFRMTPQPGVPPEEAG
                     AAVAAESSTGTWTTVWTDGLTSLDRYKGRCYGIEPVPGEDNQYIAYVAYPLDLFEEGS
                     VTNMFTSIVGNVFGFKALRPLRLEDLRIPPAYSKTFIGPPHGIQVERDKLNKYGRPLL
                     GCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFVAESLFKS
                     QAETGEIKGHYLNATAGTCEEMLKRAVFARELGAPIVMHDYLTGGFTANTTLAFYCRD
                     NGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRMSGGDHIHAGTVVGKLEGERDITLG
                     FVDFVRDDYIEKDRSRGIYFTQDWVSMPGVIPVASGGIHVWHMPALTEIFGDDSVLQF
                     GGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAREGNEIIREASK"
ORIGIN

Alignment Scores:
Pred. No.:              100             Length:         1320
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     15              Gaps:           0

US-10-758-902-9 (1-149) x OKU18644 (1-1320)

Qy         53 ThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||
Db       1022 ACGACTACATCGAAAAAGACCGTA 1045

RESULT 34
DQ013264
LOCUS       DQ013264               1364 bp    mRNA    linear   PLN 20-JUL-2005
DEFINITION  Bougainvillea x buttiana antiviral protein 1 mRNA, complete cds.
ACCESSION   DQ013264
VERSION     DQ013264.2  GI:68342547
KEYWORDS    .
SOURCE      Bougainvillea x buttiana
  ORGANISM  Bougainvillea x buttiana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Nyctaginaceae; Bougainvillea.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Choudhary,N. and Lodha,M.L.
  TITLE     cDNA Sequence of Bougainvillea Antiviral Protein (BAP1)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1364)
  AUTHORS   Choudhary,N. and Lodha,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2005) Division of Biochemistry, Indian
            Agricultural Research Institute, Pusa, New Delhi 110012, India
REFERENCE   3  (bases 1 to 1364)
  AUTHORS   Choudhary,N. and Lodha,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-2005) Division of Biochemistry, Indian
            Agricultural Research Institute, Pusa, New Delhi 110012, India
  REMARK    Sequence update by submitter
COMMENT     On Jun 30, 2005 this sequence version replaced gi:63147983.
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="Bougainvillea x buttiana"
                     /mol_type="mRNA"
                     /cultivar="Mahara"
                     /db_xref="taxon:328062"
                     /tissue_type="leaves"
     5'UTR           1. .120
     CDS             121. .1080
                     /note="BAP1"
                     /codon_start=1
                     /product="antiviral protein 1"
                     /protein_id="AAY34283.2"
                     /db_xref="GI:68342548"
                     /translation="MKPLGGLVITCIWWAIIVELVVIKPSIITKETASLGHNTVSFNL
                     EDATEQVYRSVIKSLRNELQTSTLVCKIPVTPQSLAVDKNQFVVVSLTWKSKEVQLGI
                     DVTNAYVVGYQDKLKNQDYRAFLLKDAPPLAKDKLFPGVKSETLPFGGTYPNLVKAGN
                     VDRREQFELGVEKLGHAIDSIFGKPKNDQNVARFFLNAIQIVSEAARFKYIENEVVRG
                     GLNSGLSKPNGKMLNLENSWGHISDAIHNSNQKYKCETISPALELQNADYSKWVVNKV
                     SEISPDLGILKYKSSKLTQSTTIMRSIVVEDSDELEKLETIIG"
     3'UTR           1081. .1364
ORIGIN

Alignment Scores:
Pred. No.:              104             Length:         1364
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     15              Gaps:           0

US-10-758-902-9 (1-149) x DQ013264 (1-1364)

Qy         70 TyrValValGlyTyrGlnAspLys 77
              |||||||||||||||||||||||
Db        442 TATGTGGTGGGTTATCAAGACAAA 465

RESULT 35
S76264/c
LOCUS       S76264                 1449 bp    DNA     linear   PLN 27-JUL-1995
DEFINITION  NR1=nitrate reductase (5' region) [Arabidopsis, Genomic, 1449 nt].
ACCESSION   S76264
VERSION     S76264.1  GI:913896
KEYWORDS    .
SOURCE      Arabidopsis
  ORGANISM  Arabidopsis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae.
REFERENCE   1  (bases 1 to 1449)
  AUTHORS   Lin,Y., Hwang,C.F., Brown,J.B. and Cheng,C.L.
  TITLE     5' proximal regions of Arabidopsis nitrate reductase genes direct
            nitrate-induced transcription in transgenic tobacco
  JOURNAL   Plant Physiol. 106 (2), 477-484 (1994)
   PUBMED   7991680
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 162447] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .1449
                     /organism="Arabidopsis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3701"
     gene            1. .1449
                     /gene="NR1"
                     /note="nitrate reductase"
ORIGIN

Alignment Scores:
Pred. No.:              110             Length:         1449
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     15              Gaps:           0

US-10-758-902-9 (1-149) x S76264 (1-1449)

Qy        134 LysLeuGluPheSerIleGluAla 141
              ||||||||||||||||||||||||
Db        346 AAACTTGAATTTTCAATCGAAGCA 323

RESULT 36
```

AK069521
LOCUS AK069521 1676 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023022O05, full insert sequence.
ACCESSION AK069521
VERSION AK069521.1 GI:32979545
KEYWORDS FLI_CDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
JOURNAL Science 301 (5631), 376-379 (2003)
PUBMED 12869764
REFERENCE 2 (bases 1 to 1676)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
COMMENT This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
FEATURES Location/Qualifiers
source 1. .1676
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J023022O05"
ORIGIN

Alignment Scores:

Pred. No.:	126	Length:	1676
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	15	Gaps:	0

US-10-758-902-9 (1-149) x AK069521 (1-1676)

```
Qy         29 ThrProValCysGlnLeuProVal 36
              |||||||||||||||||||||||||
Db        734 ACTCCGGTATGTCAACTACCTGTC 757
```

RESULT 37
CR848128
LOCUS CR848128 1702 bp mRNA linear VRT 12-OCT-2004
DEFINITION Xenopus tropicalis finished cDNA, clone TGas019o24.
ACCESSION CR848128
VERSION CR848128.1 GI:54110229
KEYWORDS .
SOURCE Xenopus tropicalis (Silurana tropicalis)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1702)
AUTHORS Amaya,E., Ashurst,J.L., Bonfield,J.K., Croning,M.D.R., Davies,R.M., Francis,M.D., Garrett,N., Gilchrist,M.J., Grafham,D.V., McLaren,S.R., Papalopulu,N., Rogers,J., Smith,J.C., Taylor,R.G., Voigt,J. and Zorn,A.M.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: trop@sanger.ac.uk
COMMENT Sanger Xenopus tropicalis EST/cDNA project.
This sequence is from a Xenopus Gene Collection (XGC) library, from a library constructed by Aaron M. Zorn. cDNA was prepared from RNA extracted from gastrula embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XL1-blue.
FEATURES Location/Qualifiers
source 1. .1702
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"

```
                     /clone="TGas019o24"
                     /clone_lib="XGC-gastrula"
                     /dev_stage="gastrula (stage 10.5-13 mixed)"
ORIGIN

Alignment Scores:
Pred. No.:                128             Length:         1702
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       5               Gaps:           0

US-10-758-902-9 (1-149) x CR848128 (1-1702)

Qy          96 SerLysLeuPheProGlyValThr 103
               ||||||||||||||||||||||
Db         364 AGCAAACTCTTTCCAGGAGTCACT 387

RESULT 38
CQ797957/c
LOCUS       CQ797957                1905 bp    DNA     linear   PAT 20-APR-2004
DEFINITION  Sequence 55 from Patent WO2004029631.
ACCESSION   CQ797957
VERSION     CQ797957.1  GI:46426451
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Wolf,S., Jaeger,M., Bangsow,T., Bangsow,C., Jordan,D., Pelzer,B.
            and Oppolzer,T.
  TITLE     Method for identifying bhs-specific proteins and fragments thereof
  JOURNAL   Patent: WO 2004029631-A 55 08-APR-2004;
            Esplora GmbH, c/oTU Darmstadt Institut fuer Biochemie (DE)
FEATURES             Location/Qualifiers
     source          1. .1905
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der k nstlichen Sequenz: CDNA von
                     TSC-22 aus BMEC aus Schweinehirn"
     CDS             243. .677
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAG26848.1"
                     /db_xref="GI:46426452"
                     /translation="MKSQWCRPVAMDLGVYQLRHFSISFLSSLLGTENASVRLDNSSS
                     GASVVAIDNKIEQAMDLVKSHLMYAVREEVEVLKEQIKELIEKNSQLEQENNLLKTLA
                     SPEQLAQFQAQLQTGSPPATTQPQGTTQPPAQPASQGSGPTA"
ORIGIN

Alignment Scores:
Pred. No.:                142             Length:         1905
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-9 (1-149) x CQ797957 (1-1905)

Qy          32 CysGlnLeuProValThrLeuGln 39
               |||||||||||||||||||||||
Db        1364 TGCCAGCTACCTGTCACCCTTCAG 1341

RESULT 39
AX510374/c
LOCUS       AX510374                2000 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 5069 from Patent WO0216655.
ACCESSION   AX510374
VERSION     AX510374.1  GI:23391611
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
  TITLE     Stress-regulated genes of plants, transgenic plants containing
            same, and methods of use
  JOURNAL   Patent: WO 0216655-A 5069 28-FEB-2002;
            The Scripps Research Institute (US) ; Syngenta Participations AG
            (CH)
FEATURES             Location/Qualifiers
     source          1. .2000
                     /organism="Arabidopsis thaliana"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3702"
ORIGIN

Alignment Scores:
Pred. No.:                149             Length:         2000
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-9 (1-149) x AX510374 (1-2000)

Qy         134 LysLeuGluPheSerIleGluAla 141
               |||||||||||||||||||||||
Db         819 AAACTTGAATTTTCAATCGAAGCA 796

RESULT 40
AX652416/c
LOCUS       AX652416                2000 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 2286 from Patent WO03000898.
ACCESSION   AX652416
VERSION     AX652416.1  GI:29155230
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
            Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
  TITLE     Plant genes involved in defense against pathogens
  JOURNAL   Patent: WO 03000898-A 2286 03-JAN-2003;
            Syngenta Participations AG (CH)
FEATURES             Location/Qualifiers
     source          1. .2000
                     /organism="Arabidopsis thaliana"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3702"
ORIGIN

Alignment Scores:
Pred. No.:                149             Length:         2000
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-9 (1-149) x AX652416 (1-2000)

Qy         134 LysLeuGluPheSerIleGluAla 141
               |||||||||||||||||||||||
Db         819 AAACTTGAATTTTCAATCGAAGCA 796
```

Search completed: February 20, 2006, 03:07:41
Job time : 6141.44 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:48:17 ; Search time 619.307 Seconds
(without alignments)
1603.468 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 149
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9989114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160831_4002/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US10758902_@CGN_1_1_1359_@runat_17022006_160831_4002 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	120	80.5	363	2	AAV81468	Aav81468 Ribosome-
	2	21	14.1	65	2	AAV81465	Aav81465 Ribosome-
c	3	9	6.0	110000	14	ADZ13575_0	Adz13575 Murine ca
c	4	9	6.0	110000	14	ADZ13575_1	Continuation (2 of
c	5	9	6.0	289190	13	ABD33143	Abd33143 Murine ca
c	6	8	5.4	100	3	AAA42055	Aaa42055 Human sec
	7	8	5.4	759	13	ADR59442	Adr59442 Cotton cD
c	8	8	5.4	978	4	AAF76566	Aaf76566 Human EFE
	9	8	5.4	1238	4	AAF31245	Aaf31245 Human imm
c	10	8	5.4	1686	13	ADX61939	Adx61939 Plant ful
c	11	8	5.4	1879	13	ADX61418	Adx61418 Plant ful
c	12	8	5.4	2000	6	ABZ17264	Abz17264 Arabidops
c	13	8	5.4	2000	8	ADA68963	Ada68963 Arabidops
	14	8	5.4	2143	12	ADP07317	Adp07317 Human WT1
c	15	8	5.4	2187	13	ADX59797	Adx59797 Plant ful
	16	8	5.4	2291	12	ADQ67284	Adq67284 Novel hum
	17	8	5.4	2772	10	ADE54051	Ade54051 Human pro
c	18	8	5.4	6413	4	AAS46362	Aas46362 Tumour su
c	19	8	5.4	6413	6	ABQ67000	Abq67000 Human ang
c	20	8	5.4	16363	12	ADM68765	Adm68765 Drosophil
	21	8	5.4	35076	11	ACN44688	Acn44688 Mouse gen
c	22	8	5.4	92247	11	ACN44266	Acn44266 Human gen
c	23	8	5.4	126488	14	ADZ12943	Adz12943 Human can
	24	7	4.7	23	2	AAV81463	Aav81463 PCR prime
c	25	7	4.7	23	2	AAV81464	Aav81464 PCR prime
	26	7	4.7	25	2	AAV81466	Aav81466 PCR prime
	27	7	4.7	40	2	AAQ38049	Aaq38049 Oligonucl
	28	7	4.7	90	6	AAD31055	Aad31055 Human g34
	29	7	4.7	121	10	ADH93126	Adh93126 Human gen
c	30	7	4.7	166	4	AAI27052	Aai27052 Probe #16
c	31	7	4.7	166	4	AAI55886	Aai55886 Probe #24
c	32	7	4.7	166	4	AAK23876	Aak23876 Human bra
c	33	7	4.7	166	6	ABS23443	Abs23443 Human gen
c	34	7	4.7	175	13	ADS50804	Ads50804 Bacterial
	35	7	4.7	176	12	ACH84437	Ach84437 Human gen
	36	7	4.7	222	3	AAC09175	Aac09175 Human sec
c	37	7	4.7	231	8	ACA41352	Aca41352 Prokaryot
c	38	7	4.7	234	8	ACA42037	Aca42037 Prokaryot
	39	7	4.7	236	2	AAV52126	Aav52126 Homo sapi
	40	7	4.7	263	2	AAV52122	Aav52122 Homo sapi
	41	7	4.7	264	4	ABA74599	Aba74599 Human foe
	42	7	4.7	264	4	ABA72222	Aba72222 Human foe
	43	7	4.7	264	4	ABA73113	Aba73113 Human foe
	44	7	4.7	264	4	AAI53543	Aai53543 Probe #22
	45	7	4.7	264	4	AAI52627	Aai52627 Probe #21
	46	7	4.7	264	4	AAI55082	Aai55082 Probe #23
	47	7	4.7	264	4	ABA38588	Aba38588 Probe #17
	48	7	4.7	264	4	AAK49246	Aak49246 Human bon
	49	7	4.7	264	4	AAK46788	Aak46788 Human bon
	50	7	4.7	264	4	AAK47710	Aak47710 Human bon
	51	7	4.7	264	4	AAK21549	Aak21549 Human bra
	52	7	4.7	264	4	ABS48890	Abs48890 Human liv
	53	7	4.7	264	4	ABS46560	Abs46560 Human liv
	54	7	4.7	264	4	ABS47442	Abs47442 Human liv
	55	7	4.7	264	6	ABS21748	Abs21748 Human gen
	56	7	4.7	265	12	ACH88533	Ach88533 Human gen
	57	7	4.7	279	3	AAH51673	Aah51673 Sbg1 exon
	58	7	4.7	279	3	AAH51650	Aah51650 Sbg1 exon
	59	7	4.7	280	3	AAH51685	Aah51685 Sbg1 exon
	60	7	4.7	280	3	AAH51662	Aah51662 Sbg1 exon
	61	7	4.7	280	3	AAH51697	Aah51697 Sbg1 exon
c	62	7	4.7	282	13	ADS63658	Ads63658 Bacterial
c	63	7	4.7	282	13	ADT41621	Adt41621 Bacterial
c	64	7	4.7	282	13	ADS64033	Ads64033 Bacterial
	65	7	4.7	291	4	AAS59472	Aas59472 Human KCC
	66	7	4.7	297	4	AAK54598	Aak54598 Human hae
c	67	7	4.7	297	10	ABZ40001	Abz40001 N. gonorr
	68	7	4.7	297	10	ABZ42005	Abz42005 N. gonorr
	69	7	4.7	301	12	ACH88518	Ach88518 Human gen
c	70	7	4.7	339	6	ABN92388	Abn92388 Staphyloc
	71	7	4.7	350	4	AAS32389	Aas32389 Human cDN
	72	7	4.7	356	2	AAV52117	Aav52117 Homo sapi
c	73	7	4.7	356	3	AAC02555	Aac02555 Human sec
	74	7	4.7	357	13	ADU69376	Adu69376 S agalact
	75	7	4.7	357	13	ADV83633	Adv83633 Streptoco
	76	7	4.7	360	6	ABN67043	Abn67043 Streptoco
c	77	7	4.7	362	2	AAV20103	Aav20103 Probe (4)

	78	7	4.7	368	5	ABV08748 Abv08748 Human pro
	79	7	4.7	378	10	ADB51082 Adb51082 Primary r
	80	7	4.7	380	4	AAI85923 Aai85923 Human pol
c	81	7	4.7	381	8	ABZ56847 Abz56847 Aspergill
	82	7	4.7	387	5	ABV38645 Abv38645 Human pro
	83	7	4.7	388	3	AAH51671 Aah51671 Sbg1 exon
	84	7	4.7	388	3	AAH51648 Aah51648 Sbg1 exon
	85	7	4.7	389	3	AAH51660 Aah51660 Sbg1 exon
	86	7	4.7	389	3	AAH51683 Aah51683 Sbg1 exon
	87	7	4.7	389	3	AAH51695 Aah51695 Sbg1 exon
	88	7	4.7	393	8	ACA30598 Aca30598 Prokaryot
c	89	7	4.7	396	7	ADS72353 Ads72353 Human kid
c	90	7	4.7	396	7	ADW41207 Adw41207 cDNA elev
	91	7	4.7	415	5	AAS83559 Aas83559 DNA encod
	92	7	4.7	415	5	AAS75870 Aas75870 DNA encod
c	93	7	4.7	422	13	ADX10302 Adx10302 Plant ful
	94	7	4.7	423	6	ABK09719 Abk09719 Human ova
c	95	7	4.7	431	5	ABV18359 Abv18359 Human pro
c	96	7	4.7	432	3	AAA79590 Aaa79590 Pinus rad
c	97	7	4.7	435	6	ABN92461 Abn92461 Staphyloc
c	98	7	4.7	435	13	ADS03219 Ads03219 Staphyloc
	99	7	4.7	439	3	ABQ62599 Abq62599 Mycobacte
	100	7	4.7	446	6	ABQ56909 Abq56909 Human col
	101	7	4.7	447	11	ACL28076 Acl28076 Rice abio
c	102	7	4.7	461	6	ABK30424 Abk30424 Human G-p
	103	7	4.7	463	4	AAI11500 Probe #14
	104	7	4.7	463	4	ABA53172 Aba53172 Human foe
	105	7	4.7	463	4	AAI32776 Probe #14
	106	7	4.7	463	4	ABA42745 Human bre
	107	7	4.7	463	4	ABA22946 Aba22946 Probe #14
	108	7	4.7	463	4	AAK26870 Aak26870 Human bon
	109	7	4.7	463	4	AAK01419 Aak01419 Human bra
	110	7	4.7	463	4	ABS26461 Abs26461 Human liv
	111	7	4.7	463	5	AAI01414 Aai01414 Probe #14
	112	7	4.7	463	6	ABS01470 Abs01470 Human gen
c	113	7	4.7	471	12	ADP95365 Adp95365 Cotton ex
c	114	7	4.7	472	4	AAS35302 Aas35302 Human car
c	115	7	4.7	472	10	ADE45381 Ade45381 Human car
c	116	7	4.7	472	13	ADJ06799 Adj06799 Human car
c	117	7	4.7	475	4	AAI15764 Aai15764 Probe #56
c	118	7	4.7	475	4	ABA57914 Aba57914 Human foe
c	119	7	4.7	475	4	AAI37508 Aai37508 Probe #61
c	120	7	4.7	475	4	ABA27232 Aba27232 Probe #56
c	121	7	4.7	475	4	AAK31630 Aak31630 Human bon
c	122	7	4.7	475	4	AAK05987 Aak05987 Human bra
c	123	7	4.7	475	4	ABS31314 Abs31314 Human liv
c	124	7	4.7	475	6	ABS06384 Abs06384 Human gen
	125	7	4.7	476	8	ABZ22294 Abz22294 Human DAO
	126	7	4.7	476	9	AAL60249 Aal60249 Human g34
c	127	7	4.7	478	4	AAL24118 Aal24118 Human bre
c	128	7	4.7	483	5	AAD11426 Aad11426 Zygosacch
c	129	7	4.7	483	10	ADH89183 Adh89183 Z. rouxii
	130	7	4.7	484	4	AAS60028 Aas60028 Human can
c	131	7	4.7	484	13	ADT06364 Adt06364 Nicotiana
c	132	7	4.7	489	12	ADL10550 Adl10550 Cat flea
	133	7	4.7	496	9	ACH27691 Ach27691 Human adu
c	134	7	4.7	498	5	ABV48145 Abv48145 Human pro
c	135	7	4.7	498	9	ACC72976 Acc72976 Cat flea
c	136	7	4.7	498	12	ADL09618 Adl09618 Cat flea
	137	7	4.7	507	12	ACH77903 Ach77903 Human gen
	138	7	4.7	512	4	ABA62105 Aba62105 Human foe
	139	7	4.7	512	4	AAI42049 Probe #10
	140	7	4.7	512	4	AAK36326 Aak36326 Human bon
	141	7	4.7	512	4	ABS36006 Abs36006 Human liv
c	142	7	4.7	512	12	ADI15566 Adi15566 Human pho
	143	7	4.7	513	4	AAS60640 Aas60640 Human can
	144	7	4.7	513	5	AAS74344 Aas74344 DNA encod
	145	7	4.7	516	6	ABV95643 Abv95643 Human pan
c	146	7	4.7	516	10	ABT21989 Abt21989 Breast ca
	147	7	4.7	522	6	ABQ39331 Abq39331 Oligonucl
c	148	7	4.7	522	6	ABQ39330 Abq39330 Oligonucl
	149	7	4.7	528	9	ACH35091 Ach35091 Human end
c	150	7	4.7	528	10	ADK59530 Adk59530 Plant DNA
c	151	7	4.7	543	5	ADL40080 Adl40080 Human ova
c	152	7	4.7	543	6	ABQ92793 Abq92793 Triticum
	153	7	4.7	545	6	ABN75913 Abn75913 Human ORF
	154	7	4.7	549	8	ACA54043 Aca54043 Prokaryot
	155	7	4.7	552	6	ABQ42957 Abq42957 Oligonucl
c	156	7	4.7	552	6	ABQ42956 Abq42956 Oligonucl
c	157	7	4.7	555	9	ACH38914 Ach38914 Human foe
	158	7	4.7	557	2	AAV52114 Aav52114 Homo sapi
	159	7	4.7	557	5	ADI69918 Adi69918 Human ova
	160	7	4.7	557	5	ADI76251 Adi76251 Human ova
c	161	7	4.7	562	14	ACL61717 Acl61717 Human col
c	162	7	4.7	566	4	AAI17858 Aai17858 Probe #77
c	163	7	4.7	566	4	AAI42829 Aai42829 Probe #11
c	164	7	4.7	566	4	AAK11212 Aak11212 Human bra
c	165	7	4.7	566	6	ABS11015 Abs11015 Human gen
	166	7	4.7	566	12	ACH70737 Ach70737 Human gen
	167	7	4.7	567	6	ABQ23402 Abq23402 Oligonucl
c	168	7	4.7	567	6	ABQ23403 Abq23403 Oligonucl
c	169	7	4.7	568	13	ACN56436 Acn56436 Cotton an
	170	7	4.7	570	10	ADD35080 Add35080 Mouse mit
	171	7	4.7	573	6	ABK80075 Abk80075 Bacillus
c	172	7	4.7	574	4	AAI18683 Aai18683 Probe #86
c	173	7	4.7	574	4	ABA63684 Aba63684 Human foe
c	174	7	4.7	574	4	AAI43796 Aai43796 Probe #12
c	175	7	4.7	574	4	ABA30874 Aba30874 Probe #93
c	176	7	4.7	574	4	AAK37922 Aak37922 Human bon
c	177	7	4.7	574	4	AAK12200 Aak12200 Human bra
c	178	7	4.7	574	4	ABS37544 Abs37544 Human liv
c	179	7	4.7	574	6	ABS11918 Abs11918 Human gen
c	180	7	4.7	585	11	ACH96810 Ach96810 Klebsiell
	181	7	4.7	586	4	ABA60575 Aba60575 Human foe
	182	7	4.7	586	4	AAI40465 Aai40465 Probe #91
	183	7	4.7	586	4	ABA28711 Aba28711 Probe #71
	184	7	4.7	586	4	AAK34745 Aak34745 Human bon
	185	7	4.7	586	4	AAK08858 Aak08858 Human bra
	186	7	4.7	586	4	ABS34515 Abs34515 Human liv
	187	7	4.7	586	6	ABS09316 Abs09316 Human gen
	188	7	4.7	586	12	ACH74833 Ach74833 Human gen
	189	7	4.7	588	5	ABV55005 Abv55005 Human pro
	190	7	4.7	588	6	ABK77612 Abk77612 Bacillus
	191	7	4.7	596	6	ABS73204 Abs73204 DNA encod
	192	7	4.7	596	6	ABS73205 Abs73205 DNA encod
	193	7	4.7	600	4	ABA59680 Aba59680 Human foe
	194	7	4.7	600	4	AAI39545 Aai39545 Probe #82
	195	7	4.7	600	4	AAK33819 Aak33819 Human bon
	196	7	4.7	600	4	ABS33629 Abs33629 Human liv
	197	7	4.7	600	12	ACH74818 Ach74818 Human gen
c	198	7	4.7	603	13	ADQ79191 Adq79191 Novel can
	199	7	4.7	611	6	ABQ36047 Abq36047 Oligonucl
c	200	7	4.7	611	6	ABQ36046 Abq36046 Oligonucl
	201	7	4.7	615	5	ADL41487 Adl41487 Human ova
	202	7	4.7	637	5	AAS74347 Aas74347 DNA encod
	203	7	4.7	651	10	ADH82120 Adh82120 Enterococ
c	204	7	4.7	659	12	ADI15567 Adi15567 Human pho
	205	7	4.7	662	6	ABQ54113 Abq54113 Oligonucl
c	206	7	4.7	662	6	ABQ54112 Abq54112 Oligonucl
	207	7	4.7	664	6	ABQ14025 Abq14025 Oligonucl
c	208	7	4.7	664	6	ABQ14024 Abq14024 Oligonucl
c	209	7	4.7	666	6	ABQ26648 Abq26648 Oligonucl
	210	7	4.7	666	6	ABQ26649 Abq26649 Oligonucl
	211	7	4.7	681	14	ADZ26421 Adz26421 Human KIR
	212	7	4.7	687	10	ACD96254 Acd96254 Human col
	213	7	4.7	693	6	ABK77619 Abk77619 Bacillus
	214	7	4.7	704	6	ABQ37157 Abq37157 Oligonucl
c	215	7	4.7	704	6	ABQ37156 Abq37156 Oligonucl
	216	7	4.7	712	6	ABQ22937 Abq22937 Oligonucl
c	217	7	4.7	712	6	ABQ22936 Abq22936 Oligonucl
	218	7	4.7	727	4	AAS60769 Aas60769 Human can
	219	7	4.7	727	5	ABV21445 Abv21445 Human pro
	220	7	4.7	727	5	ABV25617 Abv25617 Human pro
	221	7	4.7	727	5	ABV27263 Abv27263 Human pro
	222	7	4.7	727	5	ABV24738 Abv24738 Human pro
	223	7	4.7	727	5	ABV28255 Abv28255 Human pro

224	7	4.7	727	5	ABV22441	Abv22441 Human pro
225	7	4.7	727	5	ADL62315	Adl62315 Human ova
226	7	4.7	731	3	AAA27409	Aaa27409 Soybean g
227	7	4.7	742	3	AAH51619	Aah51619 Human sbg
228	7	4.7	742	8	ABZ22293	Abz22293 Human DAO
229	7	4.7	742	9	AAL60248	Aal60248 Human g34
230	7	4.7	748	6	ABA92990	Aba92990 Human cDN
231	7	4.7	774	2	AAQ22981	Aaq22981 Gelonin t
232	7	4.7	775	8	ACA21910	Aca21910 Prokaryot
233	7	4.7	776	3	AAH51625	Aah51625 Human sbg
234	7	4.7	777	3	AAH51613	Aah51613 Human sbg
235	7	4.7	783	2	AAQ38041	Aaq38041 Synthetic
236	7	4.7	790	4	AAH03503	Aah03503 Human cDN
237	7	4.7	807	6	AAS62086	Aas62086 Porcine m
238	7	4.7	809	3	AAZ60388	Aaz60388 A diacylg
239	7	4.7	811	3	AAH51621	Aah51621 Human sbg
240	7	4.7	813	2	AAQ48031	Aaq48031 Encodes p
241	7	4.7	813	2	AAQ42222	Aaq42222 Encodes p
242	7	4.7	813	2	AAQ75532	Aaq75532 Type I ri
243	7	4.7	813	2	AAQ92342	Aaq92342 Type I ri
244	7	4.7	822	3	AAH51624	Aah51624 Human sbg
245	7	4.7	823	3	AAH51614	Aah51614 Human sbg
246	7	4.7	823	6	ABQ31823	Abq31823 Oligonucl
c 247	7	4.7	823	6	ABQ31822	Abq31822 Oligonucl
c 248	7	4.7	826	13	ADX63182	Adx63182 Plant ful
c 249	7	4.7	828	3	AAC41606	Aac41606 Arabidops
c 250	7	4.7	833	3	AAC33409	Aac33409 Arabidops
251	7	4.7	836	3	AAH51615	Aah51615 Human sbg
252	7	4.7	851	3	AAH51618	Aah51618 Human sbg
c 253	7	4.7	855	6	ABZ12756	Abz12756 Arabidops
c 254	7	4.7	855	8	ADA68146	Ada68146 Arabidops
255	7	4.7	863	3	AAH51606	Aah51606 Human sbg
256	7	4.7	882	3	AAH51616	Aah51616 Human sbg
257	7	4.7	897	3	AAH51612	Aah51612 Human sbg
c 258	7	4.7	897	10	ADG73066	Adg73066 DNA encod
c 259	7	4.7	897	10	ADL12121	Adl12121 Pseudomon
c 260	7	4.7	899	6	ABQ38188	Abq38188 Oligonucl
261	7	4.7	899	6	ABQ38189	Abq38189 Oligonucl
c 262	7	4.7	914	10	ABZ79889	Abz79889 Human nuc
263	7	4.7	920	3	AAH51620	Aah51620 Human sbg
c 264	7	4.7	927	12	ADL02634	Adl02634 DNA encod
c 265	7	4.7	935	6	ABQ18402	Abq18402 Oligonucl
266	7	4.7	935	6	ABQ18403	Abq18403 Oligonucl
267	7	4.7	947	3	AAH51626	Aah51626 Human sbg
268	7	4.7	951	6	ABL01106	Abl01106 Human AKR
269	7	4.7	955	2	AAT86336	Aat86336 BPI pepti
270	7	4.7	955	3	AAH51617	Aah51617 Human sbg
271	7	4.7	960	4	AAH52699	Aah52699 S. epider
272	7	4.7	960	4	AAH53307	Aah53307 S. epider
273	7	4.7	978	3	AAH51622	Aah51622 Human sbg
274	7	4.7	993	3	AAH51623	Aah51623 Human sbg
275	7	4.7	995	3	AAH51602	Aah51602 Human sbg
276	7	4.7	1003	2	AAT86341	Aat86341 BPI pepti
277	7	4.7	1009	3	AAH51611	Aah51611 Human sbg
278	7	4.7	1011	5	AAS74349	Aas74349 DNA encod
c 279	7	4.7	1014	6	ABN98448	Abn98448 Arabidops
c 280	7	4.7	1020	6	ABQ27516	Abq27516 Oligonucl
281	7	4.7	1020	6	ABQ27517	Abq27517 Oligonucl
c 282	7	4.7	1024	10	ABZ83251	Abz83251 Toxicolog
c 283	7	4.7	1032	3	AAC38509	Aac38509 Arabidops
c 284	7	4.7	1040	12	ADI15568	Adi15568 Human pho
285	7	4.7	1050	3	AAA75129	Aaa75129 Open read
286	7	4.7	1050	5	AAH45489	Aah45489 Human red
287	7	4.7	1053	3	AAA08839	Aaa08839 Human DKR
288	7	4.7	1072	2	AAT86332	Aat86332 BPI pepti
c 289	7	4.7	1074	2	AAV23874	Aav23874 Plant OMT
c 290	7	4.7	1074	2	AAZ06877	Aaz06877 Pine O-me
c 291	7	4.7	1074	3	AAA67961	Aaa67961 Pinus rad
c 292	7	4.7	1074	10	ADD41711	Add41711 O-methyl
c 293	7	4.7	1075	2	AAV23875	Aav23875 Plant OMT
c 294	7	4.7	1075	2	AAZ06878	Aaz06878 Pine O-me
c 295	7	4.7	1075	3	AAA67962	Aaa67962 Pinus rad
296	7	4.7	1075	4	AAH32611	Aah32611 Human sec
c 297	7	4.7	1075	10	ADD41712	Add41712 O-methyl
c 298	7	4.7	1077	3	AAC33123	Aac33123 Arabidops
c 299	7	4.7	1077	9	ADB09263	Adb09263 Alloiococ
c 300	7	4.7	1077	9	ADB09261	Adb09261 Alloiococ
c 301	7	4.7	1077	9	ADB09259	Adb09259 Alloiococ
302	7	4.7	1089	6	ABN92370	Abn92370 Staphyloc
303	7	4.7	1089	13	ADS03069	Ads03069 Staphyloc
c 304	7	4.7	1089	13	ADS59132	Ads59132 Bacterial
305	7	4.7	1101	14	ADZ26431	Adz26431 Human KIR
306	7	4.7	1105	5	AAS74350	Aas74350 DNA encod
c 307	7	4.7	1141	8	ABZ75404	Abz75404 Sugarcane
308	7	4.7	1143	6	ABQ86138	Abq86138 Novel hum
309	7	4.7	1143	6	ABQ86139	Abq86139 Novel hum
c 310	7	4.7	1146	2	AAQ86989	Aaq86989 Creatine-
c 311	7	4.7	1146	14	AEB67450	Aeb67450 Rice geno
c 312	7	4.7	1155	10	ADF01341	Adf01341 Bacterial
c 313	7	4.7	1161	13	ADT45785	Adt45785 Bacterial
c 314	7	4.7	1167	8	ACA49107	Aca49107 Prokaryot
315	7	4.7	1176	6	ABS56021	Abs56021 cDNA enco
c 316	7	4.7	1176	7	ADZ75096	Adz75096 Arabidops
317	7	4.7	1178	8	AAL60076	Aal60076 Scolymia
c 318	7	4.7	1179	6	ABQ18317	Abq18317 Oligonucl
319	7	4.7	1179	6	ABQ18316	Abq18316 Oligonucl
c 320	7	4.7	1182	4	ABL16933	Abl16933 Drosophil
c 321	7	4.7	1185	2	AAV05039	Aav05039 Alcaligen
c 322	7	4.7	1185	2	AAZ08784	Aaz08784 A. eutrop
c 323	7	4.7	1185	3	AAA71692	Aaa71692 A. eutrop
c 324	7	4.7	1185	4	AAD09824	Aad09824 Alcaligen
325	7	4.7	1201	13	ADX09618	Adx09618 Plant ful
326	7	4.7	1205	5	AAS69916	Aas69916 DNA encod
327	7	4.7	1206	9	ADB10739	Adb10739 Alloiococ
328	7	4.7	1206	9	ADB10741	Adb10741 Alloiococ
329	7	4.7	1206	9	ADB10743	Adb10743 Alloiococ
330	7	4.7	1227	5	AAS81404	Aas81404 DNA encod
331	7	4.7	1228	6	ABQ16381	Abq16381 Oligonucl
c 332	7	4.7	1228	6	ABQ16380	Abq16380 Oligonucl
333	7	4.7	1229	5	AAS80802	Aas80802 DNA encod
334	7	4.7	1245	10	ADF02190	Adf02190 Bacterial
c 335	7	4.7	1263	3	AAC50871	Aac50871 Arabidops
c 336	7	4.7	1290	8	ADA70154	Ada70154 Rice gene
337	7	4.7	1297	6	ABK35873	Abk35873 cDNA sequ
338	7	4.7	1312	2	AAT60571	Aat60571 Cotton fi
339	7	4.7	1317	14	ADZ26439	Adz26439 Human KIR
c 340	7	4.7	1320	8	ACA38934	Aca38934 Prokaryot
c 341	7	4.7	1323	3	AAZ08255	Aaz08255 Moraxella
c 342	7	4.7	1323	3	AAZ08257	Aaz08257 Moraxella
c 343	7	4.7	1323	3	AAZ08254	Aaz08254 Moraxella
c 344	7	4.7	1323	3	AAZ08256	Aaz08256 Moraxella
345	7	4.7	1331	12	ADQ15139	Adq15139 Human can
346	7	4.7	1335	11	ADI31684	Adi31684 Human cDN
347	7	4.7	1335	13	ADS83751	Ads83751 Human lym
c 348	7	4.7	1339	6	ABQ70249	Abq70249 Listeria
c 349	7	4.7	1355	13	ACN39756	Acn39756 Tumour-as
c 350	7	4.7	1360	6	ABL62370	Abl62370 Colon ade
c 351	7	4.7	1360	6	ABN95771	Abn95771 Gene #226
352	7	4.7	1367	6	ABK09795	Abk09795 Human ova
353	7	4.7	1367	8	ABZ71966	Abz71966 Human cDN
354	7	4.7	1367	10	ADH28733	Adh28733 Human chr
355	7	4.7	1367	12	ADP13553	Adp13553 Renal cel
356	7	4.7	1367	13	ADR24780	Adr24780 Breast ca
357	7	4.7	1367	13	ACN38727	Acn38727 Tumour-as
358	7	4.7	1367	13	ADP23163	Adp23163 PRO polyp
359	7	4.7	1368	6	ABL58970	Abl58970 Human tum
360	7	4.7	1371	2	AAQ14946	Aaq14946 Human ald
c 361	7	4.7	1376	2	AAQ51619	Aaq51619 Human cre
362	7	4.7	1380	5	AAS75873	Aas75873 DNA encod
c 363	7	4.7	1390	4	ABL29325	Abl29325 Drosophil
364	7	4.7	1390	6	ABQ54381	Abq54381 Human ova
365	7	4.7	1394	2	AAQ05879	Aaq05879 Placenta-
c 366	7	4.7	1395	6	ABQ13934	Abq13934 Oligonucl
367	7	4.7	1395	6	ABQ13935	Abq13935 Oligonucl
368	7	4.7	1403	5	AAS75874	Aas75874 DNA encod
369	7	4.7	1416	12	ADF54870	Adf54870 Human ant

	370	7	4.7	1416	14	ADZ48799 Adz48799 Insulin s
c	371	7	4.7	1431	14	ADZ48855 Adz48855 Insulin s
c	372	7	4.7	1431	14	AEA81138 Aea81138 Human cre
c	373	7	4.7	1432	12	ADP10454 Adp10454 Reference
c	374	7	4.7	1432	13	ADR14270 Adr14270 Human NF-
c	375	7	4.7	1432	14	ADX07813 Adx07813 Cyclin-de
c	376	7	4.7	1432	14	ADZ22658 Adz22658 Creatine
c	377	7	4.7	1432	14	AEA04437 Aea04437 Human cDN
c	378	7	4.7	1495	4	AAS02545 Aas02545 Human sec
	379	7	4.7	1500	14	AEB68721 Aeb68721 scFv23-ge
	380	7	4.7	1517	14	AEB68719 Aeb68719 scFv23-ge
	381	7	4.7	1518	14	AEB68724 Aeb68724 scFv23-ge
	382	7	4.7	1527	6	ABS56029 Abs56029 DNA encod
c	383	7	4.7	1539	8	ACA51659 Aca51659 Prokaryot
	384	7	4.7	1554	6	ABQ70468 Abq70468 Listeria
	385	7	4.7	1557	13	ADP56235 Adp56235 Human PRO
	386	7	4.7	1557	14	ADZ26443 Adz26443 Human KIR
	387	7	4.7	1572	13	ADP56253 Adp56253 Human PRO
	388	7	4.7	1572	14	ADZ26433 Adz26433 Human KIR
	389	7	4.7	1584	10	ACF68150 Photorhab
	390	7	4.7	1587	13	ADP56151 Adp56151 Human PRO
	391	7	4.7	1587	14	ADZ26427 Adz26427 Human KIR
	392	7	4.7	1593	11	ADI32172 Adi32172 Human cDN
	393	7	4.7	1593	13	ADS84239 Ads84239 Human lym
	394	7	4.7	1593	14	ADZ26435 Adz26435 Human KIR
	395	7	4.7	1594	2	AAV54656 Aav54656 Human p58
	396	7	4.7	1596	5	AAS74355 Aas74355 DNA encod
	397	7	4.7	1596	11	ADI32150 Adi32150 Human cDN
	398	7	4.7	1596	13	ADP56396 Adp56396 Human PRO
	399	7	4.7	1596	13	ADS84217 Ads84217 Human lym
c	400	7	4.7	1611	3	AAA47339 Aaa47339 Type II F
c	401	7	4.7	1611	3	AAA47312 Aaa47312 FtsZ2 gen
	402	7	4.7	1612	5	AAS83560 Aas83560 DNA encod
	403	7	4.7	1613	7	ADQ82178 Adq82178 Human tes
c	404	7	4.7	1628	2	AAV05550 Aav05550 Arabidops
c	405	7	4.7	1659	4	AAS56326 Aas56326 Salmonell
	406	7	4.7	1686	13	ADT42168 Adt42168 Bacterial
	407	7	4.7	1708	13	ADT05171 Adt05171 Haemophil
	408	7	4.7	1724	4	AAH32609 Aah32609 Human sec
c	409	7	4.7	1761	4	AAK68428 Aak68428 Human imm
c	410	7	4.7	1761	4	AAK68427 Aak68427 Human imm
	411	7	4.7	1779	6	AAD31054 Aad31054 Human g34
	412	7	4.7	1818	13	ADT44156 Adt44156 Bacterial
	413	7	4.7	1849	4	AAH99579 Aah99579 Human pro
	414	7	4.7	1849	5	AAS74356 Aas74356 DNA encod
c	415	7	4.7	1864	2	AAZ24942 Aaz24942 Wild type
c	416	7	4.7	1869	10	ABX07302 Abx07302 S. pneumo
c	417	7	4.7	1872	4	AAS55764 Aas55764 Streptoco
c	418	7	4.7	1872	8	ACA50031 Aca50031 Prokaryot
c	419	7	4.7	1872	13	ADK44148 Adk44148 Streptoco
	420	7	4.7	1897	11	ADM76429 Adm76429 cDNA sequ
c	421	7	4.7	1902	8	ABZ42283 Abz42283 Streptoco
c	422	7	4.7	1902	13	ADR92853 Adr92853 Novel S.
c	423	7	4.7	1902	14	AEA56723 Aea56723 Streptoco
c	424	7	4.7	1912	3	AAA39806 Aaa39806 C. versic
c	425	7	4.7	1917	3	AAA39805 Aaa39805 C. versic
c	426	7	4.7	1929	8	ACA27546 Aca27546 Prokaryot
c	427	7	4.7	1938	11	ACL27929 Acl27929 Rice abio
c	428	7	4.7	1954	14	ADY49567 Ady49567 Mouse cDN
c	429	7	4.7	1974	12	ADQ78351 Adq78351 Human pho
c	430	7	4.7	1983	5	AAS69882 Aas69882 DNA encod
c	431	7	4.7	1983	14	AEA20548 Aea20548 Novel hum
c	432	7	4.7	1996	10	ADB62065 Adb62065 Human cDN
c	433	7	4.7	2000	6	ABZ16201 Abz16201 Arabidops
	434	7	4.7	2000	8	ADA72982 Ada72982 Rice gene
	435	7	4.7	2000	11	ACL38181 Acl38181 Rice stre
c	436	7	4.7	2024	10	ADE53679 Ade53679 Human pro
c	437	7	4.7	2024	12	ADE77003 Ade77003 Human cDN
c	438	7	4.7	2025	12	ADI15646 Adi15646 Human pho
c	439	7	4.7	2062	13	ADT15436 Adt15436 Plant cDN
c	440	7	4.7	2064	8	ACA25360 Aca25360 Prokaryot
	441	7	4.7	2071	12	ADQ08731 Adq08731 Ciona int
c	442	7	4.7	2082	13	ADT16478 Adt16478 Plant cDN
	443	7	4.7	2088	10	ADC31886 Adc31886 Human nov
	444	7	4.7	2102	6	AAS62284 Aas62284 cDNA sequ
c	445	7	4.7	2103	13	ADR85690 Adr85690 Aspergill
c	446	7	4.7	2107	3	AAD01017 Aad01017 Expressio
c	447	7	4.7	2115	2	AAZ32263 Aaz32263 Human dun
c	448	7	4.7	2115	3	AAA88198 Aaa88198 pPDE39 hu
c	449	7	4.7	2121	4	AAH16285 Aah16285 Human cDN
	450	7	4.7	2124	8	ABX75346 Abx75346 Human cDN
	451	7	4.7	2124	8	AAD52567 Aad52567 DKK 3 DNA
	452	7	4.7	2124	8	ABZ81839 Abz81839 DKK-2 nuc
	453	7	4.7	2124	10	ADK66944 Adk66944 Gene #34
c	454	7	4.7	2133	13	ADR85694 Adr85694 Aspergill
c	455	7	4.7	2133	13	ADR85581 Adr85581 Aspergill
c	456	7	4.7	2169	3	AAA39804 Aaa39804 C. versic
c	457	7	4.7	2186	13	ADR85107 Adr85107 Aspergill
c	458	7	4.7	2186	13	ADR85103 Adr85103 Aspergill
c	459	7	4.7	2186	13	ADR84994 Adr84994 Aspergill
	460	7	4.7	2190	10	ADB62072 Adb62072 Human cDN
	461	7	4.7	2229	12	ADP98789 Adp98789 C. albica
c	462	7	4.7	2322	12	ADN72966 Adn72966 Thale cre
	463	7	4.7	2337	8	ACA23740 Aca23740 Prokaryot
c	464	7	4.7	2343	2	AAX99989 Aax99989 Creatine
	465	7	4.7	2378	4	ABL28118 Abl28118 Drosophil
c	466	7	4.7	2394	3	AAA15156 Aaa15156 DNA encod
c	467	7	4.7	2394	4	AAS07277 Aas07277 Neisseria
c	468	7	4.7	2394	4	AAS07279 Aas07279 Neisseria
c	469	7	4.7	2394	4	AAH42130 Aah42130 Nucleotid
c	470	7	4.7	2394	4	AAH42128 Aah42128 Nucleotid
c	471	7	4.7	2394	14	ADZ09416 Adz09416 Neisseria
	472	7	4.7	2403	12	ADQ87163 Adq87163 Human tum
	473	7	4.7	2403	12	ADQ84887 Adq84887 Human tum
	474	7	4.7	2403	13	ADQ87505 Adq87505 Human tum
	475	7	4.7	2434	3	AAC47609 Aac47609 Arabidops
c	476	7	4.7	2435	4	AAI66017 Aai66017 Human pho
c	477	7	4.7	2435	8	ACC47497 Acc47497 Gene sequ
c	478	7	4.7	2436	3	AAD01018 Aad01018 Expressio
	479	7	4.7	2450	8	ABX75308 Abx75308 Human cDN
	480	7	4.7	2450	8	AAD52535 Aad52535 Human dic
	481	7	4.7	2450	8	ABZ81805 Abz81805 Human dic
	482	7	4.7	2452	13	ADR25716 Adr25716 Breast ca
c	483	7	4.7	2453	3	AAC47606 Aac47606 Arabidops
c	484	7	4.7	2456	6	ABQ67104 Abq67104 Human ang
	485	7	4.7	2467	13	ACN40955 Acn40955 Tumour-as
	486	7	4.7	2467	13	ADP23024 Adp23024 PRO polyp
	487	7	4.7	2468	6	ABA92702 Aba92702 Rice leaf
	488	7	4.7	2479	2	AAV07906 Aav07906 Human cys
	489	7	4.7	2479	3	AAA75128 Aaa75128 cDNA enco
	490	7	4.7	2479	4	AAI69309 Aai69309 Human DKK
	491	7	4.7	2479	11	ADP65490 Adp65490 Human dic
	492	7	4.7	2479	11	ADP65007 Adp65007 Human dic
	493	7	4.7	2479	13	ADR25561 Adr25561 Breast ca
	494	7	4.7	2490	2	AAV38798 Aav38798 Homo sapi
	495	7	4.7	2498	8	ABZ69889 Abz69889 Human Pur
	496	7	4.7	2502	10	ADJ56223 Adj56223 Human cDN
	497	7	4.7	2576	6	ABK52591 Abk52591 DNA encod
	498	7	4.7	2580	2	AAX18802 Aax18802 Mitochond
	499	7	4.7	2585	3	ADC78555 Adc78555 Human PRO
	500	7	4.7	2585	12	ADI65864 Adi65864 Human sec
	501	7	4.7	2585	13	ADT03707 Adt03707 Human sec
	502	7	4.7	2586	2	AAX52255 Aax52255 Protein P
	503	7	4.7	2586	4	AAF72413 Aaf72413 Human PRO
	504	7	4.7	2586	4	AAF92061 Aaf92061 Human PRO
	505	7	4.7	2586	6	ABS74381 Abs74381 Human cDN
	506	7	4.7	2586	6	ABL88096 Abl88096 Human PRO
	507	7	4.7	2586	6	ABL95585 Abl95585 Human ang
	508	7	4.7	2586	8	ACA60194 Aca60194 Human cDN
	509	7	4.7	2586	8	ACD07594 Acd07594 Novel hum
	510	7	4.7	2586	8	ACA91167 Aca91167 Novel hum
	511	7	4.7	2586	8	ACD81544 Acd81544 Human cDN
	512	7	4.7	2586	8	ACA60366 Aca60366 Novel hum
	513	7	4.7	2586	8	ABX71642 Abx71642 Human cDN
	514	7	4.7	2586	8	ACH06974 Human sec
	515	7	4.7	2586	8	ACA58813 Aca58813 cDNA enco

516	7	4.7	2586	8	ACA63989	Aca63989 cDNA enco	589	7	4.7	2586	10	ADG85273	Adg85273 Novel hum
517	7	4.7	2586	8	ACA91253	Aca91253 cDNA enco	590	7	4.7	2586	10	ADH24549	Adh24549 Novel hum
518	7	4.7	2586	8	ACD45152	Acd45152 Human sec	591	7	4.7	2586	10	ADH37405	Adh37405 Human sec
519	7	4.7	2586	8	ABX96211	Abx96211 Human sec	592	7	4.7	2586	10	ADH01994	Adh01994 Human PRO
520	7	4.7	2586	8	ACA05532	Aca05532 cDNA enco	593	7	4.7	2586	10	ADH37575	Adh37575 Human sec
521	7	4.7	2586	8	ACA93700	Aca93700 Human cDN	594	7	4.7	2586	10	ADG85613	Adg85613 Novel hum
522	7	4.7	2586	8	ACD20199	Acd20199 Human sec	595	7	4.7	2586	10	ADH24209	Adh24209 Novel hum
523	7	4.7	2586	8	ACA67274	Aca67274 cDNA enco	596	7	4.7	2586	10	ADH38503	Adh38503 Novel hum
524	7	4.7	2586	8	ACH66247	Ach66247 Novel hum	597	7	4.7	2586	10	ADG83624	Adg83624 Human PRO
525	7	4.7	2586	8	ACD02301	Acd02301 Novel hum	598	7	4.7	2586	10	ADH29432	Adh29432 Novel hum
526	7	4.7	2586	8	ACA89292	Aca89292 Novel hum	599	7	4.7	2586	10	ADH27548	Adh27548 Novel hum
527	7	4.7	2586	8	ACA68929	Aca68929 Novel hum	600	7	4.7	2586	10	ADH37745	Adh37745 Human sec
528	7	4.7	2586	8	ACA55002	Aca55002 Novel hum	601	7	4.7	2586	10	ADH37922	Adh37922 Human sec
529	7	4.7	2586	8	ACA98451	Aca98451 Human PRO	602	7	4.7	2586	10	ADH57342	Adh57342 Novel hum
530	7	4.7	2586	9	ACA63376	Aca63376 cDNA enco	603	7	4.7	2586	10	ADH59351	Adh59351 Human sec
531	7	4.7	2586	9	ACD19837	Acd19837 Human sec	604	7	4.7	2586	10	ADH53484	Adh53484 Novel hum
532	7	4.7	2586	9	ADB29440	Adb29440 Human sec	605	7	4.7	2586	10	ADH53654	Adh53654 Novel hum
533	7	4.7	2586	9	ADB17064	Adb17064 Human cDN	606	7	4.7	2586	10	ADH51990	Adh51990 Novel hum
534	7	4.7	2586	9	ACH03579	Ach03579 Human sec	607	7	4.7	2586	10	ADH49845	Adh49845 Novel hum
535	7	4.7	2586	9	ADA18296	Ada18296 Human sec	608	7	4.7	2586	10	ADI25355	Adi25355 Novel hum
536	7	4.7	2586	9	ACD66984	Acd66984 Human cDN	609	7	4.7	2586	10	ADH90148	Adh90148 Novel hum
537	7	4.7	2586	9	ADA19869	Ada19869 Novel hum	610	7	4.7	2586	10	ADI25525	Adi25525 Novel hum
538	7	4.7	2586	9	ADB17252	Adb17252 Human cDN	611	7	4.7	2586	10	ADH97699	Adh97699 Novel hum
539	7	4.7	2586	9	ACD83145	Acd83145 Human PRO	612	7	4.7	2586	10	ADI38130	Adi38130 Human sec
540	7	4.7	2586	9	ADA16271	Ada16271 Human sec	613	7	4.7	2586	10	ADI03547	Adi03547 Novel hum
541	7	4.7	2586	9	ADA20041	Ada20041 Novel hum	614	7	4.7	2586	10	ADI11904	Adi11904 Human PRO
542	7	4.7	2586	9	ACD82093	Acd82093 Human sec	615	7	4.7	2586	10	ADH89978	Adh89978 Novel hum
543	7	4.7	2586	9	ADA42416	Ada42416 Human sec	616	7	4.7	2586	10	ADH98379	Adh98379 Novel hum
544	7	4.7	2586	9	ACD23323	Acd23323 Human PRO	617	7	4.7	2586	10	ADI11054	Adi11054 Human PRO
545	7	4.7	2586	9	ADA00338	Ada00338 Human sec	618	7	4.7	2586	10	ADI11564	Adi11564 Human PRO
546	7	4.7	2586	9	ADA16695	Ada16695 Human sec	619	7	4.7	2586	10	ADH98209	Adh98209 Novel hum
547	7	4.7	2586	9	ADA13124	Ada13124 Human sec	620	7	4.7	2586	10	ADH98549	Adh98549 Novel hum
548	7	4.7	2586	9	ADA41992	Ada41992 Human sec	621	7	4.7	2586	10	ADH98039	Adh98039 Novel hum
549	7	4.7	2586	9	ADA17339	Ada17339 Human sec	622	7	4.7	2586	10	ACA59090	Aca59090 Human PRO
550	7	4.7	2586	9	ADA42842	Ada42842 Human sec	623	7	4.7	2586	10	ACA58487	Aca58487 cDNA enco
551	7	4.7	2586	9	ACD23685	Acd23685 Human PRO	624	7	4.7	2586	10	ADI05027	Adi05027 Novel hum
552	7	4.7	2586	9	ADB85580	Adb85580 Novel hum	625	7	4.7	2586	10	ADI03377	Adi03377 Novel hum
553	7	4.7	2586	10	ADB77761	Adb77761 Human sec	626	7	4.7	2586	10	ADI04772	Adi04772 Novel hum
554	7	4.7	2586	10	ADB74897	Adb74897 Human sec	627	7	4.7	2586	10	ADH78226	Adh78226 Human PRO
555	7	4.7	2586	10	ADB68259	Adb68259 Human PRO	628	7	4.7	2586	10	ADI19570	Adi19570 Novel hum
556	7	4.7	2586	10	ADB68066	Adb68066 Human PRO	629	7	4.7	2586	10	ADH90318	Adh90318 Novel hum
557	7	4.7	2586	10	ADB90883	Adb90883 Novel hum	630	7	4.7	2586	10	ADI03037	Adi03037 Novel hum
558	7	4.7	2586	10	ADC28543	Adc28543 Human sec	631	7	4.7	2586	10	ADH77886	Adh77886 Human PRO
559	7	4.7	2586	10	ADC39743	Adc39743 Human sec	632	7	4.7	2586	10	ADH97869	Adh97869 Novel hum
560	7	4.7	2586	10	ADC40257	Adc40257 Human sec	633	7	4.7	2586	10	ADI01254	Adi01254 Novel hum
561	7	4.7	2586	10	ADC19081	Adc19081 Human sec	634	7	4.7	2586	10	ADI01949	Adi01949 Novel hum
562	7	4.7	2586	10	ADC34381	Adc34381 Human sec	635	7	4.7	2586	10	ADI03207	Adi03207 Novel hum
563	7	4.7	2586	10	ADC29436	Adc29436 Human sec	636	7	4.7	2586	10	ADI11394	Adi11394 Human PRO
564	7	4.7	2586	10	ADC28967	Adc28967 Human sec	637	7	4.7	2586	10	ADI02296	Adi02296 Novel hum
565	7	4.7	2586	10	ADC40852	Adc40852 Human sec	638	7	4.7	2586	10	ADI11734	Adi11734 Human PRO
566	7	4.7	2586	10	ADC19509	Adc19509 Human sec	639	7	4.7	2586	10	ADI05371	Adi05371 Novel hum
567	7	4.7	2586	10	ADC06963	Adc06963 Human PRO	640	7	4.7	2586	10	ADH79443	Adh79443 Novel hum
568	7	4.7	2586	10	ADC17142	Adc17142 cDNA sequ	641	7	4.7	2586	10	ADI19400	Adi19400 Novel hum
569	7	4.7	2586	10	ADC33957	Adc33957 Human sec	642	7	4.7	2586	10	ADI05201	Adi05201 Novel hum
570	7	4.7	2586	10	ADC13027	Adc13027 Human sec	643	7	4.7	2586	10	ADH79613	Adh79613 Novel hum
571	7	4.7	2586	10	ADC14840	Adc14840 Novel hum	644	7	4.7	2586	10	ADI01439	Adi01439 Novel hum
572	7	4.7	2586	10	ADC52335	Adc52335 Novel hum	645	7	4.7	2586	10	ADI01609	Adi01609 Novel hum
573	7	4.7	2586	10	ADC12479	Adc12479 Human sec	646	7	4.7	2586	10	ADI01779	Adi01779 Novel hum
574	7	4.7	2586	10	ADD10338	Add10338 Human sec	647	7	4.7	2586	10	ADH79783	Adh79783 Novel hum
575	7	4.7	2586	10	ADD05034	Add05034 Human sec	648	7	4.7	2586	10	ADI04601	Adi04601 Novel hum
576	7	4.7	2586	10	ADD11298	Add11298 Human sec	649	7	4.7	2586	10	ADI02737	Adi02737 Novel hum
577	7	4.7	2586	10	ADD04040	Add04040 Human sec	650	7	4.7	2586	10	ADH78056	Adh78056 Human PRO
578	7	4.7	2586	10	ADD03616	Add03616 Human sec	651	7	4.7	2586	10	ADI25695	Adi25695 Novel hum
579	7	4.7	2586	10	ADD37091	Add37091 Human sec	652	7	4.7	2586	10	ADI25865	Adi25865 Novel hum
580	7	4.7	2586	10	ADD36011	Add36011 Novel hum	653	7	4.7	2586	10	ADK65377	Adk65377 Novel hum
581	7	4.7	2586	10	ADE34868	Ade34868 Human sec	654	7	4.7	2586	10	ADH98719	Adh98719 Novel hum
582	7	4.7	2586	10	ADG01012	Adg01012 Novel hum	655	7	4.7	2586	10	ADH79960	Adh79960 Novel hum
583	7	4.7	2586	10	ADG08565	Adg08565 Novel hum	656	7	4.7	2586	10	ADJ26398	Adj26398 Human sec
584	7	4.7	2586	10	ADF95186	Adf95186 Novel hum	657	7	4.7	2586	11	ADL93691	Adl93691 Novel hum
585	7	4.7	2586	10	ADH24039	Adh24039 Novel hum	658	7	4.7	2586	12	ADC52145	Adc52145 Novel hum
586	7	4.7	2586	10	ADH34065	Adh34065 Novel hum	659	7	4.7	2586	12	ADE79313	Ade79313 Human sec
587	7	4.7	2586	10	ADH29898	Adh29898 Novel hum	660	7	4.7	2586	12	ADE79737	Ade79737 Human sec
588	7	4.7	2586	10	ADH23869	Adh23869 Novel hum	661	7	4.7	2586	12	ADE73413	Ade73413 Human sec

662	7	4.7	2586	12	ADE41299	Ade41299 Human sec
663	7	4.7	2586	12	ADE73948	Ade73948 Human sec
664	7	4.7	2586	12	ADE99502	Ade99502 Human sec
665	7	4.7	2586	12	ADE98621	Ade98621 Human sec
666	7	4.7	2586	12	ADE99048	Ade99048 Human sec
667	7	4.7	2586	12	ADG40518	Adg40518 Human sec
668	7	4.7	2586	12	ADF73912	Adf73912 Human sec
669	7	4.7	2586	12	ADF73488	Adf73488 Human sec
670	7	4.7	2586	12	ADH06577	Adh06577 Novel hum
671	7	4.7	2586	12	ADH06407	Adh06407 Novel hum
672	7	4.7	2586	12	ADG68828	Adg68828 Novel hum
673	7	4.7	2586	12	ADH27718	Adh27718 Novel hum
674	7	4.7	2586	12	ADH25059	Adh25059 Novel hum
675	7	4.7	2586	12	ADH33691	Adh33691 Human PRO
676	7	4.7	2586	12	ADG92331	Adg92331 Human sec
677	7	4.7	2586	12	ADH02334	Adh02334 Human PRO
678	7	4.7	2586	12	ADH07941	Adh07941 Novel hum
679	7	4.7	2586	12	ADG69338	Adg69338 Novel hum
680	7	4.7	2586	12	ADH39159	Adh39159 Novel hum
681	7	4.7	2586	12	ADG92758	Adg92758 Human sec
682	7	4.7	2586	12	ADG83899	Adg83899 Human PRO
683	7	4.7	2586	12	ADG85443	Adg85443 Novel hum
684	7	4.7	2586	12	ADH06237	Adh06237 Novel hum
685	7	4.7	2586	12	ADH30067	Adh30067 Novel hum
686	7	4.7	2586	12	ADH24379	Adh24379 Novel hum
687	7	4.7	2586	12	ADG69508	Adg69508 Novel hum
688	7	4.7	2586	12	ADH07771	Adh07771 Novel hum
689	7	4.7	2586	12	ADG85783	Adg85783 Novel hum
690	7	4.7	2586	12	ADH39329	Adh39329 Novel hum
691	7	4.7	2586	12	ADH33521	Adh33521 Human PRO
692	7	4.7	2586	12	ADH33861	Adh33861 Human PRO
693	7	4.7	2586	12	ADH01071	Adh01071 Human PRO
694	7	4.7	2586	12	ADG69678	Adg69678 Novel hum
695	7	4.7	2586	12	ADH02164	Adh02164 Human PRO
696	7	4.7	2586	12	ADG69168	Adg69168 Novel hum
697	7	4.7	2586	12	ADG85953	Adg85953 Novel hum
698	7	4.7	2586	12	ADH24889	Adh24889 Novel hum
699	7	4.7	2586	12	ADH39506	Adh39506 Novel hum
700	7	4.7	2586	12	ADH02504	Adh02504 Human PRO
701	7	4.7	2586	12	ADG68998	Adg68998 Novel hum
702	7	4.7	2586	12	ADH07601	Adh07601 Novel hum
703	7	4.7	2586	12	ADG86123	Adg86123 Novel hum
704	7	4.7	2586	12	ADH24719	Adh24719 Novel hum
705	7	4.7	2586	12	ADH25767	Adh25767 Novel hum
706	7	4.7	2586	12	ADH38333	Adh38333 Novel hum
707	7	4.7	2586	12	ADH20547	Adh20547 Human sec
708	7	4.7	2586	12	ADH57172	Adh57172 Novel hum
709	7	4.7	2586	12	ADH43482	Adh43482 Human PRO
710	7	4.7	2586	12	ADH07402	Adh07402 Human sec
711	7	4.7	2586	12	ADH52160	Adh52160 Novel hum
712	7	4.7	2586	12	ADH59947	Adh59947 Human sec
713	7	4.7	2586	12	ADH49526	Adh49526 Novel hum
714	7	4.7	2586	12	ADH06975	Adh06975 Human sec
715	7	4.7	2586	12	ADH90488	Adh90488 Novel hum
716	7	4.7	2586	12	ADI11224	Adi11224 Human PRO
717	7	4.7	2586	12	ADI18717	Adi18717 Human sec
718	7	4.7	2586	12	ADH98889	Adh98889 Novel hum
719	7	4.7	2586	12	ADI65437	Adi65437 Human sec
720	7	4.7	2586	12	ADI02119	Adi02119 Novel hum
721	7	4.7	2586	12	ADH90658	Adh90658 Novel hum
722	7	4.7	2586	12	ADI37696	Adi37696 Human sec
723	7	4.7	2586	12	ADH97496	Adh97496 Human sec
724	7	4.7	2586	12	ADH60607	Adh60607 Human sec
725	7	4.7	2586	12	ADJ99664	Adj99664 Human sec
726	7	4.7	2586	12	ADL08857	Adl08857 Human sec
727	7	4.7	2586	12	ADJ98533	Adj98533 Novel hum
728	7	4.7	2586	12	ADJ98703	Adj98703 Novel hum
729	7	4.7	2586	12	ADH78862	Adh78862 Novel hum
730	7	4.7	2586	12	ADJ99096	Adj99096 Novel hum
731	7	4.7	2586	12	ADJ99266	Adj99266 Novel hum
732	7	4.7	2586	12	ADJ98884	Adj98884 Novel hum
733	7	4.7	2586	12	ADH79032	Adh79032 Novel hum
734	7	4.7	2586	12	ADK00892	Adk00892 Human PRO
735	7	4.7	2586	12	ADK14413	Adk14413 Novel hum
736	7	4.7	2586	12	ADM25198	Adm25198 Human sec
737	7	4.7	2586	12	ADM29948	Adm29948 Human sec
738	7	4.7	2586	12	ADK82827	Adk82827 Human PRO
739	7	4.7	2586	12	ADM80862	Adm80862 Human PRO
740	7	4.7	2586	12	ADO06270	Ado06270 Human PRO
741	7	4.7	2586	12	ADR11122	Adr11122 Human sec
742	7	4.7	2586	13	ADR18031	Adr18031 Human sec
743	7	4.7	2586	13	ADS74670	Ads74670 Human sec
744	7	4.7	2586	14	ADY77702	Ady77702 Neoplasti
745	7	4.7	2586	14	AEA37945	Aea37945 Human sec
746	7	4.7	2608	6	ABL92089	Abl92089 Human Tum
747	7	4.7	2608	10	ABX72014	Abx72014 DNA encod
748	7	4.7	2619	13	ADR88591	Adr88591 Human alp
749	7	4.7	2631	4	AAH54396	Aah54396 S. epider
750	7	4.7	2632	5	AAH45491	Aah45491 Human red
751	7	4.7	2660	5	AAH45490	Aah45490 Human red
752	7	4.7	2679	10	ADB63014	Adb63014 Human cDN
c 753	7	4.7	2728	14	ADW10516	Adw10516 Colon pro
c 754	7	4.7	2728	14	ADW10514	Adw10514 Colon pro
c 755	7	4.7	2728	14	ADW10512	Adw10512 Colon pro
756	7	4.7	2735	4	AAH24911	Aah24911 Nucleotid
757	7	4.7	2738	10	ADD14790	Add14790 Human src
758	7	4.7	2744	10	ADB58531	Adb58531 Toxicity-
759	7	4.7	2744	10	ADB53139	Adb53139 Primary r
760	7	4.7	2744	10	ABT42136	Abt42136 Toxicity
761	7	4.7	2744	14	ADZ61501	Adz61501 Rat Aco2
762	7	4.7	2744	14	ADZ48781	Adz48781 Insulin s
763	7	4.7	2746	2	AAQ07044	Aaq07044 Gene enco
764	7	4.7	2777	14	ADY66017	Ady66017 S. manson
c 765	7	4.7	2790	4	AAI66849	Aai66849 Nucleotid
c 766	7	4.7	2793	3	AAA14954	Aaa14954 DNA encod
767	7	4.7	2803	14	ADZ61705	Adz61705 Murine Ac
768	7	4.7	2880	13	ADV41387	Adv41387 Rat cardi
c 769	7	4.7	2883	4	AAH55002	Aah55002 S. epider
c 770	7	4.7	2894	6	AAD37051	Aad37051 Calcium-a
c 771	7	4.7	2917	10	ADB58334	Adb58334 Toxicity-
c 772	7	4.7	2917	10	ADB52893	Adb52893 Primary r
c 773	7	4.7	2917	13	ADV41158	Adv41158 Rat cardi
774	7	4.7	2920	8	ABT17891	Abt17891 Aspergill
775	7	4.7	2943	13	ADT15889	Adt15889 Plant cDN
776	7	4.7	2987	8	ABT19705	Abt19705 Aspergill
c 777	7	4.7	3009	3	AAA14956	Aaa14956 DNA encod
c 778	7	4.7	3009	12	ADM91334	Adm91334 DNA homol
c 779	7	4.7	3009	14	ADW13990	Adw13990 Mouse cDN
c 780	7	4.7	3012	13	ACN41805	Acn41805 Human dia
c 781	7	4.7	3016	11	ADI30933	Adi30933 Human cDN
c 782	7	4.7	3016	13	ADS83000	Ads83000 Human lym
c 783	7	4.7	3039	3	AAZ51644	Aaz51644 Bacillus
c 784	7	4.7	3039	3	AAZ51645	Aaz51645 Bacillus
c 785	7	4.7	3039	10	AAD61793	Aad61793 Bt.cry3Bb
c 786	7	4.7	3039	10	AAD61792	Aad61792 Bt.cry3Bb
c 787	7	4.7	3039	10	ABX95189	Abx95189 B. thurin
c 788	7	4.7	3039	10	ABX95188	Abx95188 B. thurin
c 789	7	4.7	3041	4	ABL06950	Abl06950 Drosophil
c 790	7	4.7	3044	3	AAZ51656	Aaz51656 Bacillus
c 791	7	4.7	3044	10	AAD61804	Aad61804 Bt.cry3Bb
c 792	7	4.7	3044	10	ABX95200	Abx95200 B. thurin
c 793	7	4.7	3051	8	ACF62758	Acf62758 Human pcn
c 794	7	4.7	3083	5	ADL46055	Adl46055 Human ova
795	7	4.7	3114	10	ADF03220	Adf03220 Bacterial
796	7	4.7	3125	12	ADN05304	Adn05304 Antipsori
c 797	7	4.7	3130	2	AAZ32264	Aaz32264 Human dun
c 798	7	4.7	3130	3	AAA88199	Aaa88199 pPDE43 hu
c 799	7	4.7	3130	5	AAS71151	Aas71151 DNA encod
c 800	7	4.7	3130	12	ADI15571	Adi15571 Human pho
c 801	7	4.7	3130	12	ADO05735	Ado05735 Human pho
c 802	7	4.7	3182	4	ABL16932	Abl16932 Drosophil
c 803	7	4.7	3201	3	AAA14955	Aaa14955 DNA encod
c 804	7	4.7	3222	13	ADS58143	Ads58143 Bacterial
c 805	7	4.7	3224	3	AAA39803	Aaa39803 C. versic
806	7	4.7	3225	2	AAT47238	Aat47238 FIV env g
807	7	4.7	3225	2	AAT49091	Aat49091 Feline im

	808	7	4.7	3225	2	AAT78402 Aat78402 Feline im
	809	7	4.7	3225	2	AAT62514 Aat62514 FIV envel
	810	7	4.7	3228	6	AAI70880 Aai70880 Mouse epi
c	811	7	4.7	3233	4	ABL16938 Abl16938 Drosophil
	812	7	4.7	3319	3	AAC76201 Aac76201 Human ORF
c	813	7	4.7	3332	12	ADI15565 Adi15565 Human pho
	814	7	4.7	3367	4	ABA09035 Aba09035 Human K/C
	815	7	4.7	3447	10	ADE56893 Ade56893 Rat gene
	816	7	4.7	3447	10	ADE56896 Ade56896 Rat gene
c	817	7	4.7	3447	14	ADZ74242 Adz74242 Corynebac
c	818	7	4.7	3450	3	AAZ51643 Aaz51643 Bacillus
c	819	7	4.7	3450	10	AAD61791 Aad61791 Bt.cry3Bb
c	820	7	4.7	3450	10	ABX95187 Abx95187 B. thurin
c	821	7	4.7	3455	3	AAZ51655 Aaz51655 Bacillus
c	822	7	4.7	3455	10	AAD61803 Aad61803 Bt.cry3Bb
c	823	7	4.7	3455	10	ABX95199 Abx95199 B. thurin
	824	7	4.7	3468	13	ACN39646 Acn39646 Tumour-as
c	825	7	4.7	3469	3	AAZ51646 Aaz51646 Bacillus
c	826	7	4.7	3469	10	AAD61794 Aad61794 Bt.cry3Bb
c	827	7	4.7	3469	10	ABX95190 Abx95190 B. thurin
	828	7	4.7	3666	10	ADC90678 Adc90678 E. faeciu
	829	7	4.7	3693	5	AAS83416 Aas83416 DNA encod
	830	7	4.7	3744	13	ADR07893 Full leng
c	831	7	4.7	3754	3	AAZ51642 Aaz51642 Bacillus
c	832	7	4.7	3754	10	AAD61790 Aad61790 Bt.cry3Bb
c	833	7	4.7	3754	10	ABX95186 Abx95186 B. thurin
	834	7	4.7	3767	14	ADZ49362 Adz49362 Insulin s
	835	7	4.7	3786	10	AAD62305 Aad62305 Candida a
c	836	7	4.7	3829	12	ADI15570 Adi15570 Human pho
c	837	7	4.7	3829	12	ADJ61298 Adj61298 PDE4D enc
c	838	7	4.7	3829	12	ADO34033 Ado34033 Human pho
c	839	7	4.7	3830	12	ADO46688 Ado46688 Human oli
c	840	7	4.7	3850	12	ADQ22929 Adq22929 Human sof
c	841	7	4.7	3867	2	AAQ20358 Aaq20358 N-methylh
c	842	7	4.7	3885	4	AAH54519 S. epider
c	843	7	4.7	3995	4	ABL29324 Abl29324 Drosophil
	844	7	4.7	4000	12	ADH18905 Adh18905 Human cel
	845	7	4.7	4032	5	AAS86485 Aas86485 DNA encod
	846	7	4.7	4045	13	ACN42224 Acn42224 Human dia
	847	7	4.7	4053	13	ACN42225 Acn42225 Human dia
	848	7	4.7	4080	8	AAD49595 Aad49595 Human cyt
c	849	7	4.7	4110	8	ABZ10201 Abz10201 Haematopo
	850	7	4.7	4131	8	ABT16046 Abt16046 NOVX rela
	851	7	4.7	4131	12	ADO41693 Ado41693 Novel hum
c	852	7	4.7	4149	3	AAZ51641 Aaz51641 Bacillus
c	853	7	4.7	4149	10	AAD61789 Aad61789 Bt.cry3Bb
c	854	7	4.7	4149	10	ABX95185 Abx95185 B. thurin
	855	7	4.7	4215	4	AAS59388 Aas59388 Human cDN
	856	7	4.7	4260	4	AAS59394 Aas59394 Human cDN
	857	7	4.7	4267	5	AEB56592 Aeb56592 Mouse cDN
	858	7	4.7	4267	12	ADI80010 Adi80010 Mouse tra
	859	7	4.7	4267	12	ADJ75711 Adj75711 Marker ge
	860	7	4.7	4282	12	ADO20385 Ado20385 Human PRO
	861	7	4.7	4282	14	ADY18554 Ady18554 DNA encod
	862	7	4.7	4345	5	ABV23340 Abv23340 Human pro
	863	7	4.7	4345	5	ABV29193 Abv29193 Human pro
	864	7	4.7	4345	14	AEB25792 Aeb25792 DNA encod
	865	7	4.7	4345	14	AEB25788 Aeb25788 DNA encod
	866	7	4.7	4345	14	AEB25790 Aeb25790 DNA encod
	867	7	4.7	4345	14	AEB25786 Aeb25786 DNA encod
c	868	7	4.7	4350	4	ABL29316 Abl29316 Drosophil
	869	7	4.7	4360	8	AAD49596 Aad49596 Human cyt
	870	7	4.7	4417	3	AAA47479 Aaa47479 Murine TA
	871	7	4.7	4417	10	ADI00535 Adi00535 Murine TA
	872	7	4.7	4417	11	ADM64569 Adm64569 Mouse von
	873	7	4.7	4574	6	ABA92703 Aba92703 Rice leaf
	874	7	4.7	4633	13	ACN42223 Acn42223 Human dia
	875	7	4.7	4694	4	AAK51847 Aak51847 Human pol
	876	7	4.7	4739	4	AAK51848 Aak51848 Human pol
c	877	7	4.7	4806	1	AAN91768 Aan91768 Active re
	878	7	4.7	4829	2	AAZ35666 Aaz35666 Ovine int
	879	7	4.7	4834	13	ACN42222 Acn42222 Human dia
	880	7	4.7	4842	2	AAZ35665 Aaz35665 Ovine int
	881	7	4.7	4955	12	ADQ18863 Adq18863 Human sof
	882	7	4.7	4962	4	ABL19052 Abl19052 Drosophil
	883	7	4.7	4995	4	ABL19050 Abl19050 Drosophil
c	884	7	4.7	5059	3	AAZ36227 Aaz36227 DNA encod
c	885	7	4.7	5170	12	ADK98488 Adk98488 B thuring
	886	7	4.7	5220	6	ABL92085 Abl92085 Mouse Tum
	887	7	4.7	5220	6	ABL92138 Abl92138 Mouse Tum
	888	7	4.7	5220	10	ABX72010 Abx72010 DNA encod
	889	7	4.7	5220	10	ABX72063 Abx72063 DNA encod
	890	7	4.7	5220	14	ADZ70716 Adz70716 Tumor end
	891	7	4.7	5220	14	AEA29801 Aea29801 DNA encod
	892	7	4.7	5244	13	ADR14752 Adr14752 Nucleotid
c	893	7	4.7	5600	12	ADK98490 Adk98490 B thuring
c	894	7	4.7	5706	6	ABK84184 Abk84184 Human cDN
c	895	7	4.7	5706	12	ADI15558 Adi15558 Human pho
c	896	7	4.7	5856	6	ABL32568 Abl32568 Human imm
	897	7	4.7	5862	4	AAL04675 Aal04675 Human rep
	898	7	4.7	5862	4	ABL97582 Abl97582 Human tes
c	899	7	4.7	5876	14	ADX01446 Adx01446 Human tol
c	900	7	4.7	5952	10	ADB54002 Adb54002 PCNA geno
c	901	7	4.7	6226	4	ABL05074 Abl05074 Drosophil
	902	7	4.7	6228	4	AAS52178 Aas52178 Staphyloc
	903	7	4.7	6330	10	ADF14066 Adf14066 Human end
c	904	7	4.7	6361	6	ABL33141 Abl33141 Human imm
c	905	7	4.7	6521	6	ABL33956 Abl33956 Human imm
	906	7	4.7	6561	4	AAS55178 Aas55178 Staphyloc
c	907	7	4.7	6694	6	ABL70351 Abl70351 Chemicall
c	908	7	4.7	6694	6	AAS61312 Aas61312 Human gen
	909	7	4.7	6736	2	AAV68473 Aav68473 A. pleuro
	910	7	4.7	6736	2	AAV68471 Aav68471 A. pleuro
c	911	7	4.7	6989	13	ADR84336 Adr84336 Aspergill
c	912	7	4.7	7110	10	ADB54281 Adb54281 Pretreate
c	913	7	4.7	7110	10	ADE84195 Ade84195 Human lym
c	914	7	4.7	7110	13	ADS89579 Ads89579 Oligonucl
c	915	7	4.7	7146	5	ABV24957 Abv24957 Human pro
c	916	7	4.7	7450	14	AEA89733 Aea89733 Novel tra
	917	7	4.7	7512	12	ADO29763 Ado29763 Human nov
	918	7	4.7	7546	14	ACL64338 Acl64338 M. xanthu
c	919	7	4.7	7893	2	AAX13165 Aax13165 Enterococ
c	920	7	4.7	7893	6	ABS98960 Abs98960 Enterococ
c	921	7	4.7	7966	9	ACH03910 Ach03910 Human cDN
c	922	7	4.7	8186	13	ADR84520 Adr84520 Aspergill
c	923	7	4.7	8186	13	ADR84407 Adr84407 Aspergill
c	924	7	4.7	8186	13	ADR84516 Adr84516 Aspergill
c	925	7	4.7	8235	8	ACC46220 Acc46220 Human dit
c	926	7	4.7	8349	3	AAA15565 Aaa15565 pMON30464
	927	7	4.7	8463	12	ADO00954 Ado00954 Fruit fly
c	928	7	4.7	8553	10	ABT41821 Abt41821 Toxicity
	929	7	4.7	8865	4	ABL12959 Abl12959 Drosophil
c	930	7	4.7	8946	6	ABL32910 Abl32910 Human imm
	931	7	4.7	9370	2	AAQ75165 Aaq75165 AF-4 tran
	932	7	4.7	9390	6	ABK83836 Abk83836 Human cDN
	933	7	4.7	9390	9	ACF04208 Acf04208 Human AF4
	934	7	4.7	9390	9	ACF04206 Acf04206 Human AF4
	935	7	4.7	9390	10	ADB75439 Adb75439 Prostate
	936	7	4.7	9390	10	ADK67001 Adk67001 Gene #91
	937	7	4.7	9390	12	ADQ87230 Adq87230 Human tum
	938	7	4.7	9390	13	ADR25359 Adr25359 Breast ca
	939	7	4.7	9390	13	ADR66749 Adr66749 Human pro
	940	7	4.7	9390	13	ADR65817 Adr65817 Human pro
	941	7	4.7	9390	14	ADX07360 Adx07360 Cyclin-de
	942	7	4.7	9391	2	AAQ75164 Aaq75164 AF-4 tran
	943	7	4.7	9471	2	AAV57356 Aav57356 FIV-NCSU1
	944	7	4.7	9474	2	AAV57355 Aav57355 FIV-NCSU1
c	945	7	4.7	9591	4	AAS28906 Aas28906 Human imm
c	946	7	4.7	9591	4	AAL03355 Aal03355 Human rep
c	947	7	4.7	9591	10	ADB31747 Adb31747 Human nov
	948	7	4.7	9804	4	ABL19048 Abl19048 Drosophil
c	949	7	4.7	10048	6	ABQ67015 Abq67015 Human ang
c	950	7	4.7	10475	1	AAN80643 Aan80643 Sequence
c	951	7	4.7	10475	1	AAN80616 Aan80616 Genomic c
c	952	7	4.7	10476	6	ABL67518 Abl67518 Thyroid c
c	953	7	4.7	10476	6	ABL67064 Abl67064 Thyroid c

c 954	7	4.7	10968	2	AAV17789	Aav17789 Tomato Pr
955	7	4.7	11502	4	ABL12958	Abl12958 Drosophil
c 956	7	4.7	11800	4	AAK82152	Aak82152 Human imm
c 957	7	4.7	12415	4	AAS28907	Aas28907 Human imm
c 958	7	4.7	12415	4	AAL03356	Aal03356 Human rep
c 959	7	4.7	12415	10	ADB31748	Adb31748 Human nov
c 960	7	4.7	12669	6	ABK31522	Abk31522 Signal tr
c 961	7	4.7	12669	6	ABL70489	Abl70489 Chemicall
c 962	7	4.7	12669	6	AAS61448	Aas61448 Human gen
963	7	4.7	13365	10	ADF14061	Adf14061 Human end
964	7	4.7	14920	13	ADV87706	Adv87706 Streptoco
965	7	4.7	14920	13	ADV78959	Adv78959 Streptoco
c 966	7	4.7	15606	4	ABL16881	Abl16881 Drosophil
967	7	4.7	15613	10	ADF14058	Adf14058 Human end
968	7	4.7	16161	6	AAD36071	Aad36071 Human adi
969	7	4.7	16309	10	ADF14059	Adf14059 Human end
970	7	4.7	16387	10	ADF14060	Adf14060 Human end
971	7	4.7	16854	10	ADF14057	Adf14057 Human end
c 972	7	4.7	17350	2	AAQ72708	Aaq72708 hOP1 huma
c 973	7	4.7	17410	2	AAQ53142	Aaq53142 Sequence
c 974	7	4.7	17410	2	AAT18381	Aat18381 hOP-1 gen
c 975	7	4.7	17410	2	AAV15205	Aav15205 Human ost
c 976	7	4.7	17410	2	AAX00230	Aax00230 Human ost
c 977	7	4.7	17410	2	AAZ27575	Aaz27575 Human ost
c 978	7	4.7	17410	10	ADJ62678	Adj62678 Human ost
c 979	7	4.7	17410	12	ADE52749	Ade52749 Human ost
c 980	7	4.7	17410	12	ADM80487	Adm80487 Human ost
c 981	7	4.7	17410	13	ADO03609	Ado03609 Genomic D
c 982	7	4.7	17415	2	AAT11639	Aat11639 Human ost
c 983	7	4.7	17415	2	AAV80733	Aav80733 Human ost
c 984	7	4.7	17415	3	AAA59897	Aaa59897 Human DNA
c 985	7	4.7	18096	4	AAS59588	Aas59588 Propionib
c 986	7	4.7	18096	8	ACF64517	Acf64517 Propionib
987	7	4.7	18795	10	ADF14051	Adf14051 Human end
988	7	4.7	19027	10	ADF14048	Adf14048 Human end
989	7	4.7	19181	10	ADF14056	Adf14056 Human end
990	7	4.7	19242	10	ADF14055	Adf14055 Human end
991	7	4.7	19247	10	ADF14049	Adf14049 Human end
992	7	4.7	19267	10	ADF14050	Adf14050 Human end
993	7	4.7	19344	10	ADF14052	Adf14052 Human end
994	7	4.7	19707	10	ADF14053	Adf14053 Human end
995	7	4.7	20017	10	ADF14054	Adf14054 Human end
c 996	7	4.7	20565	4	AAK89083	Aak89083 Human dig
997	7	4.7	20565	4	AAS28908	Aas28908 Human imm
c 998	7	4.7	20565	4	AAL03357	Aal03357 Human rep
999	7	4.7	20565	10	ADB31749	Adb31749 Human nov
1000	7	4.7	21040	2	AAV52188	Aav52188 Streptoco

ALIGNMENTS

RESULT 1
AAV81468
ID AAV81468 standard; DNA; 363 BP.
XX
AC AAV81468;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE Ribosome-inactivating protein, coding sequence fragment.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; ss.
XX
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX
PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 24; 39pp; English.
XX
CC This sequence represents a fragment of the DNA encoding the ribosome-
CC inactivating protein (RIP) of the invention. The RIP is designated
CC bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,
CC where the amino-terminal end exhibits 50 % homology with the sequence
CC shown in AAW67752. The proteins and conjugates form compositions in
CC treating various human diseases or conditions, including cancer, graft-
CC versus-host disease, organ transplant rejection, type I diabetes,
CC multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC viral agents in plants and mammals. Compositions containing the
CC polynucleotide encoding bouganin are useful in gene therapy. Bouganin
CC possesses low non-specific toxicity, which makes it very suitable for use
CC as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 363 BP; 110 A; 68 C; 85 G; 100 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.26e-113	Length:	363
Score:	120.00	Matches:	120
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	80.5%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-9 (1-149) x AAV81468 (1-363)

```
Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361
```

RESULT 2
AAV81465
ID AAV81465 standard; DNA; 65 BP.
XX
AC AAV81465;
XX
DT 27-AUG-2003 (revised)

```
DT   16-APR-1999  (first entry)
XX
DE   Ribosome-inactivating protein coding sequence fragment.
XX
KW   Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW   graft-versus-host disease; organ transplant rejection; type I diabetes;
KW   rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW   anti-viral agent; gene therapy; toxic agent; immunotoxin; ss.
XX
OS   Bougainvillea spectabilis.
XX
PN   WO9855623-A1.
XX
PD   10-DEC-1998.
XX
PF   08-JUN-1998;   98WO-NL000336.
XX
PR   06-JUN-1997;   97EP-00201725.
XX
PA   (PANG-) PANGENETICS BV.
XX
PI   Stirpe F,  Bolognesi A;
XX
DR   WPI; 1999-045796/04.
XX
PT   New type-1 ribosome-inactivating protein bouganin - useful in forming
PT   immunotoxins for use in medicine and plant protection.
XX
PS   Example 8; Page 22; 39pp; English.
XX
CC   This sequence encodes a fragment of the ribosome-inactivating protein
CC   (RIP) of the invention. The RIP is designated bouganin, and comprises a
CC   linear polypeptide (26 kDa) with a pI of 9.0, where the amino-terminal
CC   end exhibits 50 % homology with the sequence shown in AAW67752. The
CC   proteins and conjugates form compositions in treating various human
CC   diseases or conditions, including cancer, graft-versus-host disease,
CC   organ transplant rejection, type I diabetes, multiple sclerosis,
CC   rheumatoid arthritis, systemic lupus erythematosus, and myasthenia
CC   gravis. The proteins are also useful as therapeutic anti-viral agents in
CC   plants and mammals. Compositions containing the polynucleotide encoding
CC   bouganin are useful in gene therapy. Bouganin possesses low non-specific
CC   toxicity, which makes it very suitable for use as the toxic agent in
CC   various immunotoxins. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 65 BP; 19 A; 18 C; 15 G; 13 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.07e-12        Length:         65
Score:                  21.00           Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-9 (1-149) x AAV81465 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 3
ADZ13575_0/c
WP Sequence split into 6 fragments  LOCUS ADZ13575 Accession Adz13575
WP      Fragment Name       Begin     End
WP      ADZ13575_0              1    110000
WP      ADZ13575_1         100001    210000
WP      ADZ13575_2         200001    310000
WP      ADZ13575_3         300001    410000
WP      ADZ13575_4         400001    510000
WP      ADZ13575_5         500001    582589
ID   ADZ13575 standard; DNA; 582589 BP.
XX
AC   ADZ13575;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Murine cancer-associated genomic DNA #96.
XX
KW   Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW   cytostatic; gene; ds.
XX
OS   Mus sp.
XX
PN   WO2005031001-A2.
XX
PD   07-APR-2005.
XX
PF   23-SEP-2004; 2004WO-US031617.
XX
PR   23-SEP-2003; 2003US-00669920.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2005-273395/28.
XX
PT   Nucleic acid array useful for detecting cancer associated nucleic acid,
PT   comprises two or more nucleic acid probes.
XX
PS   Disclosure; SEQ ID NO 1095; 198pp; English.
XX
CC   The invention relates to a nucleic acid array for detecting a cancer
CC   associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC   The invention also relates to a peptide array comprising two or more
CC   isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC   that binds to a polypeptide, an isolated antibody or its fragment which
CC   binds to a polypeptide, which is prepared by immunizing a host animal
CC   with a composition comprising the polypeptide or its antigen binding
CC   fragment and collecting cells from the host expressing antibodies against
CC   the antigen or its antigen binding fragment, a composition comprising the
CC   antibody and a carrier, a method of screening for anticancer activity, a
CC   method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC   method of treating cancer and a method of inhibiting expression of a CA
CC   nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC   nucleic acids. The antibody is useful for detecting the presence or
CC   absence of cancer cells in an individual which involves contacting cells
CC   from the individual with the antibody and detecting a complex of a CA
CC   protein from the cancer cells and the antibody, where the detection of
CC   the complex correlates with the presence of cancer cells in the
CC   individual. The composition is useful for inhibiting growth of cancer
CC   cells in an individual or for delivering a therapeutic agent to cancer
CC   cells in an individual. The invention is also useful for diagnosing
CC   cancer, for treating cancer and for inhibiting expression of a CA gene in
CC   a cell. This sequence represents murine cancer-associated genomic DNA of
CC   the invention.
XX
SQ   Sequence 582589 BP; 163894A; 120816C; 118288G; 167823T; 0U; 11768Other;

Alignment Scores:
Pred. No.:              1.56e+03        Length:         110000
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.0%            Indels:         0
DB:                     14              Gaps:           0

US-10-758-902-9 (1-149) x ADZ13575_0 (1-110000)

Qy         56 SerLysLysThrValLysValAlaIle 64
              |||||||||||||||||||||||||
Db     104609 AGCAAGAAAACTGTCAAGGTTGCCATC 104583
```

```
RESULT 4
ADZ13575_1/c
Continuation (2 of 6) of ADZ13575 from base 100001 (Murine cancer-associated genomic DNA
WP Sequence split into 6 fragments  LOCUS ADZ13575 Accession Adz13575
WP     Fragment Name      Begin     End
WP     ADZ13575_0             1     110000
WP     ADZ13575_1        100001     210000
WP     ADZ13575_2        200001     310000
WP     ADZ13575_3        300001     410000
WP     ADZ13575_4        400001     510000
WP     ADZ13575_5        500001     582589

Alignment Scores:
Pred. No.:              1.56e+03       Length:         110000
Score:                  9.00           Matches:        9
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            6.0%           Indels:         0
DB:                     14             Gaps:           0

US-10-758-902-9 (1-149) x ADZ13575_1 (1-110000)

Qy         56 SerLysLysThrValLysValAlaIle 64
              |||||||||||||||||||||||||||
Db       4609 AGCAAGAAAACTGTCAAGGTTGCCATC 4583

RESULT 5
ABD33143/c
ID   ABD33143 standard; DNA; 289190 BP.
XX
AC   ABD33143;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Murine cancer-associated (CA) gene MD07-018.
XX
KW   Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW   ds; cancer; cytostatic.
XX
OS   Mus musculus.
XX
PN   WO2004058146-A2.
XX
PD   15-JUL-2004.
XX
PF   15-DEC-2003; 2003WO-US040081.
XX
PR   17-DEC-2002; 2002US-00322281.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2004-499109/47.
XX
PT   Novel human cancer associated protein encoded within open reading frame
PT   of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS   Disclosure; SEQ ID NO 115; 182pp; English.
XX
CC   The invention relates to cancer-associated proteins (CAP) and the cancer-
CC   associated (CA) nucleic acids encoding them. The invention also relates
CC   to a method for treating cancers involving administering to a patient an
CC   inhibitor of CAP, and a method of screening for anticancer activity in a
CC   potential drug involving providing a cell that expresses a CA gene,
CC   contacting a tissue sample derived from a cancer cell with an anticancer
CC   drug candidate and monitoring the effect of the anticancer drug candidate
CC   on expression of the CA gene. The CAP proteins are useful for detecting
CC   cancer associated with expression of a CAP protein in a test cell sample
CC   and for screening for a bioactive agent capable of modulating the
CC   activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC   cancer, involving determining the expression of a CA nucleic acid in a
CC   tissue. This sequence represents a murine CA gene of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 289190 BP; 79193 A; 58337 C; 57759 G; 83755 T; 0 U; 10146 Other;

Alignment Scores:
Pred. No.:              3.77e+03       Length:         289190
Score:                  9.00           Matches:        9
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            6.0%           Indels:         0
DB:                     13             Gaps:           0

US-10-758-902-9 (1-149) x ABD33143 (1-289190)

Qy         56 SerLysLysThrValLysValAlaIle 64
              |||||||||||||||||||||||||||
Db     104584 AGCAAGAAAACTGTCAAGGTTGCCATC 104558

RESULT 6
AAA42055/c
ID   AAA42055 standard; cDNA; 100 BP.
XX
AC   AAA42055;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human secreted expressed sequence tag SEQ ID NO:795.
XX
KW   Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
KW   expressed sequence tag; EST; probe; chemotactic; proliferative;
KW   immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
KW   thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
KW   antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
KW   antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
KW   cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;
KW   autoimmune disorder; multiple sclerosis; allergic condition;
KW   insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW   lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW   central nervous system disorder; Alzheimer's disease; stroke;
KW   Parkinson's disease; Huntington's disease; coagulation disorder;
KW   haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;
KW   infection; depression; psoriasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200021990-A1.
XX
PD   20-APR-2000.
XX
PF   15-OCT-1999;   99WO-US024205.
XX
PR   15-OCT-1998;   98US-0104435P.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Collins-Racie LA,  Evans C;
PI   Merberg D,  Treacy M;
XX
DR   WPI; 2000-317937/27.
XX
PT   Isolated polynucleotides, and encoded proteins, comprising secreted
PT   expressed sequence tags (sESTs), useful for treating various disorders
PT   such as autoimmune, infectious, and central nervous system disorders.
XX
PS   Claim 1; Page 334; 618pp; English.
XX
CC   AAA41261 to AAA43419 represent specifically claimed secreted expressed
CC   sequence tags (sESTs), isolated from human, mouse, xenopus and rat tissue
CC   sources. The sESTs can have a range of activities depending on the
CC   tissues they were isolated from. The activities include: chemotactic;
```

```
CC   proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
CC   haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial;
CC   antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer;
CC   osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic;
CC   cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be
CC   used for gene therapy and in vaccines. The sESTs are useful as probes for
CC   the identification and isolation of full-length cDNAs and genomic DNA
CC   molecules which correspond to the sESTs. Proteins encoded by the sESTs
CC   are useful in assays for determining biological activity and raising
CC   antibodies. They may be useful for treatment of autoimmune disorders
CC   (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC   (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC   osteoporosis, osteoarthritis, central nervous system disorders
CC   (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC   disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC   disease), tumours, bacterial, fungal or viral infections, depression and
CC   psoriasis. AAA43420 to AAA43425 represent linker variants which are given
CC   in the exemplification of the present invention
XX
SQ   Sequence 100 BP; 29 A; 27 C; 24 G; 20 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                27.8          Length:          100
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              5.4%          Indels:          0
DB:                       3             Gaps:            0

US-10-758-902-9 (1-149) x AAA42055 (1-100)

Qy        128 LeuGluLeuGlyValTyrLysLeu 135
              |||||||||||||||||||||||
Db        100 CTCGAGCTTGGGGTCTATAAGCTG 77

RESULT 7
ADR59442
ID   ADR59442 standard; cDNA; 759 BP.
XX
AC   ADR59442;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Cotton cDNA sequence, SEQ ID 223.
XX
KW   Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
KW   drought tolerance; plant disease resistance; galactomannan; lignin;
KW   plant growth regulator; heat tolerance; herbicide tolerance;
KW   homologous recombination; extreme osmotic condition tolerance;
KW   pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
KW   stress resistance.
XX
OS   Gossypium hirsutum.
XX
PN   US2004181830-A1.
XX
PD   16-SEP-2004.
XX
PF   29-JAN-2004; 2004US-00767795.
XX
PR   07-MAY-2001; 2001US-00849529.
PR   12-DEC-2001; 2001US-00021323.
XX
PA   (KOVA/) KOVALIC D K.
PA   (ZHOU/) ZHOU Y.
PA   (CAOY/) CAO Y.
XX
PI   Kovalic DK,  Zhou Y,  Cao Y;
XX
DR   WPI; 2004-667718/65.
XX
PT   New recombinant nucleic acid molecules and polypeptides from Gossypium
PT   hirsutum, useful for producing plants with improved biological
PT   characteristics (e.g. improved plant cold or drought tolerance).
XX
PS   Claim 1; SEQ ID NO 223; 14pp; English.
XX
CC   The invention relates to a recombinant polynucleotide comprising any of
CC   the 58798 Cotton plant cDNA sequences mentioned in the specification.
CC   Also a recombinant polypeptide comprising any of the 58798 amino acid
CC   sequences mentioned in the specification and producing a plant having an
CC   improved property. Producing a plant having an improved property
CC   comprises transforming a plant with a recombinant construct comprising a
CC   promoter region functional in a plant cell operably joined to a
CC   polynucleotide comprising a coding sequence for a polypeptide associated
CC   with the property, and growing the transformed plant. The polypeptide is
CC   useful for improving plant cold tolerance, manipulating growth rate in
CC   plant cells by modification of the cell cycle pathway, improving plant
CC   drought tolerance, providing increased resistance to plant disease,
CC   producing galactomannan (or lignin or plant growth regulators), improving
CC   plant heat tolerance, improving plant tolerance to herbicides, increasing
CC   the rate of homologous recombination in plants, improving plant tolerance
CC   to extreme osmotic conditions or to pathogens or pests, improving yield
CC   by modification of photosynthesis, modifying seed oil or protein yield
CC   and/or content, improving yield by modification of carbohydrate, nitrogen
CC   or phosphorus use and/or uptake, or improving yield by providing improved
CC   plant growth and development under at least one stress condition. The
CC   polynucleotide and polypeptide may also be used in recombinant DNA
CC   constructs, in physical arrays of molecules, as plant breeding markers,
CC   or in computer-based storage and analysis systems. The present sequence
CC   is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585
CC   polynucleotide sequences were available, the remaining 52213
CC   polynucleotides and all 58798 protein sequences were not present.
XX
SQ   Sequence 759 BP; 163 A; 234 C; 106 G; 256 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                176           Length:          759
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              5.4%          Indels:          0
DB:                       13            Gaps:            0

US-10-758-902-9 (1-149) x ADR59442 (1-759)

Qy         91 ProThrValAlaThrSerLysLeu 98
              |||||||||||||||||||||||
Db         91 CCCACAGTGGCCACTTCCAAGCTC 114

RESULT 8
AAF76566/c
ID   AAF76566 standard; DNA; 978 BP.
XX
AC   AAF76566;
XX
DT   11-MAY-2001  (first entry)
XX
DE   Human EFEMP1 gene fragment #25.
XX
KW   Human; EGF-containing fibrillin-like extracellular matrix protein 1;
KW   EFEMP1; macular degeneration; chromosome 2; ds.
XX
OS   Homo sapiens.
XX
PN   WO200112823-A2.
XX
PD   22-FEB-2001.
XX
PF   30-MAY-2000; 2000WO-US014965.
XX
PR   28-MAY-1999;   99US-00322357.
XX
```

PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Stone EM, Sheffield VC;
XX
DR WPI; 2001-218354/22.
XX
PT Screening assays to identify compounds that modulate EGF-containing
PT fibrillin like extracellular matrix protein 1 bioactivity, which are
PT useful for treating or preventing macular degeneration.
XX
PS Disclosure; Fig 5; 92pp; English.
XX
CC The present invention describes a method for identifying compounds which
CC modulate the activity of epidermal growth factor-containing fibrillin
CC like extracellular matrix protein 1 (EFEMP1). The human EFEMP1 coding and
CC protein sequences are also provided. Compounds of the invention can be
CC used in the treatment of macular degeneration and other diseases related
CC to EFEMP1. The present sequence is a fragment of the EFEMP1 gene
XX
SQ Sequence 978 BP; 266 A; 233 C; 170 G; 308 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	222	Length:	978
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-9 (1-149) x AAF76566 (1-978)

```
Qy         33 GlnLeuProValThrLeuGlnThr 40
              |||||||||||||||||||||||
Db        946 CAGTTACCGGTAACTCTGCAAACT 923
```

RESULT 9
AAF31245
ID AAF31245 standard; DNA; 1238 BP.
XX
AC AAF31245;
XX
DT 09-APR-2001 (first entry)
XX
DE Human immune response molecule (IMUN) coding sequence SEQ ID NO: 12.
XX
KW Human; IMUN; immune response molecule; autoimmune disorder;
KW inflammatory disorder; cell proliferation disorder; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200102569-A2.
XX
PD 11-JAN-2001.
XX
PF 06-JUL-2000; 2000WO-US018505.
XX
PR 06-JUL-1999; 99US-0142572P.
PR 09-SEP-1999; 99US-0153170P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Tang YT, Yue H, Yang J, Azimzai Y, Baughn MR, Lu DAM;
XX
DR WPI; 2001-123113/13.
DR P-PSDB; AAB67048.
XX
PT Novel human immune response molecules (IMUN), useful for diagnosing,
PT treating and preventing disorders associated with abnormal expression of
PT IMUN, e.g. Addison's disease, allergies, anemia, asthma and
PT atherosclerosis.
XX
PS Claim 5; Page 90; 95pp; English.
XX
CC The present invention provides the protein and coding sequences for ten
CC human immune response molecules (designated IMUN-1 to IMUN-10). The
CC sequences can be used in the diagnosis, treatment and prevention of
CC autoimmune and inflammatory disorders such as AIDS, atherosclerosis,
CC asthma, allergies, Crohn's disease, multiple sclerosis, irritable bowel
CC syndrome, psoriasis, rheumatoid arthritis and infections, and cell
CC proliferation disorders including arteriosclerosis, cirrhosis and cancer
XX
SQ Sequence 1238 BP; 363 A; 249 C; 302 G; 324 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	275	Length:	1238
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-9 (1-149) x AAF31245 (1-1238)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        994 ACAGTGTCATTTAATTTGGGAGAG 1017
```

RESULT 10
ADX61939/c
ID ADX61939 standard; cDNA; 1686 BP.
XX
AC ADX61939;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 32782.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 32782; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1686 BP; 485 A; 322 C; 380 G; 499 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	364	Length:	1686
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-9 (1-149) x ADX61939 (1-1686)

```
Qy         96 SerLysLeuPheProGlyValThr 103
              ||||||||||||||||||||||
Db        112 TCTAAGTTGTTCCCAGGGGTTACC 89
```

RESULT 11
ADX61418/c
ID ADX61418 standard; cDNA; 1879 BP.
XX
AC ADX61418;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 32261.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 32261; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1879 BP; 529 A; 369 C; 438 G; 543 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	402	Length:	1879
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-9 (1-149) x ADX61418 (1-1879)

```
Qy         96 SerLysLeuPheProGlyValThr 103
              ||||||||||||||||||||||
Db        382 TCTAAGTTGTTCCCAGGGGTTACC 359
```

RESULT 12
ABZ17264/c
ID ABZ17264 standard; DNA; 2000 BP.
XX
AC ABZ17264;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 5069.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.
XX
PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Kreps J, Wang X, Zhu T;
XX

DR WPI; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 5069; 577pp + Sequence Listing; English.
XX
CC The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 2000 BP; 640 A; 375 C; 264 G; 721 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	425	Length:	2000
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-9 (1-149) x ABZ17264 (1-2000)

```
Qy        134 LysLeuGluPheSerIleGluAla 141
              |||||||||||||||||||||||
Db        819 AAACTTGAATTTTCAATCGAAGCA 796
```

RESULT 13
ADA68963/c
ID ADA68963 standard; DNA; 2000 BP.
XX
AC ADA68963;
XX
DT 20-NOV-2003 (first entry)
XX
DE Arabidopsis thaliana gene, SEQ ID 2286.
XX
KW Plant; bacterial infection; fungal infection; viral infection; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 27; SEQ ID NO 2286; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 640 A; 375 C; 264 G; 721 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	425	Length:	2000
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-9 (1-149) x ADA68963 (1-2000)

```
Qy        134 LysLeuGluPheSerIleGluAla 141
              |||||||||||||||||||||||
Db        819 AAACTTGAATTTTCAATCGAAGCA 796
```

RESULT 14
ADP07317
ID ADP07317 standard; DNA; 2143 BP.
XX
AC ADP07317;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human WT1 DNA.
XX
KW ds; proliferative disease; breast; methylation; CpG; bisulfite; human.
XX
OS Homo sapiens.
XX
PN DE10255104-A1.
XX
PD 11-MAR-2004.
XX
PF 26-NOV-2002; 2002DE-01055104.
XX
PR 27-AUG-2002; 2002DE-01039313.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Maier S;
XX
DR WPI; 2004-284340/27.
DR GENBANK; NM_004906.
XX
PT Analyzing proliferative diseases of breast cells, useful e.g. for
PT diagnosis, prognosis and treatment of breast cancer, by determining
PT methylation status of specific genes.
XX
PS Claim 1; Page; 22pp; German.
XX
CC This invention describes a novel method of analysing proliferative
CC diseases of breast cells by determining the methylation status of certain
CC genes. The invention also describes nucleic acids or their complements,
CC oligomers, especially oligonucleotides or peptide nucleic acid oligomers,
CC that hybridise to, or are identical with, any of the nucleic acids, the
CC preparation of an oligomer array for analysing proliferative diseases of
CC breast cells that are associated with the methylation status of CpG
CC dinucleotides of the genes by bonding at least one oligomer to a solid
CC phase and a kit comprising a bisulfite reagent and the oligomer. The
CC nucleic acids are genomic sequences (5'- and/or regulatory and/or CpG-
CC rich regions). The base sequence of the oligomer includes at least one
CC CpG island, especially with C in the middle third of the sequence. The

CC process involves a genomic DNA sample treated chemically, specifically
CC with a bisulfite reagent, to convert non-methylated C to uracil or some
CC other base having base-pairing properties different from those of C.
CC Fragments of the treated DNA are then amplified, using primers and a
CC polymerase and the methylation status of the genomic CpG dinucleotides is
CC determined by analysis of the amplicons, particularly by hybridisation to
CC the oligomer, optionally with extension of the hybridised oligomer by at
CC least one base, or detection is by sequencing. The amplification may use
CC methylation-specific primers. Alternatively, genomic DNA is extracted
CC from a sample and digested with methylation-specific restriction enzymes,
CC then the digestion fragments detected, optionally after amplification. In
CC either method, more than 10 fragments of 100-200 bp are amplified in a
CC single reaction vessel, using a heat-resistant DNA polymerase in PCR. The
CC amplicons carry detectable markers, e.g. fluorophores, radioisotopes
CC and/or releasable fragments of known mass that can be detected by mass
CC spectrometry. The method is used for characterisation, classification,
CC differentiation, staging, phase-estimation, diagnosis and/or therapy of
CC proliferative diseases of breast cells. The method provides very specific
CC classification of proliferative diseases, allowing better treatment. It
CC can both characterise methylation status and detect single-nucleotide
CC polymorphisms. This sequence represents human gene used to illustrate the
CC method of the invention. NOTE: This sequence does not appear in the
CC printed specification but has been retrieved from Genbank.
XX
SQ Sequence 2143 BP; 619 A; 431 C; 498 G; 595 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	453	Length:	2143
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-9 (1-149) x ADP07317 (1-2143)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db       1436 ACAGTGTCATTTAATTTGGGAGAG 1459
```

RESULT 15
ADX59797/c
ID ADX59797 standard; cDNA; 2187 BP.
XX
AC ADX59797;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 30640.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 30640; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 2187 BP; 630 A; 433 C; 509 G; 615 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	461	Length:	2187
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-9 (1-149) x ADX59797 (1-2187)

```
Qy         96 SerLysLeuProGlyValThr 103
              |||||||||||||||||||||
Db        689 TCTAAGTTGTTCCCAGGGGTTACC 666
```

RESULT 16
ADQ67284
ID ADQ67284 standard; cDNA; 2291 BP.
XX
AC ADQ67284;
XX
DT 07-OCT-2004 (first entry)
XX
DE Novel human cDNA sequence #2257.
XX
KW ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX
OS Homo sapiens.
XX
PN EP1440981-A2.
XX
PD 28-JUL-2004.
XX
PF 21-JAN-2004; 2004EP-00001196.
XX

PR 21-JAN-2003; 2003JP-00102206.
PR 09-MAY-2003; 2003JP-00131392.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX
DR WPI; 2004-535376/52.
DR P-PSDB; ADQ67591.
XX
PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 4445; 2449pp; English.
XX
CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.
XX
SQ Sequence 2291 BP; 642 A; 393 C; 498 G; 758 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	481	Length:	2291
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-9 (1-149) x ADQ67284 (1-2291)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db       1604 ACAGTGTCATTTAATTTGGGAGAG 1627
```

RESULT 17
ADE54051
ID ADE54051 standard; cDNA; 2772 BP.
XX
AC ADE54051;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human prostate cancer cDNA #398.
XX
KW Human; prostate cancer; ss; cDNA combination; differential expression;
KW gene.
XX
OS Homo sapiens.
XX
PN US2003190640-A1.
XX
PD 09-OCT-2003.
XX
PF 29-MAY-2002; 2002US-00252157.
XX
PR 31-MAY-2001; 2001US-0295048P.
XX
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
XX
PI Faris M, Pearson CI;
XX
DR WPI; 2003-831619/77.
XX
PT New combination comprising cDNAs that are differentially expressed in
PT prostate cancer, useful for diagnosing, treating or monitoring the
PT progression of treatment of prostate cancer.
XX
PS Claim 1; SEQ ID NO 398; 42pp; English.
XX
CC The invention relates to a combination comprising a number of cDNAs
CC expressed in prostate cancer. The invention also relates to a method for
CC detecting differential expression of one or more cDNAs in a sample
CC containing nucleic acids by hybridising a substrate with the nucleic
CC acids, thus forming one or more hybridisation complexes, detecting
CC hybridisation complex formation and comparing the complexes formed with
CC standard complexes, where differences between the standard and the sample
CC complex formation indicate differential expression of cDNAs in the
CC sample. The differential expression is diagnostic of prostate cancer. The
CC invention also relates to proteins and antibodies related to the cDNAs.
CC The combination is useful for diagnosing, treating or monitoring the
CC progression of treatment of prostate cancer. The antibodies are useful
CC for detecting prostate cancer. This sequence represents a human prostate
CC cancer cDNA of the invention.
XX
SQ Sequence 2772 BP; 740 A; 680 C; 664 G; 688 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	572	Length:	2772
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	10	Gaps:	0

US-10-758-902-9 (1-149) x ADE54051 (1-2772)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db       2634 ACAGTGTCATTTAATTTGGGAGAG 2657
```

RESULT 18
AAS46362/c
ID AAS46362 standard; DNA; 6413 BP.
XX
AC AAS46362;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #84.
XX
KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-EP002955.
XX
PR 15-MAR-2000; 2000DE-01013847.
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.

XX
PS Claim 1; SEQ ID NO 84; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Sequences with even
CC numbered Seq ID numbers are the complementary sequence of the
CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
CC 535, except for those whose partner sequence is missing). Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 6413 BP; 1401 A; 100 C; 1647 G; 3263 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	1.23e+03	Length:	6413
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-9 (1-149) x AAS46362 (1-6413)

```
Qy         52 IleThrThrThrSerLysLysThr 59
              |||||||||||||||||||||||
Db         87 ATAACAACTACCTCAAAAAAAACT 64
```

RESULT 19
ABQ67000/c
ID ABQ67000 standard; DNA; 6413 BP.
XX
AC ABQ67000;
XX
DT 28-AUG-2002 (first entry)
XX
DE Human angiogenesis associated polynucleotide SEQ ID NO 30.
XX
KW Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
KW inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds;
KW macular degeneration; inflammatory bowel disease; Crohn's disease;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiarteriosclerotic; ds.
XX
OS Homo sapiens.
XX
PN WO200246454-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-EP014320.
XX
PR 06-DEC-2000; 2000DE-01061338.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Schacht O;
XX
DR WPI; 2002-500450/53.
XX
PT New nucleic acid fragments from chemically treated angiogenesis-
PT associated genes, useful for determining methylation status, e.g. in
PT diagnosis or treatment of cancer.
XX
PS Claim 1; SEQ ID NO 30; 41pp + Sequence Listing; German.
XX
CC The invention relates to a nucleic acid (I) comprising a segment of 18
CC bases of chemically pretreated DNA of angiogenesis-associated genes (II)
CC having sequences (ABQ66971-ABQ67178) or their complements. (I), also
CC related oligomers, are used to evaluate the methylation status and/or
CC single-nucleotide polymorphisms, in angiogenesis-related genes, for
CC diagnosis and treatment of eye diseases, proliferative retinopathy,
CC neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis,
CC diabetic retinopathy, macular degeneration caused by neovascularisation,
CC psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and
CC Crohn's disease. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 6413 BP; 1401 A; 100 C; 1647 G; 3263 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	1.23e+03	Length:	6413
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-9 (1-149) x ABQ67000 (1-6413)

```
Qy         52 IleThrThrThrSerLysLysThr 59
              |||||||||||||||||||||||
Db         87 ATAACAACTACCTCAAAAAAAACT 64
```

RESULT 20
ADM68765/c
ID ADM68765 standard; DNA; 16363 BP.
XX
AC ADM68765;
XX
DT 17-JUN-2004 (first entry)
XX
DE Drosophila melanogaster ryanodine receptor encoding DNA SEQ ID NO:9.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Drosophila melanogaster.
XX
FH Key Location/Qualifiers
FT CDS 1. .15330
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.

DR P-PSDB; ADM68766.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 9; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 16363 BP; 3940 A; 4448 C; 4559 G; 3414 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	2.88e+03	Length:	16363
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-9 (1-149) x ADM68765 (1-16363)

```
Qy        105 ArgValThrLeuThrPheAspGly 112
              |||||||||||||||||||||||
Db       7218 CGGGTAACGCTCACCTTCGACGGG 7195
```

RESULT 21
ACN44688
ID ACN44688 standard; DNA; 35076 BP.
XX
AC ACN44688;
XX
DT 18-NOV-2004 (first entry)
XX
DE Mouse genomic sequence mCG2435.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
XX
OS Mus musculus.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 1261; 0pp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 35076 BP; 9106 A; 8143 C; 7853 G; 9488 T; 0 U; 486 Other;

Alignment Scores:

Pred. No.:	5.77e+03	Length:	35076
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	11	Gaps:	0

US-10-758-902-9 (1-149) x ACN44688 (1-35076)

```
Qy         30 ProValCysGlnLeuProValThr 37
              |||||||||||||||||||||||
Db      31394 CCTGTTTGTCAGCTTCCTGTTACT 31417
```

RESULT 22
ACN44266/c
ID ACN44266 standard; DNA; 92247 BP.
XX
AC ACN44266;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genomic sequence hCG37968.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX

DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 628; 0pp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 92247 BP; 25525 A; 18183 C; 20429 G; 27884 T; 0 U; 226 Other;

Alignment Scores:

Pred. No.:	1.39e+04	Length:	92247
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	11	Gaps:	0

US-10-758-902-9 (1-149) x ACN44266 (1-92247)

```
Qy        101 GlyValThrAsnArgValThrLeu 108
              ||||||||||||||||||||||||
Db      10645 GGAGTCACAAACCGGGTCACCCTA 10622
```

RESULT 23
ADZ12943/c
ID ADZ12943 standard; DNA; 126488 BP.
XX
AC ADZ12943;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated genomic DNA #40.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 463; 198pp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents human cancer-associated genomic DNA of
CC the invention.
XX
SQ Sequence 126488 BP; 34053 A; 25980 C; 28325 G; 37898 T; 0 U; 232 Other;

Alignment Scores:

Pred. No.:	1.85e+04	Length:	126488
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	14	Gaps:	0

US-10-758-902-9 (1-149) x ADZ12943 (1-126488)

```
Qy        101 GlyValThrAsnArgValThrLeu 108
              ||||||||||||||||||||||||
Db      44198 GGAGTCACAAACCGGGTCACCCTA 44175
```

RESULT 24
AAV81463
ID AAV81463 standard; DNA; 23 BP.
XX
AC AAV81463;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE PCR primer 102 for Ribosome-inactivating protein, bouganin.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; PCR primer; ss.
XX
OS Synthetic.
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX

PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 22; 39pp; English.
XX
CC This sequence represents a PCR primer for DNA encoding the ribosome-
CC inactivating protein (RIP) of the invention. The RIP is designated
CC bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,
CC where the amino-terminal end exhibits 50 % homology with the sequence
CC shown in AAW67752. The proteins and conjugates form compositions in
CC treating various human diseases or conditions, including cancer, graft-
CC versus-host disease, organ transplant rejection, type I diabetes,
CC multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC viral agents in plants and mammals. Compositions containing the
CC polynucleotide encoding bouganin are useful in gene therapy. Bouganin
CC possesses low non-specific toxicity, which makes it very suitable for use
CC as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 23 BP; 5 A; 4 C; 5 G; 2 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.:	76.1	Length:	23
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-9 (1-149) x AAV81463 (1-23)

```
Qy          9 GlyGluAlaTyrGluTyrPro 15
              |||||||||||||||||||||
Db          1 GGNGARGCNTAYGARTAYCCN 21
```

RESULT 25
AAV81464/c
ID AAV81464 standard; DNA; 23 BP.
XX
AC AAV81464;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE PCR primer 116 for Ribosome-inactivating protein, bouganin.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; PCR primer; ss.
XX
OS Synthetic.
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX
PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 22; 39pp; English.
XX
CC This sequence represents a PCR primer for DNA encoding the ribosome-
CC inactivating protein (RIP) of the invention. The RIP is designated
CC bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,
CC where the amino-terminal end exhibits 50 % homology with the sequence
CC shown in AAW67752. The proteins and conjugates form compositions in
CC treating various human diseases or conditions, including cancer, graft-
CC versus-host disease, organ transplant rejection, type I diabetes,
CC multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC viral agents in plants and mammals. Compositions containing the
CC polynucleotide encoding bouganin are useful in gene therapy. Bouganin
CC possesses low non-specific toxicity, which makes it very suitable for use
CC as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 23 BP; 1 A; 4 C; 5 G; 6 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.:	76.1	Length:	23
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-9 (1-149) x AAV81464 (1-23)

```
Qy         23 AsnGluLeuAlaLysGlyThr 29
              |||||||||||||||||||||
Db         23 AAYGARCTNGCNAARGGNACN 3
```

RESULT 26
AAV81466
ID AAV81466 standard; DNA; 25 BP.
XX
AC AAV81466;
XX
DT 27-AUG-2003 (revised)
DT 16-APR-1999 (first entry)
XX
DE PCR primer 125 for Ribosome-inactivating protein, bouganin.
XX
KW Ribosome-inactivating protein; RIP; bouganin; cancer; multiple sclerosis;
KW graft-versus-host disease; organ transplant rejection; type I diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis;
KW anti-viral agent; gene therapy; toxic agent; immunotoxin; PCR primer; ss.
XX
OS Synthetic.
OS Bougainvillea spectabilis.
XX
PN WO9855623-A1.
XX
PD 10-DEC-1998.
XX
PF 08-JUN-1998; 98WO-NL000336.
XX
PR 06-JUN-1997; 97EP-00201725.
XX
PA (PANG-) PANGENETICS BV.
XX
PI Stirpe F, Bolognesi A;
XX
DR WPI; 1999-045796/04.
XX
PT New type-1 ribosome-inactivating protein bouganin - useful in forming
PT immunotoxins for use in medicine and plant protection.
XX
PS Example 8; Page 22; 39pp; English.
XX
CC This sequence represents a PCR primer for DNA encoding the ribosome-
CC inactivating protein (RIP) of the invention. The RIP is designated
CC bouganin, and comprises a linear polypeptide (26 kDa) with a pI of 9.0,

CC where the amino-terminal end exhibits 50 % homology with the sequence
CC shown in AAW67752. The proteins and conjugates form compositions in
CC treating various human diseases or conditions, including cancer, graft-
CC versus-host disease, organ transplant rejection, type I diabetes,
CC multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
CC and myasthenia gravis. The proteins are also useful as therapeutic anti-
CC viral agents in plants and mammals. Compositions containing the
CC polynucleotide encoding bouganin are useful in gene therapy. Bouganin
CC possesses low non-specific toxicity, which makes it very suitable for use
CC as the toxic agent in various immunotoxins. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 25 BP; 8 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	82.1	Length:	25
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-9 (1-149) x AAV81466 (1-25)

```
Qy         17 PheIleGlnAspLeuArgAsn 23
              |||||||||||||||||||||
Db          3 TTTATACAAGATTTGCGCAAC 23
```

RESULT 27
AAQ38049
ID AAQ38049 standard; DNA; 40 BP.
XX
AC AAQ38049;
XX
DT 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX
DE Oligonucleotide gel6, for prodn. of synthetic gelonin gene.
XX
KW Seed; toxin; plant; cloning; ribosomal; protein synthesis; ss;
KW Gelonium multiflorum.
XX
OS Synthetic.
XX
PN WO9305168-A1.
XX
PD 18-MAR-1993.
XX
PF 21-AUG-1992; 92WO-US007066.
XX
PR 06-SEP-1991; 91US-00755949.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Rosenblum MG, Beattie KL;
XX
DR WPI; 1993-100990/12.
XX
PT Synthetic DNA encoding gelonin plant toxin - provides nucleotide sequence
PT for synthetic gene for prodn. and cloning.
XX
PS Example 4; Fig 5; 45pp; English.
XX
CC The synthetic gelonin gene based on the sequence of Gelonium multiflorum
CC gelonin was prepd. by synthesising a number of oligonucleotides corresp.
CC to fragments of the gelonin gene and annealing and ligating to assemble
CC the intact gene. The oligonucleotides were designed to contain a codon
CC triplet for each amino acid in the corresp. gelonin fragment. Gelonin is
CC a ribosomal- inactivating plant toxin which inhibits protein synthesis.
CC The synthetic form of gelonin provides a plentiful, reproducible source
CC of gelonin which may be modified. See also AAQ38041-82. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 40 BP; 8 A; 9 C; 13 G; 10 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	126	Length:	40
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-9 (1-149) x AAQ38049 (1-40)

```
Qy         69 ValTyrValValGlyTyrGln 75
              ||||||||||||||||||||
Db          4 GTGTACGTAGTTGGCTATCAG 24
```

RESULT 28
AAD31055
ID AAD31055 standard; DNA; 90 BP.
XX
AC AAD31055;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human g34872 peptide encoding DNA.
XX
KW Human; PAPAP protein; schizophrenia candidate gene; g34872 gene;
KW schizophrenia; bipolar disorder; central nervous system disorder;
KW psychotic disorder; mood disorder; autism; mental retardation;
KW psychiatric disease; anxiety disorder; impulse-control disorder;
KW eating disorder; cognitive disorder; personality disorder; vaccine;
KW chromosome 1p35-p36; neuroleptic; antialcoholic; tranquiliser;
KW antidepressant; nootropic; antiaddictive; alkaline phosphatase; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .90
FT /*tag= b
FT /product= "Human g34872 peptide"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
PN WO200212279-A2.
XX
PD 14-FEB-2002.
XX
PF 26-JUL-2001; 2001WO-IB001891.
XX
PR 07-AUG-2000; 2000US-0223482P.
XX
PA (GEST) GENSET.
XX
PI Bihain B, Bour B, Bougueleret L;
XX
DR WPI; 2002-241732/29.
DR P-PSDB; AAE19433.
XX
PT Novel isolated and purified or recombinant polynucleotide encoding PAPAP
PT protein, useful for diagnosing and treating schizophrenia, bipolar
PT disorder and other central nervous system disorders.
XX
PS Example 1; Page 94; 96pp; English.
XX
CC The invention relates to human PAPAP polypeptides and polynucleotides.
CC The invention also concerns the interaction of PAPAP with schizophrenia
CC candidate gene g34872. PAPAP polypeptides, gene and anti-PAPAP antibodies
CC are useful for treating schizophrenia, bipolar disorder or related
CC central nervous system (CNS) disorders e.g. psychotic disorders, mood
CC disorders, autism, substance dependence and alcoholism, mental
CC retardation and other psychiatric diseases including cognitive, anxiety,
CC eating, impulse-control and personality disorders. They are also used in
CC vaccines. The present sequence is human g34872 peptide encoding DNA

```
XX
SQ   Sequence 90 BP; 37 A; 25 C; 15 G; 13 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              264          Length:         90
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            4.7%         Indels:         0
DB:                     6            Gaps:           0

US-10-758-902-9 (1-149) x AAD31055 (1-90)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||||
Db         29 ACTACAACCAGCAAAAAGACC 49

RESULT 29
ADH93126
ID   ADH93126 standard; DNA; 121 BP.
XX
AC   ADH93126;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human gene sequence #963.
XX
KW   human; gene sequence; single nucleotide polymorphism; SNP;
KW   disease diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   JP2003174883-A.
XX
PD   24-JUN-2003.
XX
PF   11-DEC-2001; 2001JP-00377637.
XX
PR   11-DEC-2001; 2001JP-00377637.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2003-819215/77.
XX
PT   Polynucleotide for detecting single nucleotide polymorphisms existing in
PT   human gene, contains isolated human gene having specified sequence.
XX
PS   Claim 1; SEQ ID NO 963; 529pp; Japanese.
XX
CC   The invention comprises isolated human gene sequences and PCR primer
CC   sequences which can be used to detect single nucleotide polymorphisms
CC   (SNPs). The DNA sequences of the invention are useful for detecting SNPs
CC   existing in human genes and for the diagnosis of human disease. The
CC   present DNA sequence represents a human gene sequence of the invention.
XX
SQ   Sequence 121 BP; 26 A; 36 C; 28 G; 30 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              345          Length:         121
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            4.7%         Indels:         0
DB:                     10           Gaps:           0

US-10-758-902-9 (1-149) x ADH93126 (1-121)

Qy         32 CysGlnLeuProValThrLeu 38
              ||||||||||||||||||||
Db         62 TGTCAGCTCCCAGTGACCCTC 82

RESULT 30
AAI27052/c
ID   AAI27052 standard; DNA; 166 BP.
XX
AC   AAI27052;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Probe #16985 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000670.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human cervical epithelial cells.
XX
PS   Claim 25; SEQ ID NO 16985; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
CC   expression, the probes are therefore useful in grading and/or staging of
CC   diseases of the cervix, notably cervical cancer. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 166 BP; 30 A; 62 C; 37 G; 37 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              460          Length:         166
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            4.7%         Indels:         0
DB:                     4            Gaps:           0

US-10-758-902-9 (1-149) x AAI27052 (1-166)

Qy         60 ValLysValAlaIleAspVal 66
              ||||||||||||||||||||
Db        142 GTGAAGGTGGCCATTGACGTC 122

RESULT 31
AAI55886/c
ID   AAI55886 standard; DNA; 166 BP.
XX
AC   AAI55886;
XX
DT   17-OCT-2001  (first entry)
XX
```

DE Probe #24572 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 25; SEQ ID NO 24572; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
SQ Sequence 166 BP; 30 A; 62 C; 37 G; 37 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	460	Length:	166
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-9 (1-149) x AAI55886 (1-166)

```
Qy         60 ValLysValAlaIleAspVal 66
              ||||||||||||||||||||
Db        142 GTGAAGGTGGCCATTGACGTC 122
```

RESULT 32
AAK23876/c
ID AAK23876 standard; DNA; 166 BP.
XX
AC AAK23876;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 23867.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 23867; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 166 BP; 30 A; 62 C; 37 G; 37 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	460	Length:	166
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-9 (1-149) x AAK23876 (1-166)

```
Qy         60 ValLysValAlaIleAspVal 66
              ||||||||||||||||||||
Db        142 GTGAAGGTGGCCATTGACGTC 122
```

RESULT 33
ABS23443/c
ID ABS23443 standard; DNA; 166 BP.
XX
AC ABS23443;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 23434.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesis; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.

```
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2002-114183/15.
XX
PT   Spatially-addressable set of single exon nucleic acid probes, used to
PT   measure gene expression in human lung samples.
XX
PS   Claim 4; SEQ ID NO 23434; 634pp; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human lung comprising single exon nucleic acid probes having one of
CC   12614 nucleic acid sequences mentioned in the specification, or their
CC   complements or the 12387 open reading frames derived from the 12614
CC   probes. Also included are a microarray comprising the novel set of probes
CC   ; the novel set of probes which hybridise at high stringency to a nucleic
CC   acid expressed in the human lung; measuring gene expression in a sample
CC   derived from human lung, comprising (a) contacting the array with a
CC   collection of detectably labeled nucleic acids derived from human lung
CC   mRNA, and (b) measuring the label detectably bound to each probe of the
CC   array; identifying exons in a eukaryotic genome, comprising (a)
CC   algorithmically predicting at least one exon from genomic sequences of
CC   the eukaryote; and (b) detecting specific hybridisation of detectably
CC   labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC   having a fragment identical to the predicted exon, the probe is included
CC   in the above mentioned microarray; assigning exons to a single gene,
CC   comprising (a) identifying exons from genomic sequence by the method
CC   above and (b) measuring the expression of each of the exons in several
CC   tissues and/or cell types using hybridisation to a single exon
CC   microarrays having a probe with the exon, where a common pattern of
CC   expression of the exons in the tissues and/or cell types indicates that
CC   the exons should be assigned to a single gene; a peptide comprising one
CC   of 12011 sequences, mentioned in the specification, or encoded by the
CC   probes/open reading frames (ORF). The probes are used for gene expression
CC   analysis, and for identifying exons in a gene, particularly using human
CC   lung derived mRNA and for the study of lung diseases such as asthma, lung
CC   cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC   disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC   tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC   Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC   histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis,
CC   Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC   dyskinesis, pulmonary hypertension and hyaline membrane disease. The
CC   present sequence is a single exon probe open reading frame of the
CC   invention. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 166 BP; 30 A; 62 C; 37 G; 37 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              460          Length:          166
Score:                  7.00         Matches:         7
Percent Similarity:     100.0%       Conservative:    0
Best Local Similarity:  100.0%       Mismatches:      0
Query Match:            4.7%         Indels:          0
DB:                     6            Gaps:            0

US-10-758-902-9 (1-149) x ABS23443 (1-166)

Qy         60 ValLysValAlaIleAspVal 66
              ||||||||||||||||||||
Db        142 GTGAAGGTGGCCATTGACGTC 122

RESULT 34
ADS50804/c
ID   ADS50804 standard; cDNA; 175 BP.
XX
AC   ADS50804;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Bacterial polynucleotide #5547.
XX
KW   Recombinant DNA construct; transformed plant; improved plant property;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW   pathogen tolerance; pest tolerance; plant disease resistance;
KW   cell cycle pathway modification; plant growth regulator;
KW   homologous recombination; seed oil yield; protein yield; carbohydrate;
KW   nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW   bacterial polynucleotide; gene; ss.
XX
OS   Bacteria.
XX
PN   US2003233675-A1.
XX
PD   18-DEC-2003.
XX
PF   20-FEB-2003; 2003US-00369493.
XX
PR   21-FEB-2002; 2002US-0360039P.
XX
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
XX
PI   Cao Y,  Hinkle GJ,  Slater SC,  Chen X,  Goldman BS;
XX
DR   WPI; 2004-061375/06.
XX
PT   New recombinant DNA construct comprising a promoter positioned to provide
PT   for expression of a polynucleotide encoding a polypeptide from a
PT   microbial source, useful for producing plants with improved properties.
XX
PS   Claim 1; SEQ ID NO 29234; 122pp; English.
XX
CC   The invention relates to a recombinant DNA construct comprising a
CC   promoter functional in a plant cell, where the promoter is positioned to
CC   provide for expression of a polynucleotide encoding a polypeptide from a
CC   microbial source. The invention also relates to a transformed plant
CC   comprising the recombinant DNA construct and a method of producing a
CC   transformed plant having an improved property. The plant is a crop plant
CC   such as maize or soybean. The method of producing a transformed plant
CC   having an improved property comprises transforming a plant with the
CC   recombinant DNA construct and growing the transformed plant, where the
CC   polynucleotide or polypeptide is useful for improving plant properties.
CC   The recombinant DNA construct is useful for producing plants with
CC   improved plant properties, e.g. improved cold, heat or drought tolerance,
CC   tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC   increased resistance to plant disease, better growth rate by modification
CC   of the cell cycle pathway with plant growth regulators, increased rate of
CC   homologous recombination, modified seed oil or protein yield and/or
CC   content, improved yield by modification of carbohydrate, nitrogen or
CC   phosphorus use and/or uptake, by modification of photosynthesis or by
CC   providing improved plant growth and development under at least one stress
CC   condition, improved lignin production or improved galactomannan
CC   production. This sequence represents a bacterial polynucleotide used in
CC   the scope of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification but was obtained in electronic
CC   format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 175 BP; 52 A; 48 C; 32 G; 43 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              483             Length:         175
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     13              Gaps:           0

US-10-758-902-9 (1-149) x ADS50804 (1-175)

Qy        108 LeuThrPheAspGlySerTyr 114
              ||||||||||||||||||||
Db         80 CTCACCTTCGATGGATCGTAT 60

RESULT 35
ACH84437
ID   ACH84437 standard; DNA; 176 BP.
XX
AC   ACH84437;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human genome derived single exon probe #17632.
XX
KW   Human; probe; ss; gene expression; single exon probe; microarray;
KW   alternative splicing event; genomic alteration.
XX
OS   Homo sapiens.
XX
PN   US2003194704-A1.
XX
PD   16-OCT-2003.
XX
PF   03-APR-2002; 2002US-00029386.
XX
PR   03-APR-2002; 2002US-00029386.
XX
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
XX
PI   Penn SG,  Rank DR,  Hanzel DK;
XX
DR   WPI; 2004-119264/12.
XX
PT   New human genome-derived single exon nucleic acid probes useful for human
PT   gene expression analysis, for identifying or characterizing alternative
PT   splicing events, for assessing genomic alterations or as tools for
PT   surveying tissues.
XX
PS   Claim 1; SEQ ID NO 17632; 80pp; English.
XX
CC   The invention relates to a nucleic acid probe for measuring human gene
CC   expression, comprising any of the 27,400 fully defined nucleotide
CC   sequences in the specification, or their complements or fragments, and
CC   encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC   fully defined in the specification. The probe is a single exon probe that
CC   hybridises under high stringency conditions to a nucleic acid molecule
CC   expressed in human cells or tissues. Also included are a spatially-
CC   addressable set of single exon nucleic acid probes for measuring human
CC   gene expression (comprising a plurality of single exon nucleic acid
CC   probes cited above, where each of the plurality of probes is separately
CC   and addressably isolatable or amplifiable from the plurality), a single
CC   exon microarray for measuring human gene expression, a method of
CC   measuring human gene expression, a vector comprising the single exon
CC   probe cited above, an ORF-encoded peptide comprising at least 8
CC   contiguous amino acids of any of the above- mentioned amino acid
CC   sequences (optionally with conservative amino acid substitutions), an
CC   isolated antibody that binds specifically to a peptide cited above,
CC   methods of selling and/or licensing single exon probes or microarrays to
CC   a customer desiring to measure gene expression, a method of providing
CC   human gene expression data by subscription, and a computer-readable
CC   storage medium which contains a database having a plurality of records
CC   (each record including data on the expression of a single exon probe
CC   cited above. The probe, methods and apparatus are useful in gene
CC   expression analysis. The probes may be used as tools for surveying
CC   tissues to detect the presence of expressed messages that contain their
CC   specific exon, or in constructing genome-derived single exon microarrays.
CC   In addition, the probes are used in identifying and characterising
CC   alternative splicing events, in detecting and characterising gross
CC   alterations in the genomic locus that includes their exon, in assessing
CC   smaller genomic alterations, in priming the synthesis of nucleic acids,
CC   or in expressing the ORF-encoded peptide. The present sequence is a human
CC   single exon probe of the invention. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ   Sequence 176 BP; 39 A; 41 C; 63 G; 33 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              485             Length:         176
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     12              Gaps:           0

US-10-758-902-9 (1-149) x ACH84437 (1-176)

Qy         60 ValLysValAlaIleAspVal 66
              ||||||||||||||||||||
Db         31 GTGAAGGTGGCCATTGACGTC 51

RESULT 36
AAC09175
ID   AAC09175 standard; cDNA; 222 BP.
XX
AC   AAC09175;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 13250.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-00200610.
XX
PR   26-FEB-1999;   99US-0122487P.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS   Claim 1; SEQ ID NO 13250; 71pp + Sequence Listing; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
```

CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
SQ Sequence 222 BP; 42 A; 67 C; 75 G; 37 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	600	Length:	222
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-9 (1-149) x AAC09175 (1-222)

```
Qy         60 ValLysValAlaIleAspVal 66
              ||||||||||||||||||||
Db        167 GTGAAGGTGGCCATTGACGTC 187
```

RESULT 37
ACA41352/c
ID ACA41352 standard; DNA; 231 BP.
XX
AC ACA41352;
XX
DT 27-OCT-2003 (revised)
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #23009.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Neisseria gonorrhoeae.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU37482.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 29222; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 27-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 231 BP; 57 A; 61 C; 59 G; 54 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	622	Length:	231
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-9 (1-149) x ACA41352 (1-231)

```
Qy         34 LeuProValThrLeuGlnThr 40
              ||||||||||||||||||||
Db         29 TTACCGGTCACTTTGCAAACT 9
```

RESULT 38
ACA42037/c
ID ACA42037 standard; DNA; 234 BP.
XX
AC ACA42037;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #23694.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Neisseria meningitidis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU38167.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 29907; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 234 BP; 59 A; 63 C; 59 G; 53 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	629	Length:	234
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-9 (1-149) x ACA42037 (1-234)

```
Qy         34 LeuProValThrLeuGlnThr 40
              ||||||||||||||||||||
Db         29 TTGCCGGTCACTTTGCAAACT 9
```

RESULT 39
AAV52126
ID AAV52126 standard; cDNA; 236 BP.
XX
AC AAV52126;
XX
DT 09-NOV-1998 (first entry)
XX
DE Homo sapiens CESP gene related EST clone.
XX
KW CESP; cerebellum and embryo specific protein; restenosis;
KW myocardial infarction; arrhythmia; heart disease; atherosclerosis;
KW expressed sequence tag; ds.
XX
OS Homo sapiens.
XX
PN WO9827932-A2.
XX
PD 02-JUL-1998.
XX
PF 18-DEC-1997; 97WO-US023518.
XX
PR 20-DEC-1996; 96US-0033870P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Ruben SM;
XX
DR WPI; 1998-377366/32.
XX
PT New isolated cerebellum and embryo specific polypeptide - used to develop
PT products for treating e.g. coronary restenosis, myocardial infarction,
PT heart disease and artery or venous thrombosis.
XX
PS Disclosure; Page 60; 77pp; English.
XX
CC The sequence is that of an EST clone related to the cerebellum and embryo
CC specific protein (CESP) gene
XX
SQ Sequence 236 BP; 68 A; 60 C; 62 G; 44 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	634	Length:	236
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-9 (1-149) x AAV52126 (1-236)

```
Qy         30 ProValCysGlnLeuProVal 36
              ||||||||||||||||||||
Db        167 CCAGTTTGCCAGCTTCCAGTA 187
```

RESULT 40
AAV52122
ID AAV52122 standard; cDNA; 263 BP.
XX
AC AAV52122;
XX
DT 09-NOV-1998 (first entry)
XX
DE Homo sapiens CESP gene related EST clone.
XX
KW CESP; cerebellum and embryo specific protein; restenosis;
KW myocardial infarction; arrhythmia; heart disease; atherosclerosis;
KW expressed sequence tag; ds.
XX
OS Homo sapiens.
XX
PN WO9827932-A2.
XX
PD 02-JUL-1998.
XX
PF 18-DEC-1997; 97WO-US023518.
XX
PR 20-DEC-1996; 96US-0033870P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Ruben SM;
XX
DR WPI; 1998-377366/32.
XX
PT New isolated cerebellum and embryo specific polypeptide - used to develop
PT products for treating e.g. coronary restenosis, myocardial infarction,
PT heart disease and artery or venous thrombosis.

XX
PS Disclosure; Page 58-59; 77pp; English.
XX
CC The sequence is that of an EST clone related to the cerebellum and embryo
CC specific protein (CESP) gene
XX
SQ Sequence 263 BP; 69 A; 69 C; 72 G; 50 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.:	700	Length:	263
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	2	Gaps:	0

US-10-758-902-9 (1-149) x AAV52122 (1-263)

```
Qy         30 ProValCysGlnLeuProVal 36
              ||||||||||||||||||||
Db        157 CCAGTTTGCCAGCTTCCAGTA 177
```

Search completed: February 20, 2006, 01:11:43
Job time : 747.307 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 01:03:22 ; Search time 226.413 Seconds
(without alignments)
1169.792 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 149
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2599929

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160837_4110/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10758902_@CGN_1_1_237_@runat_17022006_160837_4110 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	120	80.5	363	3	US-09-445-160B-8	Sequence 8, Appli
	2	21	14.1	65	3	US-09-445-160B-5	Sequence 5, Appli
	3	8	5.4	601	3	US-09-949-016-146445	Sequence 146445,
c	4	8	5.4	979	3	US-09-322-357-71	Sequence 71, Appl
	5	8	5.4	55195	3	US-09-949-016-15854	Sequence 15854, A
c	6	8	5.4	76247	3	US-09-949-016-16136	Sequence 16136, A
	7	7	4.7	23	3	US-09-445-160B-3	Sequence 3, Appli
c	8	7	4.7	23	3	US-09-445-160B-4	Sequence 4, Appli
	9	7	4.7	25	3	US-09-445-160B-6	Sequence 6, Appli
	10	7	4.7	222	3	US-09-513-999C-13250	Sequence 13250, A
	11	7	4.7	279	3	US-09-539-333D-62	Sequence 62, Appl
	12	7	4.7	279	3	US-09-539-333D-85	Sequence 85, Appl
	13	7	4.7	280	3	US-09-539-333D-74	Sequence 74, Appl
	14	7	4.7	280	3	US-09-539-333D-97	Sequence 97, Appl
	15	7	4.7	280	3	US-09-539-333D-109	Sequence 109, App
c	16	7	4.7	339	3	US-09-134-001C-1851	Sequence 1851, Ap
c	17	7	4.7	356	3	US-09-513-999C-2553	Sequence 2553, Ap
	18	7	4.7	388	3	US-09-539-333D-60	Sequence 60, Appl
	19	7	4.7	388	3	US-09-539-333D-83	Sequence 83, Appl
	20	7	4.7	389	3	US-09-539-333D-72	Sequence 72, Appl
	21	7	4.7	389	3	US-09-539-333D-95	Sequence 95, Appl
	22	7	4.7	389	3	US-09-539-333D-107	Sequence 107, App
c	23	7	4.7	432	3	US-10-101-464A-391	Sequence 391, App
c	24	7	4.7	435	3	US-09-134-001C-1924	Sequence 1924, Ap
	25	7	4.7	439	3	US-09-060-756-98	Sequence 98, Appl
	26	7	4.7	439	3	US-09-670-314-98	Sequence 98, Appl
c	27	7	4.7	461	3	US-09-280-116-194	Sequence 194, App
	28	7	4.7	491	3	US-09-270-767-13340	Sequence 13340, A
c	29	7	4.7	585	3	US-09-489-039A-2605	Sequence 2605, Ap
	30	7	4.7	601	3	US-09-949-016-21916	Sequence 21916, A
	31	7	4.7	601	3	US-09-949-016-21917	Sequence 21917, A
	32	7	4.7	601	3	US-09-949-016-47002	Sequence 47002, A
	33	7	4.7	601	3	US-09-949-016-60813	Sequence 60813, A
	34	7	4.7	601	3	US-09-949-016-84175	Sequence 84175, A
	35	7	4.7	601	3	US-09-949-016-84176	Sequence 84176, A
c	36	7	4.7	601	3	US-09-949-016-94256	Sequence 94256, A
c	37	7	4.7	601	3	US-09-949-016-94257	Sequence 94257, A
c	38	7	4.7	601	3	US-09-949-016-95022	Sequence 95022, A
c	39	7	4.7	601	3	US-09-949-016-95134	Sequence 95134, A
	40	7	4.7	601	3	US-09-949-016-120534	Sequence 120534,
c	41	7	4.7	601	3	US-09-949-016-124164	Sequence 124164,
c	42	7	4.7	601	3	US-09-949-016-124165	Sequence 124165,
	43	7	4.7	601	3	US-09-949-016-146880	Sequence 146880,
	44	7	4.7	601	3	US-09-949-016-148868	Sequence 148868,
c	45	7	4.7	601	3	US-09-949-016-181749	Sequence 181749,
c	46	7	4.7	601	3	US-09-949-016-181868	Sequence 181868,
c	47	7	4.7	601	3	US-09-949-016-181987	Sequence 181987,
c	48	7	4.7	601	3	US-09-949-016-190166	Sequence 190166,
c	49	7	4.7	601	3	US-09-949-016-200635	Sequence 200635,
c	50	7	4.7	601	3	US-09-949-016-200636	Sequence 200636,
c	51	7	4.7	601	3	US-09-949-016-200637	Sequence 200637,
c	52	7	4.7	601	3	US-09-949-016-200781	Sequence 200781,
c	53	7	4.7	601	3	US-09-949-016-200782	Sequence 200782,
c	54	7	4.7	601	3	US-09-949-016-200783	Sequence 200783,
	55	7	4.7	651	3	US-09-134-000C-5	Sequence 5, Appli
	56	7	4.7	663	3	US-09-270-767-14225	Sequence 14225, A
	57	7	4.7	723	3	US-09-248-796A-14	Sequence 14, Appl
	58	7	4.7	731	3	US-09-831-683B-13	Sequence 13, Appl
	59	7	4.7	742	3	US-09-539-333D-19	Sequence 19, Appl
	60	7	4.7	774	6	PCT-US91-05766-1	Sequence 1, Appli
	61	7	4.7	776	3	US-09-539-333D-25	Sequence 25, Appl
	62	7	4.7	777	3	US-09-539-333D-13	Sequence 13, Appl
	63	7	4.7	783	2	US-08-327-440-1	Sequence 1, Appli
	64	7	4.7	809	3	US-10-121-857-61	Sequence 61, Appl
	65	7	4.7	811	3	US-09-539-333D-21	Sequence 21, Appl
	66	7	4.7	813	2	US-07-901-707-11	Sequence 11, Appl
	67	7	4.7	813	2	US-07-901-707-57	Sequence 57, Appl
	68	7	4.7	813	2	US-07-988-430-11	Sequence 11, Appl
	69	7	4.7	813	2	US-07-988-430-57	Sequence 57, Appl
	70	7	4.7	813	2	US-08-425-336-11	Sequence 11, Appl
	71	7	4.7	813	2	US-08-488-113B-11	Sequence 11, Appl
	72	7	4.7	813	2	US-08-477-484B-11	Sequence 11, Appl
	73	7	4.7	813	2	US-08-646-360-11	Sequence 11, Appl
	74	7	4.7	813	2	US-08-621-803-246	Sequence 246, App
	75	7	4.7	813	3	US-08-839-765-11	Sequence 11, Appl
	76	7	4.7	813	3	US-09-136-389-11	Sequence 11, Appl
	77	7	4.7	813	3	US-09-217-352-246	Sequence 246, App
	78	7	4.7	813	3	US-09-610-838-11	Sequence 11, Appl
	79	7	4.7	813	3	US-09-711-485-11	Sequence 11, Appl
	80	7	4.7	813	6	PCT-US92-09487-11	Sequence 11, Appl
	81	7	4.7	813	6	PCT-US92-09487-57	Sequence 57, Appl
	82	7	4.7	822	3	US-09-539-333D-24	Sequence 24, Appl

	83	7	4.7	823	3	US-09-539-333D-14	Sequence 14, Appl
	84	7	4.7	836	3	US-09-539-333D-15	Sequence 15, Appl
	85	7	4.7	851	3	US-09-539-333D-18	Sequence 18, Appl
	86	7	4.7	863	3	US-09-539-333D-6	Sequence 6, Appli
	87	7	4.7	882	3	US-09-539-333D-16	Sequence 16, Appl
	88	7	4.7	897	3	US-09-539-333D-12	Sequence 12, Appl
	89	7	4.7	920	3	US-09-539-333D-20	Sequence 20, Appl
c	90	7	4.7	927	3	US-09-540-236-320	Sequence 320, App
	91	7	4.7	947	3	US-09-539-333D-26	Sequence 26, Appl
	92	7	4.7	955	2	US-08-621-803-258	Sequence 258, App
	93	7	4.7	955	3	US-09-217-352-258	Sequence 258, App
	94	7	4.7	955	3	US-09-539-333D-17	Sequence 17, Appl
	95	7	4.7	960	3	US-09-710-279-791	Sequence 791, App
	96	7	4.7	960	3	US-09-710-279-2007	Sequence 2007, Ap
	97	7	4.7	978	3	US-09-539-333D-22	Sequence 22, Appl
	98	7	4.7	993	3	US-09-539-333D-23	Sequence 23, Appl
	99	7	4.7	995	3	US-09-539-333D-2	Sequence 2, Appli
	100	7	4.7	1003	2	US-08-621-803-252	Sequence 252, App
	101	7	4.7	1003	3	US-09-217-352-252	Sequence 252, App
	102	7	4.7	1009	3	US-09-539-333D-11	Sequence 11, Appl
	103	7	4.7	1053	3	US-09-161-241-2	Sequence 2, Appli
	104	7	4.7	1072	2	US-08-621-803-250	Sequence 250, App
	105	7	4.7	1072	3	US-09-217-352-250	Sequence 250, App
c	106	7	4.7	1074	2	US-08-975-316-54	Sequence 54, Appl
c	107	7	4.7	1074	3	US-09-615-192A-54	Sequence 54, Appl
c	108	7	4.7	1074	3	US-09-169-789-54	Sequence 54, Appl
c	109	7	4.7	1075	2	US-08-975-316-55	Sequence 55, Appl
c	110	7	4.7	1075	3	US-09-615-192A-55	Sequence 55, Appl
c	111	7	4.7	1075	3	US-09-169-789-55	Sequence 55, Appl
	112	7	4.7	1089	3	US-09-134-001C-1833	Sequence 1833, Ap
c	113	7	4.7	1155	3	US-09-543-681A-1626	Sequence 1626, Ap
c	114	7	4.7	1185	2	US-08-628-039-9	Sequence 9, Appli
c	115	7	4.7	1185	3	US-08-912-205-9	Sequence 9, Appli
c	116	7	4.7	1185	3	US-09-440-400-9	Sequence 9, Appli
c	117	7	4.7	1185	3	US-09-942-891-9	Sequence 9, Appli
	118	7	4.7	1245	3	US-09-543-681A-2475	Sequence 2475, Ap
	119	7	4.7	1312	2	US-08-580-545B-9	Sequence 9, Appli
	120	7	4.7	1312	3	US-09-262-653A-9	Sequence 9, Appli
	121	7	4.7	1335	3	US-09-023-655-1010	Sequence 1010, Ap
c	122	7	4.7	1414	3	US-09-949-016-2364	Sequence 2364, Ap
c	123	7	4.7	1487	3	US-09-722-971-3	Sequence 3, Appli
	124	7	4.7	1593	3	US-09-023-655-1498	Sequence 1498, Ap
	125	7	4.7	1594	2	US-08-248-628A-1	Sequence 1, Appli
	126	7	4.7	1596	3	US-09-023-655-1476	Sequence 1476, Ap
c	127	7	4.7	1628	2	US-08-883-515-3	Sequence 3, Appli
	128	7	4.7	1829	3	US-09-270-767-11181	Sequence 11181, A
c	129	7	4.7	1864	2	US-08-673-388-9	Sequence 9, Appli
c	130	7	4.7	1864	2	US-08-614-877-9	Sequence 9, Appli
c	131	7	4.7	1872	3	US-09-583-110-663	Sequence 663, App
c	132	7	4.7	1902	3	US-09-107-433-1488	Sequence 1488, Ap
c	133	7	4.7	1996	3	US-10-104-047-219	Sequence 219, App
c	134	7	4.7	2024	3	US-09-919-039-168	Sequence 168, App
c	135	7	4.7	2107	3	US-09-441-340-29	Sequence 29, Appl
c	136	7	4.7	2115	2	US-08-474-379C-60	Sequence 60, Appl
c	137	7	4.7	2115	3	US-09-146-249A-60	Sequence 60, Appl
c	138	7	4.7	2115	3	US-08-206-188B-60	Sequence 60, Appl
	139	7	4.7	2190	3	US-10-104-047-226	Sequence 226, App
c	140	7	4.7	2343	2	US-09-018-760-3	Sequence 3, Appli
c	141	7	4.7	2394	3	US-09-994-192-3	Sequence 3, Appli
c	142	7	4.7	2436	3	US-09-441-340-31	Sequence 31, Appl
	143	7	4.7	2556	3	US-08-811-682-18	Sequence 18, Appl
	144	7	4.7	2580	2	US-08-887-798-1	Sequence 1, Appli
c	145	7	4.7	2583	3	US-09-248-796A-4482	Sequence 4482, Ap
	146	7	4.7	2586	3	US-09-907-794A-235	Sequence 235, App
	147	7	4.7	2586	3	US-09-905-125A-235	Sequence 235, App
	148	7	4.7	2586	3	US-09-902-775A-235	Sequence 235, App
	149	7	4.7	2586	3	US-09-906-700-235	Sequence 235, App
	150	7	4.7	2586	3	US-09-903-603A-235	Sequence 235, App
	151	7	4.7	2586	3	US-09-904-920A-235	Sequence 235, App
	152	7	4.7	2586	3	US-09-909-064-235	Sequence 235, App
	153	7	4.7	2586	3	US-09-905-381A-235	Sequence 235, App
	154	7	4.7	2586	3	US-09-906-618-235	Sequence 235, App
	155	7	4.7	2586	3	US-09-906-646-235	Sequence 235, App
	156	7	4.7	2586	3	US-09-904-462-235	Sequence 235, App
	157	7	4.7	2586	3	US-09-902-736A-235	Sequence 235, App
	158	7	4.7	2586	3	US-09-906-722A-235	Sequence 235, App
	159	7	4.7	2608	3	US-09-949-016-1985	Sequence 1985, Ap
	160	7	4.7	2608	3	US-09-949-016-1986	Sequence 1986, Ap
	161	7	4.7	2608	3	US-09-949-016-1987	Sequence 1987, Ap
	162	7	4.7	2631	3	US-09-710-279-3760	Sequence 3760, Ap
	163	7	4.7	2679	3	US-10-104-047-1168	Sequence 1168, Ap
	164	7	4.7	2871	3	US-09-949-016-5027	Sequence 5027, Ap
c	165	7	4.7	2883	3	US-09-710-279-4366	Sequence 4366, Ap
c	166	7	4.7	3016	3	US-09-023-655-259	Sequence 259, App
c	167	7	4.7	3039	3	US-09-377-466B-19	Sequence 19, Appl
c	168	7	4.7	3039	3	US-09-377-466B-21	Sequence 21, Appl
c	169	7	4.7	3039	3	US-10-232-665-19	Sequence 19, Appl
c	170	7	4.7	3039	3	US-10-232-665-21	Sequence 21, Appl
c	171	7	4.7	3044	3	US-09-377-466B-38	Sequence 38, Appl
c	172	7	4.7	3044	3	US-10-232-665-38	Sequence 38, Appl
	173	7	4.7	3114	3	US-09-543-681A-3505	Sequence 3505, Ap
c	174	7	4.7	3130	2	US-08-474-379C-62	Sequence 62, Appl
c	175	7	4.7	3130	3	US-09-146-249A-62	Sequence 62, Appl
c	176	7	4.7	3130	3	US-08-206-188B-62	Sequence 62, Appl
	177	7	4.7	3225	2	US-08-482-090-14	Sequence 14, Appl
	178	7	4.7	3225	2	US-08-481-700B-7	Sequence 7, Appli
	179	7	4.7	3225	2	US-09-007-383-14	Sequence 14, Appl
c	180	7	4.7	3450	3	US-09-377-466B-17	Sequence 17, Appl
c	181	7	4.7	3450	3	US-10-232-665-17	Sequence 17, Appl
c	182	7	4.7	3455	3	US-09-377-466B-36	Sequence 36, Appl
c	183	7	4.7	3455	3	US-10-232-665-36	Sequence 36, Appl
c	184	7	4.7	3469	3	US-09-377-466B-23	Sequence 23, Appl
c	185	7	4.7	3469	3	US-10-232-665-23	Sequence 23, Appl
	186	7	4.7	3666	3	US-09-107-532A-305	Sequence 305, App
c	187	7	4.7	3754	3	US-09-377-466B-15	Sequence 15, Appl
c	188	7	4.7	3754	3	US-10-232-665-15	Sequence 15, Appl
	189	7	4.7	3767	3	US-09-949-016-4537	Sequence 4537, Ap
c	190	7	4.7	3867	2	US-07-727-814B-1	Sequence 1, Appli
c	191	7	4.7	3867	2	US-08-258-614-1	Sequence 1, Appli
c	192	7	4.7	3885	3	US-09-710-279-3883	Sequence 3883, Ap
c	193	7	4.7	4149	3	US-09-377-466B-13	Sequence 13, Appl
c	194	7	4.7	4149	3	US-10-232-665-13	Sequence 13, Appl
	195	7	4.7	4267	3	US-09-661-753-47	Sequence 47, Appl
c	196	7	4.7	5059	3	US-09-700-687-1	Sequence 1, Appli
	197	7	4.7	6736	3	US-09-057-570-1	Sequence 1, Appli
	198	7	4.7	6736	3	US-09-057-570-5	Sequence 5, Appli
	199	7	4.7	6736	3	US-09-387-693-1	Sequence 1, Appli
	200	7	4.7	6736	3	US-09-387-693-5	Sequence 5, Appli
	201	7	4.7	7004	3	US-09-057-570-3	Sequence 3, Appli
	202	7	4.7	7004	3	US-09-387-693-3	Sequence 3, Appli
	203	7	4.7	7546	3	US-09-902-540-801	Sequence 801, App
c	204	7	4.7	8349	3	US-09-186-002-16	Sequence 16, Appl
c	205	7	4.7	8959	3	US-09-949-016-12114	Sequence 12114, A
c	206	7	4.7	9030	3	US-09-949-016-16338	Sequence 16338, A
	207	7	4.7	9370	2	US-08-320-559-27	Sequence 27, Appl
	208	7	4.7	9370	3	US-08-545-860D-27	Sequence 27, Appl
	209	7	4.7	9370	6	PCT-US94-04496-27	Sequence 27, Appl
	210	7	4.7	9391	2	US-08-320-559-25	Sequence 25, Appl
	211	7	4.7	9391	3	US-08-545-860D-25	Sequence 25, Appl
	212	7	4.7	9391	6	PCT-US94-04496-25	Sequence 25, Appl
	213	7	4.7	9471	3	US-08-811-682-1	Sequence 1, Appli
c	214	7	4.7	10713	3	US-09-949-016-15928	Sequence 15928, A
c	215	7	4.7	10968	2	US-08-680-327-2	Sequence 2, Appli
c	216	7	4.7	10968	3	US-09-228-246-1	Sequence 1, Appli
c	217	7	4.7	14205	3	US-09-949-016-14464	Sequence 14464, A
	218	7	4.7	16780	3	US-09-949-002-796	Sequence 796, App
c	219	7	4.7	17410	2	US-07-841-646-3	Sequence 3, Appli
c	220	7	4.7	17410	2	US-08-147-023-3	Sequence 3, Appli
c	221	7	4.7	17410	2	US-08-447-570-3	Sequence 3, Appli
c	222	7	4.7	17410	2	US-08-449-700-3	Sequence 3, Appli
c	223	7	4.7	17410	2	US-08-449-699A-3	Sequence 3, Appli
c	224	7	4.7	17410	3	US-09-148-925C-3	Sequence 3, Appli
c	225	7	4.7	17410	3	US-08-957-425-3	Sequence 3, Appli
c	226	7	4.7	17410	3	US-10-321-799-3	Sequence 3, Appli
c	227	7	4.7	17415	3	US-08-486-343A-1	Sequence 1, Appli
c	228	7	4.7	17415	3	US-09-423-821B-1	Sequence 1, Appli

c 229	7	4.7	17415	6	PCT-US95-07349-1	Sequence 1, Appli
230	7	4.7	17580	3	US-09-949-016-16055	Sequence 16055, A
231	7	4.7	21040	3	US-08-961-527-55	Sequence 55, Appl
c 232	7	4.7	23219	3	US-09-949-016-13556	Sequence 13556, A
c 233	7	4.7	25235	3	US-10-164-230-2	Sequence 2, Appli
234	7	4.7	28592	3	US-09-949-002-806	Sequence 806, App
235	7	4.7	29357	3	US-09-949-016-16676	Sequence 16676, A
c 236	7	4.7	33753	3	US-09-949-016-15741	Sequence 15741, A
c 237	7	4.7	33756	3	US-09-949-016-12006	Sequence 12006, A
c 238	7	4.7	35355	3	US-09-949-016-14197	Sequence 14197, A
239	7	4.7	37059	3	US-09-949-016-15865	Sequence 15865, A
240	7	4.7	46899	2	US-08-471-119A-1	Sequence 1, Appli
241	7	4.7	48522	3	US-09-949-002-740	Sequence 740, App
242	7	4.7	49359	3	US-09-949-002-690	Sequence 690, App
243	7	4.7	49931	3	US-09-949-016-13727	Sequence 13727, A
244	7	4.7	49931	3	US-09-949-016-13728	Sequence 13728, A
245	7	4.7	49931	3	US-09-949-016-13729	Sequence 13729, A
246	7	4.7	55328	3	US-09-949-016-12747	Sequence 12747, A
247	7	4.7	55330	3	US-09-949-016-17146	Sequence 17146, A
248	7	4.7	63982	3	US-09-949-016-16769	Sequence 16769, A
249	7	4.7	68529	3	US-09-949-016-12140	Sequence 12140, A
250	7	4.7	68529	3	US-09-949-016-15671	Sequence 15671, A
251	7	4.7	69764	3	US-09-949-016-15638	Sequence 15638, A
252	7	4.7	77772	3	US-09-949-016-17417	Sequence 17417, A
253	7	4.7	77997	3	US-09-949-016-12249	Sequence 12249, A
c 254	7	4.7	87190	3	US-09-949-016-16335	Sequence 16335, A
255	7	4.7	88240	3	US-09-949-016-16279	Sequence 16279, A
256	7	4.7	90150	3	US-09-949-016-17383	Sequence 17383, A
257	7	4.7	90776	3	US-09-949-016-17230	Sequence 17230, A
c 258	7	4.7	93894	3	US-09-949-016-13629	Sequence 13629, A
c 259	7	4.7	99748	3	US-09-949-016-11990	Sequence 11990, A
c 260	7	4.7	99749	3	US-09-949-016-16518	Sequence 16518, A
c 261	7	4.7	100848	3	US-09-596-002-39	Sequence 39, Appl
c 262	7	4.7	105733	3	US-09-949-016-13080	Sequence 13080, A
c 263	7	4.7	106256	3	US-09-949-016-16858	Sequence 16858, A
c 264	7	4.7	110243	3	US-09-949-016-13698	Sequence 13698, A
c 265	7	4.7	112114	3	US-09-949-016-17292	Sequence 17292, A
266	7	4.7	113042	3	US-09-949-016-12343	Sequence 12343, A
267	7	4.7	113042	3	US-09-949-016-15246	Sequence 15246, A
268	7	4.7	113538	3	US-09-949-016-16329	Sequence 16329, A
269	7	4.7	131978	3	US-09-949-016-13117	Sequence 13117, A
c 270	7	4.7	133719	3	US-09-949-016-15092	Sequence 15092, A
271	7	4.7	143644	3	US-09-949-016-15238	Sequence 15238, A
c 272	7	4.7	145241	3	US-09-949-016-17394	Sequence 17394, A
c 273	7	4.7	145241	3	US-09-949-016-17395	Sequence 17395, A
c 274	7	4.7	152393	3	US-09-949-016-14514	Sequence 14514, A
c 275	7	4.7	152393	3	US-09-949-016-14515	Sequence 14515, A
c 276	7	4.7	152582	3	US-09-949-016-12086	Sequence 12086, A
c 277	7	4.7	152583	3	US-09-949-016-17390	Sequence 17390, A
c 278	7	4.7	152583	3	US-09-949-016-17391	Sequence 17391, A
c 279	7	4.7	154605	3	US-09-949-016-11894	Sequence 11894, A
280	7	4.7	154626	3	US-09-949-016-14000	Sequence 14000, A
c 281	7	4.7	155266	3	US-09-949-016-13870	Sequence 13870, A
c 282	7	4.7	156894	3	US-09-949-016-12765	Sequence 12765, A
c 283	7	4.7	156894	3	US-09-949-016-12766	Sequence 12766, A
c 284	7	4.7	156895	3	US-09-949-016-16957	Sequence 16957, A
c 285	7	4.7	156895	3	US-09-949-016-16958	Sequence 16958, A
c 286	7	4.7	156895	3	US-09-949-016-16959	Sequence 16959, A
287	7	4.7	187848	3	US-09-949-016-12111	Sequence 12111, A
c 288	7	4.7	194790	3	US-09-949-016-15393	Sequence 15393, A
289	7	4.7	235064	3	US-09-949-016-15390	Sequence 15390, A
c 290	7	4.7	255679	3	US-09-949-016-17189	Sequence 17189, A
c 291	7	4.7	264206	3	US-09-949-016-12731	Sequence 12731, A
c 292	7	4.7	264304	3	US-09-949-016-13249	Sequence 13249, A
293	7	4.7	283538	3	US-09-949-016-13506	Sequence 13506, A
294	7	4.7	317366	3	US-09-949-016-16001	Sequence 16001, A
c 295	7	4.7	319608	3	US-09-539-333D-1	Sequence 1, Appli
c 296	7	4.7	319608	3	US-09-679-409-1	Sequence 1, Appli
c 297	7	4.7	373182	3	US-09-949-016-17371	Sequence 17371, A
c 298	7	4.7	373694	3	US-09-949-016-12062	Sequence 12062, A
c 299	7	4.7	421491	3	US-09-949-016-12805	Sequence 12805, A
c 300	7	4.7	421494	3	US-09-949-016-14060	Sequence 14060, A
301	7	4.7	455726	3	US-09-949-016-14157	Sequence 14157, A
302	7	4.7	481115	3	US-09-949-016-11940	Sequence 11940, A
c 303	7	4.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 304	7	4.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 305	6	4.0	25	3	US-09-590-759-104	Sequence 104, App
c 306	6	4.0	25	3	US-09-396-196G-982	Sequence 982, App
307	6	4.0	25	3	US-09-396-196G-38564	Sequence 38564, A
308	6	4.0	25	3	US-09-396-196G-125449	Sequence 125449,
309	6	4.0	28	3	US-09-023-082A-48	Sequence 48, Appl
310	6	4.0	28	3	US-09-248-998-48	Sequence 48, Appl
311	6	4.0	28	3	US-09-610-651-48	Sequence 48, Appl
312	6	4.0	28	3	US-09-345-373-48	Sequence 48, Appl
313	6	4.0	28	3	US-10-075-446-48	Sequence 48, Appl
314	6	4.0	31	2	US-08-390-850-57	Sequence 57, Appl
315	6	4.0	31	2	US-08-390-850-58	Sequence 58, Appl
316	6	4.0	31	2	US-08-435-634-57	Sequence 57, Appl
317	6	4.0	31	2	US-08-435-634-58	Sequence 58, Appl
318	6	4.0	36	2	US-08-464-531-10	Sequence 10, Appl
319	6	4.0	36	2	US-08-461-598-10	Sequence 10, Appl
320	6	4.0	36	3	US-08-322-137-10	Sequence 10, Appl
c 321	6	4.0	39	3	US-09-023-082A-36	Sequence 36, Appl
c 322	6	4.0	39	3	US-09-564-805-134	Sequence 134, App
c 323	6	4.0	39	3	US-09-248-998-36	Sequence 36, Appl
c 324	6	4.0	39	3	US-09-610-651-36	Sequence 36, Appl
c 325	6	4.0	39	3	US-09-434-382-134	Sequence 134, App
c 326	6	4.0	39	3	US-09-345-373-36	Sequence 36, Appl
c 327	6	4.0	39	3	US-10-075-446-36	Sequence 36, Appl
c 328	6	4.0	41	3	US-10-165-873D-32	Sequence 32, Appl
c 329	6	4.0	47	3	US-09-023-082A-51	Sequence 51, Appl
c 330	6	4.0	47	3	US-09-248-998-51	Sequence 51, Appl
c 331	6	4.0	47	3	US-09-610-651-51	Sequence 51, Appl
c 332	6	4.0	47	3	US-09-345-373-51	Sequence 51, Appl
c 333	6	4.0	47	3	US-10-075-446-51	Sequence 51, Appl
334	6	4.0	50	3	US-10-131-827-7466	Sequence 7466, Ap
335	6	4.0	51	2	US-07-936-163-33	Sequence 33, Appl
336	6	4.0	51	3	US-08-729-601A-80	Sequence 80, Appl
337	6	4.0	52	3	US-08-675-773B-11	Sequence 11, Appl
c 338	6	4.0	54	3	US-08-679-645-1220	Sequence 1220, Ap
339	6	4.0	56	3	US-09-513-999C-28175	Sequence 28175, A
340	6	4.0	59	2	US-08-464-531-23	Sequence 23, Appl
341	6	4.0	59	2	US-08-461-598-23	Sequence 23, Appl
342	6	4.0	59	3	US-08-322-137-23	Sequence 23, Appl
343	6	4.0	59	3	US-08-582-333A-20	Sequence 20, Appl
c 344	6	4.0	60	3	US-09-023-228B-29	Sequence 29, Appl
c 345	6	4.0	60	3	US-09-163-025B-29	Sequence 29, Appl
c 346	6	4.0	60	3	US-10-037-282-29	Sequence 29, Appl
347	6	4.0	70	2	US-08-894-578-153	Sequence 153, App
348	6	4.0	70	3	US-09-121-286-4	Sequence 4, Appli
349	6	4.0	70	3	US-09-121-286-19	Sequence 19, Appl
350	6	4.0	75	3	US-09-023-082A-35	Sequence 35, Appl
351	6	4.0	75	3	US-09-248-998-35	Sequence 35, Appl
352	6	4.0	75	3	US-09-610-651-35	Sequence 35, Appl
353	6	4.0	75	3	US-09-345-373-35	Sequence 35, Appl
354	6	4.0	75	3	US-10-075-446-35	Sequence 35, Appl
355	6	4.0	90	3	US-09-023-082A-103	Sequence 103, App
356	6	4.0	90	3	US-09-218-444-24	Sequence 24, Appl
357	6	4.0	90	3	US-09-248-998-103	Sequence 103, App
358	6	4.0	90	3	US-09-853-666-24	Sequence 24, Appl
359	6	4.0	90	3	US-09-610-651-103	Sequence 103, App
360	6	4.0	90	3	US-09-345-373-103	Sequence 103, App
361	6	4.0	90	3	US-10-075-446-103	Sequence 103, App
362	6	4.0	93	3	US-09-513-999C-18774	Sequence 18774, A
c 363	6	4.0	105	2	US-08-611-757-84	Sequence 84, Appl
c 364	6	4.0	105	6	PCT-US95-05980-84	Sequence 84, Appl
c 365	6	4.0	114	3	US-09-641-931F-43	Sequence 43, Appl
366	6	4.0	121	3	US-08-903-446A-4	Sequence 4, Appli
c 367	6	4.0	121	3	US-09-818-875-1765	Sequence 1765, Ap
368	6	4.0	121	3	US-09-818-875-1766	Sequence 1766, Ap
369	6	4.0	126	3	US-09-513-999C-23655	Sequence 23655, A
370	6	4.0	132	3	US-10-021-338A-66	Sequence 66, Appl
c 371	6	4.0	138	3	US-09-621-976-9945	Sequence 9945, Ap
372	6	4.0	139	3	US-09-513-999C-27754	Sequence 27754, A
373	6	4.0	147	3	US-09-513-999C-13216	Sequence 13216, A
c 374	6	4.0	152	3	US-09-513-999C-22048	Sequence 22048, A

c 375	6	4.0	154	3	US-09-856-221-2	Sequence 2, Appli
c 376	6	4.0	155	3	US-09-513-999C-22586	Sequence 22586, A
c 377	6	4.0	158	3	US-09-945-703B-10	Sequence 10, Appl
c 378	6	4.0	164	3	US-09-513-999C-13209	Sequence 13209, A
c 379	6	4.0	171	3	US-10-125-258-122	Sequence 122, App
c 380	6	4.0	177	3	US-09-513-999C-18003	Sequence 18003, A
c 381	6	4.0	183	3	US-09-328-352-672	Sequence 672, App
382	6	4.0	186	3	US-09-248-796A-12158	Sequence 12158, A
c 383	6	4.0	189	3	US-09-134-000C-3378	Sequence 3378, Ap
384	6	4.0	189	3	US-09-248-796A-8597	Sequence 8597, Ap
c 385	6	4.0	189	3	US-09-248-796A-13621	Sequence 13621, A
386	6	4.0	190	3	US-09-513-999C-23294	Sequence 23294, A
387	6	4.0	192	3	US-09-489-039A-7126	Sequence 7126, Ap
388	6	4.0	195	3	US-09-328-352-644	Sequence 644, App
389	6	4.0	195	3	US-09-540-236-509	Sequence 509, App
390	6	4.0	196	3	US-09-270-767-27150	Sequence 27150, A
391	6	4.0	201	3	US-09-640-211A-456	Sequence 456, App
392	6	4.0	204	3	US-09-543-681A-3703	Sequence 3703, Ap
393	6	4.0	213	3	US-09-513-999C-34308	Sequence 34308, A
c 394	6	4.0	219	3	US-09-401-064-133	Sequence 133, App
c 395	6	4.0	219	3	US-09-248-796A-12324	Sequence 12324, A
c 396	6	4.0	226	3	US-09-270-767-25231	Sequence 25231, A
c 397	6	4.0	228	3	US-09-583-110-504	Sequence 504, App
398	6	4.0	228	3	US-09-248-796A-9611	Sequence 9611, Ap
c 399	6	4.0	229	3	US-09-513-999C-12936	Sequence 12936, A
c 400	6	4.0	239	3	US-09-513-999C-3326	Sequence 3326, Ap
c 401	6	4.0	243	3	US-09-513-999C-11619	Sequence 11619, A
c 402	6	4.0	243	3	US-10-125-258-120	Sequence 120, App
403	6	4.0	246	3	US-09-484-906-3	Sequence 3, Appli
c 404	6	4.0	247	3	US-09-016-434-771	Sequence 771, App
c 405	6	4.0	248	3	US-09-195-106-11	Sequence 11, Appl
c 406	6	4.0	249	3	US-09-107-433-1012	Sequence 1012, Ap
c 407	6	4.0	249	3	US-09-902-540-4694	Sequence 4694, Ap
408	6	4.0	252	3	US-08-906-769-98	Sequence 98, Appl
409	6	4.0	252	3	US-08-906-616-98	Sequence 98, Appl
410	6	4.0	252	3	US-08-817-795-98	Sequence 98, Appl
411	6	4.0	252	3	US-08-639-075A-98	Sequence 98, Appl
412	6	4.0	252	3	US-09-012-431-98	Sequence 98, Appl
413	6	4.0	252	3	US-09-012-692-98	Sequence 98, Appl
414	6	4.0	252	3	US-08-906-613-98	Sequence 98, Appl
415	6	4.0	252	3	US-09-270-767-2843	Sequence 2843, Ap
416	6	4.0	252	3	US-09-270-767-18125	Sequence 18125, A
417	6	4.0	252	6	PCT-US95-14442A-98	Sequence 98, Appl
c 418	6	4.0	256	3	US-09-513-999C-15822	Sequence 15822, A
c 419	6	4.0	258	3	US-09-513-999C-26204	Sequence 26204, A
420	6	4.0	270	3	US-09-621-976-11226	Sequence 11226, A
421	6	4.0	271	3	US-09-513-999C-21595	Sequence 21595, A
422	6	4.0	273	3	US-09-583-110-2542	Sequence 2542, Ap
423	6	4.0	273	3	US-09-107-433-1483	Sequence 1483, Ap
424	6	4.0	276	3	US-09-023-082A-81	Sequence 81, Appl
425	6	4.0	276	3	US-09-248-998-81	Sequence 81, Appl
426	6	4.0	276	3	US-09-489-039A-7135	Sequence 7135, Ap
427	6	4.0	276	3	US-09-610-651-81	Sequence 81, Appl
428	6	4.0	276	3	US-09-248-796A-10344	Sequence 10344, A
429	6	4.0	276	3	US-09-345-373-81	Sequence 81, Appl
430	6	4.0	276	3	US-10-075-446-81	Sequence 81, Appl
c 431	6	4.0	284	3	US-09-313-294A-5334	Sequence 5334, Ap
432	6	4.0	285	3	US-09-248-796A-3910	Sequence 3910, Ap
c 433	6	4.0	285	3	US-09-248-796A-7658	Sequence 7658, Ap
434	6	4.0	289	3	US-09-313-294A-6645	Sequence 6645, Ap
c 435	6	4.0	294	3	US-09-313-294A-4236	Sequence 4236, Ap
436	6	4.0	294	3	US-09-513-999C-21677	Sequence 21677, A
437	6	4.0	295	3	US-09-313-294A-4305	Sequence 4305, Ap
438	6	4.0	295	3	US-09-313-294A-7009	Sequence 7009, Ap
c 439	6	4.0	300	3	US-09-489-039A-2448	Sequence 2448, Ap
c 440	6	4.0	307	3	US-09-854-133-663	Sequence 663, App
441	6	4.0	308	3	US-09-513-999C-21934	Sequence 21934, A
c 442	6	4.0	309	3	US-09-270-767-7193	Sequence 7193, Ap
c 443	6	4.0	309	3	US-09-270-767-22475	Sequence 22475, A
444	6	4.0	315	3	US-09-614-221A-71	Sequence 71, Appl
c 445	6	4.0	321	3	US-09-195-106-4	Sequence 4, Appli
446	6	4.0	321	3	US-09-248-796A-3225	Sequence 3225, Ap
447	6	4.0	332	3	US-09-188-930-83	Sequence 83, Appl
448	6	4.0	332	3	US-09-312-283C-83	Sequence 83, Appl
449	6	4.0	335	3	US-09-513-999C-11476	Sequence 11476, A
450	6	4.0	339	3	US-10-101-464A-244	Sequence 244, App
451	6	4.0	344	3	US-09-702-705-658	Sequence 658, App
452	6	4.0	344	3	US-09-736-457-658	Sequence 658, App
453	6	4.0	344	3	US-09-614-124B-658	Sequence 658, App
454	6	4.0	344	3	US-09-671-325-658	Sequence 658, App
455	6	4.0	344	3	US-09-589-184-658	Sequence 658, App
456	6	4.0	344	3	US-09-658-824-658	Sequence 658, App
c 457	6	4.0	344	3	US-09-513-999C-2920	Sequence 2920, Ap
c 458	6	4.0	344	3	US-09-513-999C-23641	Sequence 23641, A
459	6	4.0	344	3	US-10-017-754-658	Sequence 658, App
460	6	4.0	344	3	US-09-651-563-658	Sequence 658, App
461	6	4.0	344	3	US-09-519-642-658	Sequence 658, App
462	6	4.0	345	3	US-09-710-279-2297	Sequence 2297, Ap
c 463	6	4.0	346	3	US-09-513-999C-31898	Sequence 31898, A
464	6	4.0	351	3	US-09-614-221A-312	Sequence 312, App
465	6	4.0	354	3	US-09-134-001C-2769	Sequence 2769, Ap
466	6	4.0	356	3	US-09-640-211A-1951	Sequence 1951, Ap
467	6	4.0	357	3	US-09-023-082A-79	Sequence 79, Appl
468	6	4.0	357	3	US-09-248-998-79	Sequence 79, Appl
469	6	4.0	357	3	US-09-610-651-79	Sequence 79, Appl
470	6	4.0	357	3	US-09-345-373-79	Sequence 79, Appl
471	6	4.0	357	3	US-10-075-446-79	Sequence 79, Appl
472	6	4.0	359	3	US-09-621-976-10224	Sequence 10224, A
c 473	6	4.0	360	2	US-08-967-101-97	Sequence 97, Appl
c 474	6	4.0	360	2	US-08-592-541-97	Sequence 97, Appl
c 475	6	4.0	360	3	US-09-124-698-97	Sequence 97, Appl
c 476	6	4.0	360	3	US-09-127-480-97	Sequence 97, Appl
c 477	6	4.0	360	3	US-08-496-841C-97	Sequence 97, Appl
c 478	6	4.0	360	3	US-09-124-523-97	Sequence 97, Appl
c 479	6	4.0	360	3	US-09-636-796A-97	Sequence 97, Appl
c 480	6	4.0	360	3	US-08-431-048F-97	Sequence 97, Appl
481	6	4.0	360	3	US-09-902-540-2822	Sequence 2822, Ap
482	6	4.0	361	3	US-09-590-759-110	Sequence 110, App
483	6	4.0	361	3	US-09-513-999C-11766	Sequence 11766, A
484	6	4.0	361	3	US-09-513-999C-13019	Sequence 13019, A
c 485	6	4.0	362	3	US-09-702-705-940	Sequence 940, App
c 486	6	4.0	362	3	US-09-736-457-940	Sequence 940, App
c 487	6	4.0	362	3	US-09-614-124B-940	Sequence 940, App
c 488	6	4.0	362	3	US-09-671-325-940	Sequence 940, App
c 489	6	4.0	362	3	US-09-658-824-940	Sequence 940, App
c 490	6	4.0	362	3	US-10-017-754-940	Sequence 940, App
c 491	6	4.0	362	3	US-09-651-563-940	Sequence 940, App
c 492	6	4.0	363	3	US-09-107-532A-1445	Sequence 1445, Ap
493	6	4.0	368	3	US-09-621-976-759	Sequence 759, App
494	6	4.0	369	3	US-09-621-976-875	Sequence 875, App
495	6	4.0	369	3	US-09-621-976-905	Sequence 905, App
496	6	4.0	370	3	US-08-956-171E-4077	Sequence 4077, Ap
497	6	4.0	370	3	US-09-621-976-711	Sequence 711, App
498	6	4.0	370	3	US-08-781-986A-4077	Sequence 4077, Ap
499	6	4.0	372	3	US-09-855-288-7	Sequence 7, Appli
500	6	4.0	373	3	US-09-621-976-12356	Sequence 12356, A
501	6	4.0	376	3	US-09-621-976-822	Sequence 822, App
502	6	4.0	378	3	US-09-621-976-789	Sequence 789, App
503	6	4.0	380	3	US-09-270-767-29325	Sequence 29325, A
504	6	4.0	381	3	US-09-270-767-6684	Sequence 6684, Ap
505	6	4.0	381	3	US-09-270-767-21966	Sequence 21966, A
506	6	4.0	384	3	US-09-248-796A-6894	Sequence 6894, Ap
507	6	4.0	385	3	US-09-513-999C-20150	Sequence 20150, A
508	6	4.0	386	3	US-09-513-999C-22547	Sequence 22547, A
c 509	6	4.0	387	3	US-09-195-106-9	Sequence 9, Appli
c 510	6	4.0	387	3	US-09-513-999C-9918	Sequence 9918, Ap
c 511	6	4.0	395	2	US-08-967-101-19	Sequence 19, Appl
c 512	6	4.0	395	2	US-08-592-541-19	Sequence 19, Appl
c 513	6	4.0	395	3	US-09-124-698-19	Sequence 19, Appl
c 514	6	4.0	395	3	US-09-127-480-19	Sequence 19, Appl
c 515	6	4.0	395	3	US-08-496-841C-19	Sequence 19, Appl
c 516	6	4.0	395	3	US-09-124-523-19	Sequence 19, Appl
c 517	6	4.0	395	3	US-09-636-796A-19	Sequence 19, Appl
c 518	6	4.0	395	3	US-08-431-048F-19	Sequence 19, Appl
c 519	6	4.0	399	3	US-09-682-597A-5	Sequence 5, Appli
c 520	6	4.0	399	3	US-09-270-767-31241	Sequence 31241, A

521	6	4.0	400	3	US-09-621-976-709	Sequence 709, App
522	6	4.0	402	3	US-09-023-082A-69	Sequence 69, Appl
523	6	4.0	402	3	US-09-248-998-69	Sequence 69, Appl
524	6	4.0	402	3	US-09-610-651-69	Sequence 69, Appl
c 525	6	4.0	402	3	US-09-513-999C-32041	Sequence 32041, A
526	6	4.0	402	3	US-09-345-373-69	Sequence 69, Appl
527	6	4.0	402	3	US-10-075-446-69	Sequence 69, Appl
c 528	6	4.0	406	3	US-09-195-106-10	Sequence 10, Appl
529	6	4.0	407	3	US-09-270-767-4087	Sequence 4087, Ap
530	6	4.0	407	3	US-09-270-767-19369	Sequence 19369, A
531	6	4.0	408	3	US-09-248-796A-2941	Sequence 2941, Ap
532	6	4.0	408	4	US-09-605-703B-1409	Sequence 1409, Ap
533	6	4.0	408	4	US-09-605-703B-1413	Sequence 1413, Ap
c 534	6	4.0	409	3	US-09-702-705-529	Sequence 529, App
c 535	6	4.0	409	3	US-09-736-457-529	Sequence 529, App
c 536	6	4.0	409	3	US-09-614-124B-529	Sequence 529, App
c 537	6	4.0	409	3	US-09-671-325-529	Sequence 529, App
c 538	6	4.0	409	3	US-09-589-184-529	Sequence 529, App
c 539	6	4.0	409	3	US-09-658-824-529	Sequence 529, App
c 540	6	4.0	409	3	US-10-017-754-529	Sequence 529, App
c 541	6	4.0	409	3	US-09-651-563-529	Sequence 529, App
c 542	6	4.0	409	3	US-09-519-642-529	Sequence 529, App
c 543	6	4.0	410	3	US-09-854-133-352	Sequence 352, App
c 544	6	4.0	411	3	US-09-389-681-309	Sequence 309, App
c 545	6	4.0	411	3	US-09-620-405B-309	Sequence 309, App
c 546	6	4.0	411	3	US-09-252-991A-8167	Sequence 8167, Ap
c 547	6	4.0	411	3	US-09-328-352-4001	Sequence 4001, Ap
c 548	6	4.0	411	3	US-09-339-338-309	Sequence 309, App
c 549	6	4.0	411	3	US-09-433-826B-309	Sequence 309, App
c 550	6	4.0	411	3	US-09-604-287A-309	Sequence 309, App
c 551	6	4.0	411	3	US-09-834-759-309	Sequence 309, App
c 552	6	4.0	411	3	US-09-710-279-911	Sequence 911, App
c 553	6	4.0	411	3	US-09-590-751A-309	Sequence 309, App
c 554	6	4.0	411	3	US-09-551-621-309	Sequence 309, App
c 555	6	4.0	411	3	US-09-551-621A-309	Sequence 309, App
c 556	6	4.0	411	3	US-10-076-622-309	Sequence 309, App
557	6	4.0	412	3	US-09-702-705-1047	Sequence 1047, Ap
558	6	4.0	412	3	US-09-736-457-1047	Sequence 1047, Ap
559	6	4.0	412	3	US-09-614-124B-1047	Sequence 1047, Ap
560	6	4.0	412	3	US-09-671-325-1047	Sequence 1047, Ap
561	6	4.0	412	3	US-09-658-824-1047	Sequence 1047, Ap
562	6	4.0	412	3	US-10-017-754-1047	Sequence 1047, Ap
563	6	4.0	412	3	US-09-651-563-1047	Sequence 1047, Ap
564	6	4.0	414	3	US-09-543-681A-1971	Sequence 1971, Ap
c 565	6	4.0	415	3	US-09-270-767-7569	Sequence 7569, Ap
c 566	6	4.0	415	3	US-09-270-767-22851	Sequence 22851, A
c 567	6	4.0	416	3	US-09-222-575-124	Sequence 124, App
c 568	6	4.0	416	3	US-09-389-681-124	Sequence 124, App
c 569	6	4.0	416	3	US-09-620-405B-124	Sequence 124, App
c 570	6	4.0	416	3	US-09-339-338-124	Sequence 124, App
c 571	6	4.0	416	3	US-09-433-826B-124	Sequence 124, App
c 572	6	4.0	416	3	US-09-604-287A-124	Sequence 124, App
c 573	6	4.0	416	3	US-09-285-480-124	Sequence 124, App
c 574	6	4.0	416	3	US-09-834-759-124	Sequence 124, App
c 575	6	4.0	416	3	US-09-590-751A-124	Sequence 124, App
c 576	6	4.0	416	3	US-09-551-621-124	Sequence 124, App
c 577	6	4.0	416	3	US-09-551-621A-124	Sequence 124, App
c 578	6	4.0	416	3	US-10-076-622-124	Sequence 124, App
579	6	4.0	423	2	US-08-470-179-175	Sequence 175, App
c 580	6	4.0	424	2	US-08-158-189-4	Sequence 4, Appli
581	6	4.0	426	3	US-09-023-082A-95	Sequence 95, Appl
582	6	4.0	426	3	US-09-023-082A-111	Sequence 111, App
583	6	4.0	426	3	US-09-023-082A-119	Sequence 119, App
584	6	4.0	426	3	US-09-023-082A-123	Sequence 123, App
585	6	4.0	426	3	US-09-023-082A-127	Sequence 127, App
586	6	4.0	426	3	US-09-023-082A-131	Sequence 131, App
587	6	4.0	426	3	US-09-023-082A-135	Sequence 135, App
588	6	4.0	426	3	US-09-023-082A-139	Sequence 139, App
589	6	4.0	426	3	US-09-023-082A-145	Sequence 145, App
590	6	4.0	426	3	US-09-218-444-16	Sequence 16, Appl
591	6	4.0	426	3	US-09-218-444-32	Sequence 32, Appl
592	6	4.0	426	3	US-09-248-998-95	Sequence 95, Appl
593	6	4.0	426	3	US-09-248-998-111	Sequence 111, App
594	6	4.0	426	3	US-09-248-998-119	Sequence 119, App
595	6	4.0	426	3	US-09-248-998-123	Sequence 123, App
596	6	4.0	426	3	US-09-248-998-127	Sequence 127, App
597	6	4.0	426	3	US-09-248-998-131	Sequence 131, App
598	6	4.0	426	3	US-09-248-998-135	Sequence 135, App
599	6	4.0	426	3	US-09-248-998-139	Sequence 139, App
600	6	4.0	426	3	US-09-248-998-145	Sequence 145, App
601	6	4.0	426	3	US-09-853-666-16	Sequence 16, Appl
602	6	4.0	426	3	US-09-853-666-32	Sequence 32, Appl
603	6	4.0	426	3	US-09-610-651-95	Sequence 95, Appl
604	6	4.0	426	3	US-09-610-651-111	Sequence 111, App
605	6	4.0	426	3	US-09-610-651-119	Sequence 119, App
606	6	4.0	426	3	US-09-610-651-123	Sequence 123, App
607	6	4.0	426	3	US-09-610-651-127	Sequence 127, App
608	6	4.0	426	3	US-09-610-651-131	Sequence 131, App
609	6	4.0	426	3	US-09-610-651-135	Sequence 135, App
610	6	4.0	426	3	US-09-610-651-139	Sequence 139, App
611	6	4.0	426	3	US-09-610-651-145	Sequence 145, App
612	6	4.0	426	3	US-09-345-373-95	Sequence 95, Appl
613	6	4.0	426	3	US-09-345-373-111	Sequence 111, App
614	6	4.0	426	3	US-09-345-373-119	Sequence 119, App
615	6	4.0	426	3	US-09-345-373-123	Sequence 123, App
616	6	4.0	426	3	US-09-345-373-127	Sequence 127, App
617	6	4.0	426	3	US-09-345-373-131	Sequence 131, App
618	6	4.0	426	3	US-09-345-373-135	Sequence 135, App
619	6	4.0	426	3	US-09-345-373-139	Sequence 139, App
620	6	4.0	426	3	US-09-345-373-145	Sequence 145, App
621	6	4.0	426	3	US-10-075-446-95	Sequence 95, Appl
622	6	4.0	426	3	US-10-075-446-111	Sequence 111, App
623	6	4.0	426	3	US-10-075-446-119	Sequence 119, App
624	6	4.0	426	3	US-10-075-446-123	Sequence 123, App
625	6	4.0	426	3	US-10-075-446-127	Sequence 127, App
626	6	4.0	426	3	US-10-075-446-131	Sequence 131, App
627	6	4.0	426	3	US-10-075-446-135	Sequence 135, App
628	6	4.0	426	3	US-10-075-446-139	Sequence 139, App
629	6	4.0	426	3	US-10-075-446-145	Sequence 145, App
630	6	4.0	428	3	US-09-513-999C-739	Sequence 739, App
631	6	4.0	431	3	US-09-513-999C-8516	Sequence 8516, Ap
632	6	4.0	435	3	US-09-270-767-4320	Sequence 4320, Ap
633	6	4.0	435	3	US-09-270-767-19602	Sequence 19602, A
c 634	6	4.0	441	3	US-09-248-796A-570	Sequence 570, App
635	6	4.0	443	3	US-09-621-976-13818	Sequence 13818, A
636	6	4.0	444	3	US-09-023-082A-67	Sequence 67, Appl
637	6	4.0	444	3	US-09-248-998-67	Sequence 67, Appl
638	6	4.0	444	3	US-09-621-976-8238	Sequence 8238, Ap
639	6	4.0	444	3	US-09-610-651-67	Sequence 67, Appl
640	6	4.0	444	3	US-09-345-373-67	Sequence 67, Appl
641	6	4.0	444	3	US-10-075-446-67	Sequence 67, Appl
c 642	6	4.0	449	3	US-09-856-221-1	Sequence 1, Appli
c 643	6	4.0	450	2	US-08-529-878B-38	Sequence 38, Appl
644	6	4.0	452	3	US-09-621-976-18629	Sequence 18629, A
c 645	6	4.0	452	3	US-09-270-767-1023	Sequence 1023, Ap
c 646	6	4.0	452	3	US-09-270-767-16305	Sequence 16305, A
647	6	4.0	453	3	US-09-191-468-89	Sequence 89, Appl
648	6	4.0	453	3	US-09-191-468-91	Sequence 91, Appl
649	6	4.0	453	3	US-09-191-468-93	Sequence 93, Appl
650	6	4.0	453	3	US-09-191-468-95	Sequence 95, Appl
651	6	4.0	453	3	US-09-191-468-97	Sequence 97, Appl
652	6	4.0	453	3	US-09-191-468-99	Sequence 99, Appl
653	6	4.0	453	3	US-09-191-468-101	Sequence 101, App
c 654	6	4.0	454	3	US-09-621-976-15184	Sequence 15184, A
c 655	6	4.0	456	3	US-09-489-039A-3975	Sequence 3975, Ap
656	6	4.0	456	3	US-09-610-651-173	Sequence 173, App
657	6	4.0	457	3	US-09-270-767-7135	Sequence 7135, Ap
c 658	6	4.0	457	3	US-09-270-767-9928	Sequence 9928, Ap
659	6	4.0	457	3	US-09-270-767-22417	Sequence 22417, A
c 660	6	4.0	457	3	US-09-513-999C-22945	Sequence 22945, A
661	6	4.0	460	3	US-09-280-116-216	Sequence 216, App
c 662	6	4.0	460	3	US-09-621-976-13826	Sequence 13826, A
c 663	6	4.0	460	3	US-09-270-767-5830	Sequence 5830, Ap
c 664	6	4.0	460	3	US-09-270-767-21112	Sequence 21112, A
c 665	6	4.0	462	3	US-09-489-039A-6317	Sequence 6317, Ap
666	6	4.0	462	3	US-09-710-279-2825	Sequence 2825, Ap

	667	6	4.0	465	3	US-09-107-433-589	Sequence 589, App
	668	6	4.0	466	3	US-09-621-976-1443	Sequence 1443, Ap
	669	6	4.0	468	3	US-09-134-001C-288	Sequence 288, App
	670	6	4.0	471	3	US-09-270-767-2995	Sequence 2995, Ap
	671	6	4.0	471	3	US-09-270-767-18277	Sequence 18277, A
	672	6	4.0	474	3	US-09-621-976-3253	Sequence 3253, Ap
c	673	6	4.0	475	3	US-10-178-213-391	Sequence 391, App
c	674	6	4.0	476	3	US-09-270-767-8163	Sequence 8163, Ap
c	675	6	4.0	476	3	US-09-270-767-23445	Sequence 23445, A
	676	6	4.0	476	3	US-09-513-999C-77	Sequence 77, Appl
	677	6	4.0	480	3	US-09-489-039A-2592	Sequence 2592, Ap
	678	6	4.0	481	3	US-09-949-016-52690	Sequence 52690, A
c	679	6	4.0	483	3	US-09-821-687-1	Sequence 1, Appli
c	680	6	4.0	486	3	US-09-060-756-220	Sequence 220, App
c	681	6	4.0	486	3	US-09-670-314-220	Sequence 220, App
	682	6	4.0	486	3	US-09-489-039A-4501	Sequence 4501, Ap
	683	6	4.0	486	3	US-09-248-796A-8398	Sequence 8398, Ap
	684	6	4.0	487	3	US-09-602-787A-419	Sequence 419, App
	685	6	4.0	490	2	US-08-133-711-43	Sequence 43, Appl
c	686	6	4.0	490	3	US-09-621-976-15213	Sequence 15213, A
	687	6	4.0	492	3	US-09-134-000C-1371	Sequence 1371, Ap
c	688	6	4.0	492	3	US-09-270-767-5138	Sequence 5138, Ap
c	689	6	4.0	492	3	US-09-270-767-20420	Sequence 20420, A
	690	6	4.0	494	3	US-09-389-681-290	Sequence 290, App
	691	6	4.0	494	3	US-09-620-405B-290	Sequence 290, App
	692	6	4.0	494	3	US-09-339-338-290	Sequence 290, App
	693	6	4.0	494	3	US-09-433-826B-290	Sequence 290, App
	694	6	4.0	494	3	US-09-604-287A-290	Sequence 290, App
	695	6	4.0	494	3	US-09-834-759-290	Sequence 290, App
	696	6	4.0	494	3	US-09-590-751A-290	Sequence 290, App
	697	6	4.0	494	3	US-09-551-621-290	Sequence 290, App
	698	6	4.0	494	3	US-09-551-621A-290	Sequence 290, App
	699	6	4.0	494	3	US-10-076-622-290	Sequence 290, App
	700	6	4.0	495	3	US-09-621-976-1430	Sequence 1430, Ap
	701	6	4.0	496	3	US-09-280-116-252	Sequence 252, App
	702	6	4.0	498	3	US-09-270-767-1036	Sequence 1036, Ap
	703	6	4.0	498	3	US-09-270-767-16318	Sequence 16318, A
c	704	6	4.0	498	3	US-09-872-051-7	Sequence 7, Appli
c	705	6	4.0	500	3	US-09-621-976-3868	Sequence 3868, Ap
c	706	6	4.0	500	3	US-09-270-767-5755	Sequence 5755, Ap
c	707	6	4.0	500	3	US-09-270-767-21037	Sequence 21037, A
	708	6	4.0	504	3	US-09-107-532A-2642	Sequence 2642, Ap
	709	6	4.0	507	3	US-09-949-016-3468	Sequence 3468, Ap
	710	6	4.0	507	4	US-09-605-703B-2283	Sequence 2283, Ap
c	711	6	4.0	513	3	US-09-702-705-314	Sequence 314, App
c	712	6	4.0	513	3	US-09-736-457-314	Sequence 314, App
c	713	6	4.0	513	3	US-09-328-352-3911	Sequence 3911, Ap
c	714	6	4.0	513	3	US-09-614-124B-314	Sequence 314, App
c	715	6	4.0	513	3	US-09-671-325-314	Sequence 314, App
c	716	6	4.0	513	3	US-09-589-184-314	Sequence 314, App
c	717	6	4.0	513	3	US-09-270-767-6571	Sequence 6571, Ap
c	718	6	4.0	513	3	US-09-270-767-21853	Sequence 21853, A
c	719	6	4.0	513	3	US-09-658-824-314	Sequence 314, App
c	720	6	4.0	513	3	US-10-017-754-314	Sequence 314, App
c	721	6	4.0	513	3	US-09-651-563-314	Sequence 314, App
c	722	6	4.0	513	3	US-09-519-642-314	Sequence 314, App
	723	6	4.0	514	2	US-08-705-625-1	Sequence 1, Appli
	724	6	4.0	514	3	US-09-220-574-1	Sequence 1, Appli
c	725	6	4.0	515	3	US-09-496-694B-231	Sequence 231, App
	726	6	4.0	515	3	US-09-517-790-1	Sequence 1, Appli
c	727	6	4.0	515	3	US-09-918-186A-231	Sequence 231, App
	728	6	4.0	516	3	US-09-023-082A-115	Sequence 115, App
	729	6	4.0	516	3	US-09-248-998-115	Sequence 115, App
	730	6	4.0	516	3	US-09-610-651-115	Sequence 115, App
	731	6	4.0	516	3	US-09-345-373-115	Sequence 115, App
	732	6	4.0	516	3	US-10-075-446-115	Sequence 115, App
	733	6	4.0	517	3	US-09-533-559-2196	Sequence 2196, Ap
	734	6	4.0	519	3	US-08-714-918-67	Sequence 67, Appl
	735	6	4.0	519	3	US-09-265-315-67	Sequence 67, Appl
	736	6	4.0	519	3	US-09-265-315-67	Sequence 67, Appl
	737	6	4.0	519	3	US-09-266-417-67	Sequence 67, Appl
	738	6	4.0	519	3	US-09-702-705-1313	Sequence 1313, Ap
	739	6	4.0	519	3	US-09-736-457-1313	Sequence 1313, Ap
	740	6	4.0	519	3	US-09-528-709-67	Sequence 67, Appl
	741	6	4.0	519	3	US-09-614-124B-1313	Sequence 1313, Ap
	742	6	4.0	519	3	US-09-527-745-67	Sequence 67, Appl
	743	6	4.0	519	3	US-09-671-325-1313	Sequence 1313, Ap
	744	6	4.0	519	3	US-09-658-824-1313	Sequence 1313, Ap
	745	6	4.0	519	3	US-10-017-754-1313	Sequence 1313, Ap
	746	6	4.0	519	3	US-09-651-563-1313	Sequence 1313, Ap
c	747	6	4.0	520	3	US-09-702-705-277	Sequence 277, App
c	748	6	4.0	520	3	US-09-736-457-277	Sequence 277, App
c	749	6	4.0	520	3	US-09-614-124B-277	Sequence 277, App
c	750	6	4.0	520	3	US-09-671-325-277	Sequence 277, App
c	751	6	4.0	520	3	US-09-589-184-277	Sequence 277, App
c	752	6	4.0	520	3	US-09-658-824-277	Sequence 277, App
c	753	6	4.0	520	3	US-10-017-754-277	Sequence 277, App
c	754	6	4.0	520	3	US-09-651-563-277	Sequence 277, App
c	755	6	4.0	520	3	US-09-519-642-277	Sequence 277, App
c	756	6	4.0	522	3	US-09-248-796A-11526	Sequence 11526, A
	757	6	4.0	523	3	US-09-517-790-4	Sequence 4, Appli
	758	6	4.0	524	3	US-09-854-133-638	Sequence 638, App
	759	6	4.0	525	3	US-09-023-082A-42	Sequence 42, Appl
	760	6	4.0	525	3	US-09-023-082A-54	Sequence 54, Appl
	761	6	4.0	525	3	US-09-023-082A-65	Sequence 65, Appl
	762	6	4.0	525	3	US-09-023-082A-83	Sequence 83, Appl
	763	6	4.0	525	3	US-09-023-082A-84	Sequence 84, Appl
c	764	6	4.0	525	3	US-09-107-532A-45	Sequence 45, Appl
	765	6	4.0	525	3	US-09-248-998-42	Sequence 42, Appl
	766	6	4.0	525	3	US-09-248-998-54	Sequence 54, Appl
	767	6	4.0	525	3	US-09-248-998-65	Sequence 65, Appl
	768	6	4.0	525	3	US-09-248-998-83	Sequence 83, Appl
	769	6	4.0	525	3	US-09-248-998-84	Sequence 84, Appl
	770	6	4.0	525	3	US-09-610-651-42	Sequence 42, Appl
	771	6	4.0	525	3	US-09-610-651-54	Sequence 54, Appl
	772	6	4.0	525	3	US-09-610-651-65	Sequence 65, Appl
	773	6	4.0	525	3	US-09-610-651-83	Sequence 83, Appl
	774	6	4.0	525	3	US-09-610-651-84	Sequence 84, Appl
	775	6	4.0	525	3	US-09-345-373-42	Sequence 42, Appl
	776	6	4.0	525	3	US-09-345-373-54	Sequence 54, Appl
	777	6	4.0	525	3	US-09-345-373-65	Sequence 65, Appl
	778	6	4.0	525	3	US-09-345-373-83	Sequence 83, Appl
	779	6	4.0	525	3	US-09-345-373-84	Sequence 84, Appl
	780	6	4.0	525	3	US-10-075-446-42	Sequence 42, Appl
	781	6	4.0	525	3	US-10-075-446-54	Sequence 54, Appl
	782	6	4.0	525	3	US-10-075-446-65	Sequence 65, Appl
	783	6	4.0	525	3	US-10-075-446-83	Sequence 83, Appl
	784	6	4.0	525	3	US-10-075-446-84	Sequence 84, Appl
	785	6	4.0	526	2	US-08-686-878A-35	Sequence 35, Appl
	786	6	4.0	526	3	US-09-175-928-35	Sequence 35, Appl
	787	6	4.0	528	3	US-09-621-976-14771	Sequence 14771, A
c	788	6	4.0	531	3	US-09-248-796A-11087	Sequence 11087, A
	789	6	4.0	536	3	US-09-517-790-5	Sequence 5, Appli
	790	6	4.0	536	3	US-09-270-767-7565	Sequence 7565, Ap
	791	6	4.0	536	3	US-09-270-767-22847	Sequence 22847, A
	792	6	4.0	537	3	US-09-621-976-15676	Sequence 15676, A
	793	6	4.0	537	3	US-09-583-110-722	Sequence 722, App
c	794	6	4.0	542	3	US-09-270-767-8846	Sequence 8846, Ap
c	795	6	4.0	542	3	US-09-270-767-24128	Sequence 24128, A
	796	6	4.0	543	3	US-09-533-559-2354	Sequence 2354, Ap
c	797	6	4.0	546	3	US-09-437-054A-13	Sequence 13, Appl
	798	6	4.0	546	3	US-09-252-991A-15256	Sequence 15256, A
	799	6	4.0	546	3	US-09-489-039A-4341	Sequence 4341, Ap
c	800	6	4.0	552	3	US-09-307-973A-5	Sequence 5, Appli
	801	6	4.0	552	3	US-09-248-796A-3866	Sequence 3866, Ap
	802	6	4.0	553	3	US-08-943-731-84	Sequence 84, Appl
	803	6	4.0	555	3	US-09-023-082A-29	Sequence 29, Appl
	804	6	4.0	555	3	US-09-248-998-29	Sequence 29, Appl
c	805	6	4.0	555	3	US-09-134-000C-3370	Sequence 3370, Ap
c	806	6	4.0	555	3	US-09-621-976-10492	Sequence 10492, A
	807	6	4.0	555	3	US-09-610-651-29	Sequence 29, Appl
	808	6	4.0	555	3	US-09-345-373-29	Sequence 29, Appl
	809	6	4.0	555	3	US-10-075-446-29	Sequence 29, Appl
	810	6	4.0	558	2	US-08-233-788A-60	Sequence 60, Appl
c	811	6	4.0	558	3	US-09-270-767-6272	Sequence 6272, Ap
c	812	6	4.0	558	3	US-09-270-767-21554	Sequence 21554, A

813	6	4.0	558	9	5486454-1	Patent No. 5486454
c 814	6	4.0	564	3	US-09-252-991A-5360	Sequence 5360, Ap
815	6	4.0	564	3	US-09-134-000C-1021	Sequence 1021, Ap
816	6	4.0	567	3	US-08-642-274D-41	Sequence 41, Appl
817	6	4.0	567	3	US-08-952-014C-41	Sequence 41, Appl
818	6	4.0	567	3	US-09-107-433-1528	Sequence 1528, Ap
819	6	4.0	567	3	US-09-949-016-52691	Sequence 52691, A
820	6	4.0	571	3	US-09-328-111-42	Sequence 42, Appl
c 821	6	4.0	572	3	US-09-949-016-5243	Sequence 5243, Ap
822	6	4.0	574	3	US-09-533-559-319	Sequence 319, App
823	6	4.0	578	3	US-09-533-559-1570	Sequence 1570, Ap
c 824	6	4.0	579	3	US-09-248-796A-4194	Sequence 4194, Ap
825	6	4.0	582	3	US-08-998-416-621	Sequence 621, App
c 826	6	4.0	582	3	US-09-248-796A-1511	Sequence 1511, Ap
827	6	4.0	589	2	US-08-700-013B-22	Sequence 22, Appl
828	6	4.0	589	2	US-08-700-013B-24	Sequence 24, Appl
829	6	4.0	591	3	US-09-533-559-2226	Sequence 2226, Ap
c 830	6	4.0	601	3	US-09-949-016-19111	Sequence 19111, A
c 831	6	4.0	601	3	US-09-949-016-19591	Sequence 19591, A
832	6	4.0	601	3	US-09-949-016-20240	Sequence 20240, A
833	6	4.0	601	3	US-09-949-016-20954	Sequence 20954, A
834	6	4.0	601	3	US-09-949-016-20955	Sequence 20955, A
835	6	4.0	601	3	US-09-949-016-21588	Sequence 21588, A
c 836	6	4.0	601	3	US-09-949-016-22613	Sequence 22613, A
837	6	4.0	601	3	US-09-949-016-24378	Sequence 24378, A
c 838	6	4.0	601	3	US-09-949-016-24400	Sequence 24400, A
c 839	6	4.0	601	3	US-09-949-016-24401	Sequence 24401, A
c 840	6	4.0	601	3	US-09-949-016-24402	Sequence 24402, A
c 841	6	4.0	601	3	US-09-949-016-24403	Sequence 24403, A
c 842	6	4.0	601	3	US-09-949-016-25029	Sequence 25029, A
c 843	6	4.0	601	3	US-09-949-016-25303	Sequence 25303, A
844	6	4.0	601	3	US-09-949-016-28029	Sequence 28029, A
c 845	6	4.0	601	3	US-09-949-016-28322	Sequence 28322, A
c 846	6	4.0	601	3	US-09-949-016-28371	Sequence 28371, A
847	6	4.0	601	3	US-09-949-016-28529	Sequence 28529, A
848	6	4.0	601	3	US-09-949-016-28699	Sequence 28699, A
849	6	4.0	601	3	US-09-949-016-28959	Sequence 28959, A
850	6	4.0	601	3	US-09-949-016-28960	Sequence 28960, A
851	6	4.0	601	3	US-09-949-016-28961	Sequence 28961, A
852	6	4.0	601	3	US-09-949-016-28985	Sequence 28985, A
853	6	4.0	601	3	US-09-949-016-30794	Sequence 30794, A
c 854	6	4.0	601	3	US-09-949-016-31770	Sequence 31770, A
c 855	6	4.0	601	3	US-09-949-016-31915	Sequence 31915, A
c 856	6	4.0	601	3	US-09-949-016-31916	Sequence 31916, A
857	6	4.0	601	3	US-09-949-016-32945	Sequence 32945, A
858	6	4.0	601	3	US-09-949-016-33708	Sequence 33708, A
859	6	4.0	601	3	US-09-949-016-33709	Sequence 33709, A
860	6	4.0	601	3	US-09-949-016-35212	Sequence 35212, A
861	6	4.0	601	3	US-09-949-016-35213	Sequence 35213, A
c 862	6	4.0	601	3	US-09-949-016-35671	Sequence 35671, A
c 863	6	4.0	601	3	US-09-949-016-35672	Sequence 35672, A
c 864	6	4.0	601	3	US-09-949-016-35786	Sequence 35786, A
c 865	6	4.0	601	3	US-09-949-016-35787	Sequence 35787, A
c 866	6	4.0	601	3	US-09-949-016-35788	Sequence 35788, A
c 867	6	4.0	601	3	US-09-949-016-35789	Sequence 35789, A
c 868	6	4.0	601	3	US-09-949-016-35864	Sequence 35864, A
c 869	6	4.0	601	3	US-09-949-016-35865	Sequence 35865, A
c 870	6	4.0	601	3	US-09-949-016-35866	Sequence 35866, A
c 871	6	4.0	601	3	US-09-949-016-35867	Sequence 35867, A
c 872	6	4.0	601	3	US-09-949-016-35941	Sequence 35941, A
c 873	6	4.0	601	3	US-09-949-016-35942	Sequence 35942, A
c 874	6	4.0	601	3	US-09-949-016-35943	Sequence 35943, A
c 875	6	4.0	601	3	US-09-949-016-35944	Sequence 35944, A
c 876	6	4.0	601	3	US-09-949-016-36028	Sequence 36028, A
c 877	6	4.0	601	3	US-09-949-016-36029	Sequence 36029, A
c 878	6	4.0	601	3	US-09-949-016-36030	Sequence 36030, A
c 879	6	4.0	601	3	US-09-949-016-36031	Sequence 36031, A
c 880	6	4.0	601	3	US-09-949-016-36227	Sequence 36227, A
881	6	4.0	601	3	US-09-949-016-37475	Sequence 37475, A
882	6	4.0	601	3	US-09-949-016-38161	Sequence 38161, A
883	6	4.0	601	3	US-09-949-016-38615	Sequence 38615, A
884	6	4.0	601	3	US-09-949-016-38616	Sequence 38616, A
c 885	6	4.0	601	3	US-09-949-016-38727	Sequence 38727, A
c 886	6	4.0	601	3	US-09-949-016-39083	Sequence 39083, A
887	6	4.0	601	3	US-09-949-016-39687	Sequence 39687, A
c 888	6	4.0	601	3	US-09-949-016-39705	Sequence 39705, A
c 889	6	4.0	601	3	US-09-949-016-40471	Sequence 40471, A
c 890	6	4.0	601	3	US-09-949-016-40529	Sequence 40529, A
c 891	6	4.0	601	3	US-09-949-016-40530	Sequence 40530, A
c 892	6	4.0	601	3	US-09-949-016-41132	Sequence 41132, A
893	6	4.0	601	3	US-09-949-016-42446	Sequence 42446, A
c 894	6	4.0	601	3	US-09-949-016-42918	Sequence 42918, A
895	6	4.0	601	3	US-09-949-016-43096	Sequence 43096, A
896	6	4.0	601	3	US-09-949-016-43097	Sequence 43097, A
897	6	4.0	601	3	US-09-949-016-44718	Sequence 44718, A
898	6	4.0	601	3	US-09-949-016-46442	Sequence 46442, A
c 899	6	4.0	601	3	US-09-949-016-46579	Sequence 46579, A
c 900	6	4.0	601	3	US-09-949-016-46580	Sequence 46580, A
c 901	6	4.0	601	3	US-09-949-016-46931	Sequence 46931, A
902	6	4.0	601	3	US-09-949-016-47641	Sequence 47641, A
903	6	4.0	601	3	US-09-949-016-49577	Sequence 49577, A
904	6	4.0	601	3	US-09-949-016-50218	Sequence 50218, A
c 905	6	4.0	601	3	US-09-949-016-51923	Sequence 51923, A
c 906	6	4.0	601	3	US-09-949-016-53043	Sequence 53043, A
c 907	6	4.0	601	3	US-09-949-016-53044	Sequence 53044, A
c 908	6	4.0	601	3	US-09-949-016-53045	Sequence 53045, A
c 909	6	4.0	601	3	US-09-949-016-53046	Sequence 53046, A
910	6	4.0	601	3	US-09-949-016-53773	Sequence 53773, A
911	6	4.0	601	3	US-09-949-016-54208	Sequence 54208, A
912	6	4.0	601	3	US-09-949-016-54243	Sequence 54243, A
c 913	6	4.0	601	3	US-09-949-016-54768	Sequence 54768, A
c 914	6	4.0	601	3	US-09-949-016-55350	Sequence 55350, A
915	6	4.0	601	3	US-09-949-016-55649	Sequence 55649, A
916	6	4.0	601	3	US-09-949-016-55672	Sequence 55672, A
917	6	4.0	601	3	US-09-949-016-56564	Sequence 56564, A
918	6	4.0	601	3	US-09-949-016-56565	Sequence 56565, A
919	6	4.0	601	3	US-09-949-016-56566	Sequence 56566, A
c 920	6	4.0	601	3	US-09-949-016-57605	Sequence 57605, A
c 921	6	4.0	601	3	US-09-949-016-58090	Sequence 58090, A
c 922	6	4.0	601	3	US-09-949-016-58091	Sequence 58091, A
c 923	6	4.0	601	3	US-09-949-016-58328	Sequence 58328, A
924	6	4.0	601	3	US-09-949-016-58571	Sequence 58571, A
925	6	4.0	601	3	US-09-949-016-59311	Sequence 59311, A
c 926	6	4.0	601	3	US-09-949-016-60294	Sequence 60294, A
927	6	4.0	601	3	US-09-949-016-60966	Sequence 60966, A
c 928	6	4.0	601	3	US-09-949-016-61611	Sequence 61611, A
c 929	6	4.0	601	3	US-09-949-016-61733	Sequence 61733, A
c 930	6	4.0	601	3	US-09-949-016-62084	Sequence 62084, A
c 931	6	4.0	601	3	US-09-949-016-62085	Sequence 62085, A
932	6	4.0	601	3	US-09-949-016-63452	Sequence 63452, A
933	6	4.0	601	3	US-09-949-016-63715	Sequence 63715, A
934	6	4.0	601	3	US-09-949-016-63721	Sequence 63721, A
935	6	4.0	601	3	US-09-949-016-63727	Sequence 63727, A
936	6	4.0	601	3	US-09-949-016-63733	Sequence 63733, A
c 937	6	4.0	601	3	US-09-949-016-63868	Sequence 63868, A
c 938	6	4.0	601	3	US-09-949-016-63869	Sequence 63869, A
c 939	6	4.0	601	3	US-09-949-016-63943	Sequence 63943, A
c 940	6	4.0	601	3	US-09-949-016-63944	Sequence 63944, A
941	6	4.0	601	3	US-09-949-016-67673	Sequence 67673, A
942	6	4.0	601	3	US-09-949-016-68358	Sequence 68358, A
c 943	6	4.0	601	3	US-09-949-016-68497	Sequence 68497, A
c 944	6	4.0	601	3	US-09-949-016-69141	Sequence 69141, A
945	6	4.0	601	3	US-09-949-016-69509	Sequence 69509, A
c 946	6	4.0	601	3	US-09-949-016-70587	Sequence 70587, A
947	6	4.0	601	3	US-09-949-016-70665	Sequence 70665, A
948	6	4.0	601	3	US-09-949-016-70666	Sequence 70666, A
949	6	4.0	601	3	US-09-949-016-70667	Sequence 70667, A
950	6	4.0	601	3	US-09-949-016-70668	Sequence 70668, A
951	6	4.0	601	3	US-09-949-016-71169	Sequence 71169, A
952	6	4.0	601	3	US-09-949-016-71274	Sequence 71274, A
953	6	4.0	601	3	US-09-949-016-71275	Sequence 71275, A
c 954	6	4.0	601	3	US-09-949-016-72527	Sequence 72527, A
955	6	4.0	601	3	US-09-949-016-72655	Sequence 72655, A
956	6	4.0	601	3	US-09-949-016-74228	Sequence 74228, A
957	6	4.0	601	3	US-09-949-016-74248	Sequence 74248, A
958	6	4.0	601	3	US-09-949-016-74268	Sequence 74268, A

959	6	4.0	601	3	US-09-949-016-74288	Sequence 74288, A
960	6	4.0	601	3	US-09-949-016-74393	Sequence 74393, A
961	6	4.0	601	3	US-09-949-016-74697	Sequence 74697, A
962	6	4.0	601	3	US-09-949-016-74896	Sequence 74896, A
963	6	4.0	601	3	US-09-949-016-75095	Sequence 75095, A
964	6	4.0	601	3	US-09-949-016-75294	Sequence 75294, A
965	6	4.0	601	3	US-09-949-016-75493	Sequence 75493, A
c 966	6	4.0	601	3	US-09-949-016-75779	Sequence 75779, A
967	6	4.0	601	3	US-09-949-016-76013	Sequence 76013, A
968	6	4.0	601	3	US-09-949-016-76014	Sequence 76014, A
969	6	4.0	601	3	US-09-949-016-76015	Sequence 76015, A
c 970	6	4.0	601	3	US-09-949-016-76590	Sequence 76590, A
971	6	4.0	601	3	US-09-949-016-77277	Sequence 77277, A
972	6	4.0	601	3	US-09-949-016-77278	Sequence 77278, A
973	6	4.0	601	3	US-09-949-016-77693	Sequence 77693, A
c 974	6	4.0	601	3	US-09-949-016-78620	Sequence 78620, A
c 975	6	4.0	601	3	US-09-949-016-78621	Sequence 78621, A
c 976	6	4.0	601	3	US-09-949-016-78622	Sequence 78622, A
977	6	4.0	601	3	US-09-949-016-78678	Sequence 78678, A
c 978	6	4.0	601	3	US-09-949-016-79062	Sequence 79062, A
c 979	6	4.0	601	3	US-09-949-016-79063	Sequence 79063, A
c 980	6	4.0	601	3	US-09-949-016-79064	Sequence 79064, A
c 981	6	4.0	601	3	US-09-949-016-79065	Sequence 79065, A
c 982	6	4.0	601	3	US-09-949-016-79775	Sequence 79775, A
983	6	4.0	601	3	US-09-949-016-80034	Sequence 80034, A
c 984	6	4.0	601	3	US-09-949-016-81069	Sequence 81069, A
c 985	6	4.0	601	3	US-09-949-016-81620	Sequence 81620, A
986	6	4.0	601	3	US-09-949-016-81738	Sequence 81738, A
987	6	4.0	601	3	US-09-949-016-81739	Sequence 81739, A
988	6	4.0	601	3	US-09-949-016-81740	Sequence 81740, A
c 989	6	4.0	601	3	US-09-949-016-81911	Sequence 81911, A
990	6	4.0	601	3	US-09-949-016-82616	Sequence 82616, A
c 991	6	4.0	601	3	US-09-949-016-82946	Sequence 82946, A
c 992	6	4.0	601	3	US-09-949-016-82947	Sequence 82947, A
993	6	4.0	601	3	US-09-949-016-83868	Sequence 83868, A
994	6	4.0	601	3	US-09-949-016-84097	Sequence 84097, A
c 995	6	4.0	601	3	US-09-949-016-84109	Sequence 84109, A
996	6	4.0	601	3	US-09-949-016-84393	Sequence 84393, A
c 997	6	4.0	601	3	US-09-949-016-84607	Sequence 84607, A
998	6	4.0	601	3	US-09-949-016-86666	Sequence 86666, A
999	6	4.0	601	3	US-09-949-016-86966	Sequence 86966, A
c1000	6	4.0	601	3	US-09-949-016-88754	Sequence 88754, A

ALIGNMENTS

```
RESULT 1
US-09-445-160B-8
; Sequence 8, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;  PUBLICATION INFORMATION:
US-09-445-160B-8

Alignment Scores:
Pred. No.:              1.32e-112      Length:          363
Score:                  120.00         Matches:         120
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            80.5%          Indels:          0
DB:                     3              Gaps:            0

US-10-758-902-9 (1-149) x US-09-445-160B-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361

RESULT 2
US-09-445-160B-5
; Sequence 5, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 5
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;  PUBLICATION INFORMATION:
US-09-445-160B-5

Alignment Scores:
Pred. No.:              4e-13          Length:          65
Score:                  21.00          Matches:         21
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            14.1%          Indels:          0
DB:                     3              Gaps:            0

US-10-758-902-9 (1-149) x US-09-445-160B-5 (1-65)
```

```
Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63
```

RESULT 3
US-09-949-016-146445
; Sequence 146445, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 146445
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-146445

Alignment Scores:

Pred. No.:	41	Length:	601
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-9 (1-149) x US-09-949-016-146445 (1-601)

```
Qy         55 ThrSerLysLysThrValLysVal 62
              ||||||||||||||||||||||
Db        243 ACAAGCAAAAAAACAGTAAAGGTC 266
```

RESULT 4
US-09-322-357-71/c
; Sequence 71, Application US/09322357
; Patent No. 6593104
; GENERAL INFORMATION:
; APPLICANT: STONE, EDWIN M.
; APPLICANT: SHEFFIELD, VAL C.
; TITLE OF INVENTION: MACULAR DEGENERATION DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: UIA-018.03
; CURRENT APPLICATION NUMBER: US/09/322,357
; CURRENT FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: "n" bases at various positions throughout the sequence may
; OTHER INFORMATION: be a, t, c, g, other or unknown
US-09-322-357-71

Alignment Scores:

Pred. No.:	63.3	Length:	979
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-9 (1-149) x US-09-322-357-71 (1-979)

```
Qy         33 GlnLeuProValThrLeuGlnThr 40
              |||||||||||||||||||||||
Db        947 CAGTTACCGGTAACTCTGCAAACT 924
```

RESULT 5
US-09-949-016-15854
; Sequence 15854, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15854
; LENGTH: 55195
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15854

Alignment Scores:

Pred. No.:	2.29e+03	Length:	55195
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-9 (1-149) x US-09-949-016-15854 (1-55195)

```
Qy         55 ThrSerLysLysThrValLysVal 62
              ||||||||||||||||||||||
Db      46778 ACAAGCAAAAAAACAGTAAAGGTC 46801
```

RESULT 6
US-09-949-016-16136/c
; Sequence 16136, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16136
; LENGTH: 76247
; TYPE: DNA
; ORGANISM: Human
; FEATURE:

```
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(76247)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16136

Alignment Scores:
Pred. No.:              3.06e+03        Length:         76247
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-949-016-16136 (1-76247)

Qy        101 GlyValThrAsnArgValThrLeu 108
              ||||||||||||||||||||||||
Db       2645 GGAGTCACAAACCGGGTCACCCTA 2622

RESULT 7
US-09-445-160B-3
; Sequence 3, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;   NAME/KEY:
;   LOCATION: 3, 9, 21
;   OTHER INFORMATION: a, c, g or t
;  PUBLICATION INFORMATION:
US-09-445-160B-3

Alignment Scores:
Pred. No.:              23.1            Length:         23
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-445-160B-3 (1-23)

Qy          9 GlyGluAlaTyrGluTyrPro 15
              |||||||||||||||||||||
Db          1 GGNGARGCNTAYGARTAYCCN 21

RESULT 8
US-09-445-160B-4/c
; Sequence 4, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 4
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;   NAME/KEY:
;   LOCATION: 3, 6, 12, 15
;   OTHER INFORMATION: a, c, g or t
;  PUBLICATION INFORMATION:
US-09-445-160B-4

Alignment Scores:
Pred. No.:              23.1            Length:         23
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-445-160B-4 (1-23)

Qy         23 AsnGluLeuAlaLysGlyThr 29
              |||||||||||||||||||||
Db         23 AAYGARCTNGCNAARGGNACN 3

RESULT 9
US-09-445-160B-6
; Sequence 6, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 6
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;  PUBLICATION INFORMATION:
US-09-445-160B-6

Alignment Scores:
Pred. No.:              24.8            Length:         25
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-445-160B-6 (1-25)
```

```
Qy         17 PheIleGlnAspLeuArgAsn 23
              |||||||||||||||||||||
Db          3 TTTATACAAGATTTGCGCAAC 23

RESULT 10
US-09-513-999C-13250
; Sequence 13250, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 13250
;   LENGTH: 222
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 69
;   OTHER INFORMATION: s=g or c
US-09-513-999C-13250

Alignment Scores:
Pred. No.:              174           Length:        222
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.7%          Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-9 (1-149) x US-09-513-999C-13250 (1-222)

Qy         60 ValLysValAlaIleAspVal 66
              ||||||||||||||||||||
Db        167 GTGAAGGTGGCCATTGACGTC 187

RESULT 11
US-09-539-333D-62
; Sequence 62, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 62
;   LENGTH: 279
;   TYPE: DNA
;   ORGANISM: Pan troglodytes
US-09-539-333D-62

Alignment Scores:
Pred. No.:              213           Length:        279
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.7%          Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-9 (1-149) x US-09-539-333D-62 (1-279)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||||
Db        104 ACTACAACCAGCAAAAAGACC 124

RESULT 12
US-09-539-333D-85
; Sequence 85, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 85
;   LENGTH: 279
;   TYPE: DNA
;   ORGANISM: Gorilla gorilla
US-09-539-333D-85

Alignment Scores:
Pred. No.:              213           Length:        279
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
```

```
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-539-333D-85 (1-279)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        104 ACTACAACCAGCAAAAAGACC 124

RESULT 13
US-09-539-333D-74
; Sequence 74, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 74
;   LENGTH: 280
;   TYPE: DNA
;   ORGANISM: Hylobates sp.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 256,260,263,267,272
;   OTHER INFORMATION: n=a, g, c or t
US-09-539-333D-74

Alignment Scores:
Pred. No.:              213             Length:         280
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-539-333D-74 (1-280)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        104 ACTACAACCAGCAAAAAGACC 124

RESULT 14
US-09-539-333D-97
; Sequence 97, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 97
;   LENGTH: 280
;   TYPE: DNA
;   ORGANISM: Pongo pygmaeus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 267
;   OTHER INFORMATION: n=a, g, c or t
US-09-539-333D-97

Alignment Scores:
Pred. No.:              213             Length:         280
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-539-333D-97 (1-280)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        104 ACTACAACCAGCAAAAAGACC 124

RESULT 15
US-09-539-333D-109
; Sequence 109, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
```

```
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 109
;   LENGTH: 280
;   TYPE: DNA
;   ORGANISM: Macaca mulatta
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 268
;   OTHER INFORMATION: n=a, g, c or t
US-09-539-333D-109

Alignment Scores:
Pred. No.:                213           Length:          280
Score:                    7.00          Matches:         7
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              4.7%          Indels:          0
DB:                       3             Gaps:            0

US-10-758-902-9 (1-149) x US-09-539-333D-109 (1-280)

Qy          53 ThrThrThrSerLysLysThr 59
               |||||||||||||||||||
Db         104 ACTACAACCAGCAAAAAGACC 124

RESULT 16
US-09-134-001C-1851/c
; Sequence 1851, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1851
;   LENGTH: 339
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1851

Alignment Scores:
Pred. No.:                253           Length:          339
Score:                    7.00          Matches:         7
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              4.7%          Indels:          0
DB:                       3             Gaps:            0

US-10-758-902-9 (1-149) x US-09-134-001C-1851 (1-339)

Qy          52 IleThrThrThrSerLysLys 58
               |||||||||||||||||||
Db          48 ATTACAACAACTTCCAAGAAA 28

RESULT 17
US-09-513-999C-2553/c
; Sequence 2553, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 2553
;   LENGTH: 356
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 191..355
US-09-513-999C-2553

Alignment Scores:
Pred. No.:                264           Length:          356
Score:                    7.00          Matches:         7
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              4.7%          Indels:          0
DB:                       3             Gaps:            0

US-10-758-902-9 (1-149) x US-09-513-999C-2553 (1-356)

Qy         116 LysLeuValAsnAlaAlaLys 122
               ||||||||||||||||||||
Db         291 AAATTAGTTAATGCAGCAAAG 271

RESULT 18
US-09-539-333D-60
; Sequence 60, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
```

```
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 60
;   LENGTH: 388
;   TYPE: DNA
;   ORGANISM: Pan troglodytes
US-09-539-333D-60

Alignment Scores:
Pred. No.:              285          Length:         388
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            4.7%         Indels:         0
DB:                     3            Gaps:           0

US-10-758-902-9 (1-149) x US-09-539-333D-60 (1-388)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 19
US-09-539-333D-83
; Sequence 83, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 83
;   LENGTH: 388
;   TYPE: DNA
;   ORGANISM: Gorilla gorilla
US-09-539-333D-83

Alignment Scores:
Pred. No.:              285          Length:         388
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            4.7%         Indels:         0
DB:                     3            Gaps:           0

US-10-758-902-9 (1-149) x US-09-539-333D-83 (1-388)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 20
US-09-539-333D-72
; Sequence 72, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 72
;   LENGTH: 389
;   TYPE: DNA
;   ORGANISM: Hylobates sp.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 365,369,372,376,381
;   OTHER INFORMATION: n=a, g, c or t
US-09-539-333D-72

Alignment Scores:
Pred. No.:              286          Length:         389
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            4.7%         Indels:         0
DB:                     3            Gaps:           0

US-10-758-902-9 (1-149) x US-09-539-333D-72 (1-389)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 21
US-09-539-333D-95
; Sequence 95, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
```

```
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 95
;   LENGTH: 389
;   TYPE: DNA
;   ORGANISM: Pongo pygmaeus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 376
;   OTHER INFORMATION: n=a, g, c or t
US-09-539-333D-95

Alignment Scores:
Pred. No.:              286           Length:         389
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-9 (1-149) x US-09-539-333D-95 (1-389)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 22
US-09-539-333D-107
; Sequence 107, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 107
;   LENGTH: 389
;   TYPE: DNA
;   ORGANISM: Macaca mulatta
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 377
;   OTHER INFORMATION: n=a, g, c or t
US-09-539-333D-107

Alignment Scores:
Pred. No.:              286           Length:         389
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-9 (1-149) x US-09-539-333D-107 (1-389)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 23
US-10-101-464A-391/c
; Sequence 391, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
;  APPLICANT: Strabala, Timothy
;  APPLICANT:  Nieuwenhuizen, Nicolaas
;  APPLICANT:  Higgins, Colleen M.
;  TITLE OF INVENTION: Compositions Isolated from Plant Cells
;  TITLE OF INVENTION:  and Their Use in the Modification of Plant Cell Signaling
;  FILE REFERENCE: 11000.1020c2
;  CURRENT APPLICATION NUMBER: US/10/101,464A
;  CURRENT FILING DATE:  2002-03-18
;  PRIOR APPLICATION NUMBER: 09/704,302
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: 09/228,986
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/162,866
;  PRIOR FILING DATE: 1999-11-01
;  PRIOR APPLICATION NUMBER: PCT/US00/00724
;  PRIOR FILING DATE: 2000-01-11
;  NUMBER OF SEQ ID NOS: 989
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 391
;   LENGTH: 432
;   TYPE: DNA
;   ORGANISM: Pinus radiata
US-10-101-464A-391

Alignment Scores:
Pred. No.:              314           Length:         432
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
```

```
Query Match:            4.7%        Indels:        0
DB:                     3           Gaps:          0

US-10-758-902-9 (1-149) x US-10-101-464A-391 (1-432)

Qy         90 ValProThrValAlaThrSer 96
              ||||||||||||||||||||||
Db        402 GTTCCCACTGTAGCCACTTCT 382

RESULT 24
US-09-134-001C-1924/c
; Sequence 1924, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1924
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1924

Alignment Scores:
Pred. No.:              316         Length:        435
Score:                  7.00        Matches:       7
Percent Similarity:     100.0%      Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:            4.7%        Indels:        0
DB:                     3           Gaps:          0

US-10-758-902-9 (1-149) x US-09-134-001C-1924 (1-435)

Qy         52 IleThrThrThrSerLysLys 58
              ||||||||||||||||||||||
Db         77 ATTACAACAACTTCCAAGAAA 57

RESULT 25
US-09-060-756-98
; Sequence 98, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
;  APPLICANT: Cole, Stewart
;  APPLICANT: Buchrieser-Brosch, Roland
;  APPLICANT: Gordon, Stephen
;  APPLICANT: Billault, Alain
;  TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;  TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;  TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;  FILE REFERENCE: 3495-0169
;  CURRENT APPLICATION NUMBER: US/09/060,756
;  CURRENT FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 743
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
;   LENGTH: 439
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-060-756-98

Alignment Scores:
Pred. No.:              318         Length:        439
Score:                  7.00        Matches:       7
Percent Similarity:     100.0%      Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:            4.7%        Indels:        0
DB:                     3           Gaps:          0

US-10-758-902-9 (1-149) x US-09-060-756-98 (1-439)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db        364 CAGGATCTCAGAAACGAGCTG 384

RESULT 26
US-09-670-314-98
; Sequence 98, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
;  APPLICANT: Cole, Stewart
;  APPLICANT:  Buchrieser-Brosch, Roland
;  APPLICANT:  Gordon, Stephen
;  APPLICANT:  Billault, Alain
;  TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;  TITLE OF INVENTION:  THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;  TITLE OF INVENTION:  LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;  FILE REFERENCE: 3495-0169
;  CURRENT APPLICATION NUMBER: US/09/670,314
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 09/060,756
;  PRIOR FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 743
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
;   LENGTH: 439
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-670-314-98

Alignment Scores:
Pred. No.:              318         Length:        439
Score:                  7.00        Matches:       7
Percent Similarity:     100.0%      Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:            4.7%        Indels:        0
DB:                     3           Gaps:          0

US-10-758-902-9 (1-149) x US-09-670-314-98 (1-439)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db        364 CAGGATCTCAGAAACGAGCTG 384

RESULT 27
US-09-280-116-194/c
; Sequence 194, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
;  FILE REFERENCE: 5800-24, 035800/176965
;  CURRENT APPLICATION NUMBER: US/09/280,116A
;  CURRENT FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 194
;   LENGTH: 461
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: angiotensin-converting enzyme
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(461)
;   OTHER INFORMATION: n = a, t, c or g
US-09-280-116-194

Alignment Scores:
```

```
Pred. No.:              333             Length:         461
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-280-116-194 (1-461)

Qy         78 TrpAspGlyLysAspArgAla 84
              |||||||||||||||||||||
Db        362 TGGGATGGGAAAGACAGGGCA 342

RESULT 28
US-09-270-767-13340
; Sequence 13340, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13340
;   LENGTH: 491
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-13340

Alignment Scores:
Pred. No.:              352             Length:         491
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-270-767-13340 (1-491)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||||
Db        303 ACAACAACATCAAAAAAACA 323

RESULT 29
US-09-489-039A-2605/c
; Sequence 2605, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 2605
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2605

Alignment Scores:
Pred. No.:              411             Length:         585
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-489-039A-2605 (1-585)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||||
Db        122 ACTACTACCAGCAAAAAAACC 102

RESULT 30
US-09-949-016-21916
; Sequence 21916, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21916
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-21916

Alignment Scores:
Pred. No.:              421             Length:         601
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-949-016-21916 (1-601)

Qy         32 CysGlnLeuProValThrLeu 38
              ||||||||||||||||||||
Db        512 TGTCAATTACCAGTCACCTTG 532

RESULT 31
US-09-949-016-21917
; Sequence 21917, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21917
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-21917

Alignment Scores:
Pred. No.:              421             Length:         601
Score:                  7.00            Matches:        7
```

```
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            4.7%            Indels:        0
DB:                     3               Gaps:          0

US-10-758-902-9 (1-149) x US-09-949-016-21917 (1-601)

Qy         32 CysGlnLeuProValThrLeu 38
              ||||||||||||||||||||
Db        199 TGTCAATTACCAGTCACCTTG 219

RESULT 32
US-09-949-016-47002
; Sequence 47002, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47002
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-47002

Alignment Scores:
Pred. No.:              421             Length:        601
Score:                  7.00            Matches:       7
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            4.7%            Indels:        0
DB:                     3               Gaps:          0

US-10-758-902-9 (1-149) x US-09-949-016-47002 (1-601)

Qy         61 LysValAlaIleAspValThr 67
              |||||||||||||||||||||
Db        197 AAAGTGGCCATTGATGTTACT 217

RESULT 33
US-09-949-016-60813
; Sequence 60813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60813
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-60813

Alignment Scores:
Pred. No.:              421             Length:        601
Score:                  7.00            Matches:       7
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            4.7%            Indels:        0
DB:                     3               Gaps:          0

US-10-758-902-9 (1-149) x US-09-949-016-60813 (1-601)

Qy         29 ThrProValCysGlnLeuPro 35
              |||||||||||||||||||
Db        104 ACACCAGTCTGTCAATTACCC 124

RESULT 34
US-09-949-016-84175
; Sequence 84175, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84175
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-84175

Alignment Scores:
Pred. No.:              421             Length:        601
Score:                  7.00            Matches:       7
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            4.7%            Indels:        0
DB:                     3               Gaps:          0

US-10-758-902-9 (1-149) x US-09-949-016-84175 (1-601)

Qy         32 CysGlnLeuProValThrLeu 38
              ||||||||||||||||||||
Db        512 TGTCAATTACCAGTCACCTTG 532

RESULT 35
US-09-949-016-84176
; Sequence 84176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84176
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-84176

Alignment Scores:
Pred. No.:              421           Length:         601
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-9 (1-149) x US-09-949-016-84176 (1-601)

Qy         32 CysGlnLeuProValThrLeu 38
              ||||||||||||||||||||
Db        199 TGTCAATTACCAGTCACCTTG 219

RESULT 36
US-09-949-016-94256/c
; Sequence 94256, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94256
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-94256

Alignment Scores:
Pred. No.:              421           Length:         601
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-9 (1-149) x US-09-949-016-94256 (1-601)

Qy        125 ArgLysAspLeuGluLeuGly 131
              ||||||||||||||||||||
Db        510 AGGAAAGATCTAGAGCTGGGG 490

RESULT 37
US-09-949-016-94257/c
; Sequence 94257, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94257
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-94257

Alignment Scores:
Pred. No.:              421           Length:         601
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-9 (1-149) x US-09-949-016-94257 (1-601)

Qy        125 ArgLysAspLeuGluLeuGly 131
              ||||||||||||||||||||
Db        435 AGGAAAGATCTAGAGCTGGGG 415

RESULT 38
US-09-949-016-95022/c
; Sequence 95022, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95022
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-95022

Alignment Scores:
Pred. No.:              421           Length:         601
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-9 (1-149) x US-09-949-016-95022 (1-601)

Qy         44 AspLysArgPheValLeuVal 50
              ||||||||||||||||||||
Db        192 GACAAGAGGTTTGTCCTGGTG 172

RESULT 39
US-09-949-016-95134/c
; Sequence 95134, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

```
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95134
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-95134

Alignment Scores:
Pred. No.:              421           Length:        601
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.7%          Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-9 (1-149) x US-09-949-016-95134 (1-601)

Qy         44 AspLysArgPheValLeuVal 50
              |||||||||||||||||||||
Db        192 GACAAGAGGTTTGTCCTGGTG 172

RESULT 40
US-09-949-016-120534
; Sequence 120534, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 120534
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-120534

Alignment Scores:
Pred. No.:              421           Length:        601
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.7%          Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-9 (1-149) x US-09-949-016-120534 (1-601)

Qy         92 ThrValAlaThrSerLysLeu 98
              |||||||||||||||||||||
Db        278 ACCGTGGCCACCTCCAAATTG 298


Search completed: February 20, 2006, 03:09:12
Job time : 244.413 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 01:12:01 ; Search time 1109.59 Seconds
(without alignments)
1110.442 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 149
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygappp 60.0 , Ygapext 60.0
Fgappp 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 1

Total number of hits satisfying chosen parameters: 19572506

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/absa/ABSSWEB_spool/US10758902/runat_17022006_160840_4165/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=oligo.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05p
-USER=US10758902_@CGN_1_1_2064_@runat_17022006_160840_4165 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	122	81.9	2404	10	US-11-084-080-15	Sequence 15, Appl
2	122	81.9	2404	10	US-11-084-080-19	Sequence 19, Appl
3	122	81.9	2404	10	US-11-084-080-21	Sequence 21, Appl
4	122	81.9	2404	10	US-11-084-080-23	Sequence 23, Appl
5	122	81.9	2431	10	US-11-084-080-27	Sequence 27, Appl
6	120	80.5	363	8	US-10-758-902-8	Sequence 8, Appli
7	21	14.1	65	8	US-10-758-902-5	Sequence 5, Appli
c 8	9	6.0	289190	7	US-10-322-281-115	Sequence 115, App
9	8	5.4	201	7	US-10-741-601-14447	Sequence 14447, A
10	8	5.4	416	4	US-09-925-065A-47024	Sequence 47024, A
c 11	8	5.4	487	4	US-09-925-065A-630179	Sequence 630179,
c 12	8	5.4	524	5	US-10-027-632-281750	Sequence 281750,
c 13	8	5.4	524	6	US-10-027-632-281750	Sequence 281750,
14	8	5.4	565	4	US-09-925-065A-325312	Sequence 325312,
15	8	5.4	622	4	US-09-925-065A-787599	Sequence 787599,
16	8	5.4	759	8	US-10-767-795-223	Sequence 223, App
c 17	8	5.4	979	9	US-10-619-761-71	Sequence 71, Appl
18	8	5.4	1549	7	US-10-437-963-47027	Sequence 47027, A
c 19	8	5.4	1560	8	US-10-425-115-183970	Sequence 183970,
c 20	8	5.4	1686	7	US-10-425-114-32782	Sequence 32782, A
c 21	8	5.4	1879	7	US-10-425-114-32261	Sequence 32261, A
c 22	8	5.4	2000	3	US-09-938-842A-5069	Sequence 5069, Ap
c 23	8	5.4	2000	3	US-09-938-842A-5069	Sequence 5069, Ap
c 24	8	5.4	2187	7	US-10-425-114-30640	Sequence 30640, A
c 25	8	5.4	2443	4	US-09-925-065A-694362	Sequence 694362,
26	8	5.4	2772	6	US-10-252-157-398	Sequence 398, App
c 27	8	5.4	2797	8	US-10-425-115-87686	Sequence 87686, A
c 28	8	5.4	6413	7	US-10-221-714A-84	Sequence 84, Appl
c 29	8	5.4	6413	7	US-10-433-793-30	Sequence 30, Appl
c 30	8	5.4	12648	7	US-10-741-601-5652	Sequence 5652, Ap
c 31	8	5.4	16363	7	US-10-668-767-9	Sequence 9, Appli
32	8	5.4	31657	7	US-10-741-601-5690	Sequence 5690, Ap
33	8	5.4	35076	5	US-10-087-192-1261	Sequence 1261, Ap
34	8	5.4	41309	7	US-10-741-601-5771	Sequence 5771, Ap
c 35	8	5.4	55606	6	US-10-085-117-133	Sequence 133, App
36	8	5.4	63693	7	US-10-741-601-5650	Sequence 5650, Ap
c 37	8	5.4	77038	6	US-10-085-117-151	Sequence 151, App
c 38	8	5.4	92247	5	US-10-087-192-628	Sequence 628, App
39	8	5.4	3673778	6	US-10-312-841-1	Sequence 1, Appli
c 40	7	4.7	23	8	US-10-758-902-3	Sequence 3, Appli
c 41	7	4.7	25	7	US-10-719-956-347414	Sequence 347414,
c 42	7	4.7	25	7	US-10-719-956-347416	Sequence 347416,
43	7	4.7	25	8	US-10-758-902-6	Sequence 6, Appli
c 44	7	4.7	25	8	US-10-719-900-557809	Sequence 557809,
45	7	4.7	25	8	US-10-719-900-848834	Sequence 848834,
c 46	7	4.7	25	10	US-11-036-317-212714	Sequence 212714,
c 47	7	4.7	25	10	US-11-036-317-329781	Sequence 329781,
c 48	7	4.7	25	10	US-11-036-317-381661	Sequence 381661,
c 49	7	4.7	25	10	US-11-036-317-484022	Sequence 484022,
c 50	7	4.7	25	10	US-11-036-317-607049	Sequence 607049,
c 51	7	4.7	25	10	US-11-036-317-720121	Sequence 720121,
52	7	4.7	36	10	US-11-084-080-125	Sequence 125, App
53	7	4.7	90	6	US-10-071-645-5	Sequence 5, Appli
c 54	7	4.7	117	7	US-10-242-535A-3517	Sequence 3517, Ap
c 55	7	4.7	117	7	US-10-085-783A-3517	Sequence 3517, Ap
c 56	7	4.7	149	7	US-10-767-701-27360	Sequence 27360, A
57	7	4.7	150	7	US-10-242-535A-51509	Sequence 51509, A
58	7	4.7	150	7	US-10-085-783A-51509	Sequence 51509, A
c 59	7	4.7	153	8	US-10-425-115-136227	Sequence 136227,
c 60	7	4.7	166	3	US-09-864-761-29906	Sequence 29906, A
c 61	7	4.7	175	6	US-10-369-493-29234	Sequence 29234, A
62	7	4.7	176	6	US-10-029-386-17632	Sequence 17632, A
c 63	7	4.7	201	7	US-10-741-601-7707	Sequence 7707, Ap
c 64	7	4.7	201	7	US-10-741-601-7916	Sequence 7916, Ap
65	7	4.7	201	8	US-10-719-993-45568	Sequence 45568, A
66	7	4.7	201	8	US-10-719-993-45569	Sequence 45569, A
c 67	7	4.7	201	8	US-10-741-600-21500	Sequence 21500, A
c 68	7	4.7	201	8	US-10-741-600-21709	Sequence 21709, A
c 69	7	4.7	201	8	US-10-741-600-65936	Sequence 65936, A
c 70	7	4.7	226	8	US-10-425-115-86450	Sequence 86450, A
71	7	4.7	230	7	US-10-424-599-128909	Sequence 128909,
c 72	7	4.7	231	7	US-10-282-122A-29222	Sequence 29222, A
c 73	7	4.7	234	7	US-10-282-122A-29907	Sequence 29907, A
74	7	4.7	236	5	US-10-201-310-29	Sequence 29, Appl
c 75	7	4.7	254	7	US-10-424-599-18718	Sequence 18718, A
c 76	7	4.7	262	8	US-10-425-115-127119	Sequence 127119,
77	7	4.7	263	5	US-10-201-310-25	Sequence 25, Appl
78	7	4.7	264	3	US-09-864-761-23908	Sequence 23908, A
79	7	4.7	264	3	US-09-864-761-31252	Sequence 31252, A
80	7	4.7	264	3	US-09-864-761-31316	Sequence 31316, A

	81	7	4.7	265	6	US-10-029-386-21728	Sequence 21728, A
	82	7	4.7	279	6	US-10-147-603-62	Sequence 62, Appl
	83	7	4.7	279	6	US-10-147-603-85	Sequence 85, Appl
	84	7	4.7	280	6	US-10-147-603-74	Sequence 74, Appl
	85	7	4.7	280	6	US-10-147-603-97	Sequence 97, Appl
	86	7	4.7	280	6	US-10-147-603-109	Sequence 109, App
c	87	7	4.7	282	6	US-10-369-493-39332	Sequence 39332, A
c	88	7	4.7	282	6	US-10-369-493-39707	Sequence 39707, A
c	89	7	4.7	282	6	US-10-369-493-40059	Sequence 40059, A
	90	7	4.7	291	3	US-09-835-976B-94	Sequence 94, Appl
	91	7	4.7	297	3	US-09-796-692-323	Sequence 323, App
	92	7	4.7	297	3	US-09-796-692-6932	Sequence 6932, Ap
	93	7	4.7	297	5	US-10-040-862-323	Sequence 323, App
	94	7	4.7	297	5	US-10-040-862-6932	Sequence 6932, Ap
	95	7	4.7	297	6	US-10-057-475B-323	Sequence 323, App
	96	7	4.7	297	6	US-10-057-475B-6932	Sequence 6932, Ap
	97	7	4.7	297	6	US-10-154-884B-323	Sequence 323, App
	98	7	4.7	297	6	US-10-154-884B-6932	Sequence 6932, Ap
	99	7	4.7	297	8	US-10-764-324-323	Sequence 323, App
	100	7	4.7	297	8	US-10-764-324-6932	Sequence 6932, Ap
	101	7	4.7	301	6	US-10-029-386-21713	Sequence 21713, A
c	102	7	4.7	311	7	US-10-437-963-69055	Sequence 69055, A
	103	7	4.7	318	8	US-10-674-124A-24998	Sequence 24998, A
	104	7	4.7	336	4	US-09-925-065A-350812	Sequence 350812,
c	105	7	4.7	337	8	US-10-425-115-117253	Sequence 117253,
	106	7	4.7	350	6	US-10-074-024-149	Sequence 149, App
	107	7	4.7	356	5	US-10-201-310-20	Sequence 20, Appl
	108	7	4.7	356	8	US-10-425-115-25826	Sequence 25826, A
	109	7	4.7	368	8	US-10-357-930-8739	Sequence 8739, Ap
	110	7	4.7	387	8	US-10-357-930-38664	Sequence 38664, A
	111	7	4.7	388	6	US-10-147-603-60	Sequence 60, Appl
	112	7	4.7	388	6	US-10-147-603-83	Sequence 83, Appl
	113	7	4.7	389	6	US-10-147-603-72	Sequence 72, Appl
	114	7	4.7	389	6	US-10-147-603-95	Sequence 95, Appl
	115	7	4.7	389	6	US-10-147-603-107	Sequence 107, App
	116	7	4.7	393	7	US-10-282-122A-18468	Sequence 18468, A
c	117	7	4.7	396	5	US-10-102-524-950	Sequence 950, App
c	118	7	4.7	399	8	US-10-425-115-44011	Sequence 44011, A
c	119	7	4.7	410	4	US-09-925-065A-367811	Sequence 367811,
	120	7	4.7	415	9	US-10-450-763-11674	Sequence 11674, A
	121	7	4.7	415	9	US-10-450-763-19363	Sequence 19363, A
c	122	7	4.7	422	7	US-10-425-114-4877	Sequence 4877, Ap
	123	7	4.7	423	3	US-09-864-864-256	Sequence 256, App
c	124	7	4.7	431	8	US-10-357-930-18350	Sequence 18350, A
c	125	7	4.7	432	5	US-10-101-464A-391	Sequence 391, App
c	126	7	4.7	432	9	US-10-864-252-391	Sequence 391, App
c	127	7	4.7	435	7	US-10-724-972A-2514	Sequence 2514, Ap
	128	7	4.7	439	6	US-10-259-678-98	Sequence 98, Appl
c	129	7	4.7	440	5	US-10-027-632-53595	Sequence 53595, A
c	130	7	4.7	440	6	US-10-027-632-53595	Sequence 53595, A
	131	7	4.7	446	3	US-09-969-034-604	Sequence 604, App
	132	7	4.7	460	7	US-10-242-535A-7712	Sequence 7712, Ap
	133	7	4.7	460	7	US-10-085-783A-7712	Sequence 7712, Ap
	134	7	4.7	463	3	US-09-864-761-1412	Sequence 1412, Ap
c	135	7	4.7	471	3	US-09-732-627A-4376	Sequence 4376, Ap
c	136	7	4.7	472	3	US-09-764-869-187	Sequence 187, App
c	137	7	4.7	472	5	US-10-091-504-187	Sequence 187, App
c	138	7	4.7	472	6	US-10-227-577-187	Sequence 187, App
	139	7	4.7	473	7	US-10-242-535A-42029	Sequence 42029, A
	140	7	4.7	473	7	US-10-085-783A-42029	Sequence 42029, A
c	141	7	4.7	475	3	US-09-864-761-5698	Sequence 5698, Ap
	142	7	4.7	476	6	US-10-211-160-15	Sequence 15, Appl
	143	7	4.7	476	6	US-10-051-681A-15	Sequence 15, Appl
	144	7	4.7	482	7	US-10-437-963-52322	Sequence 52322, A
c	145	7	4.7	483	3	US-09-908-744-38	Sequence 38, Appl
	146	7	4.7	484	3	US-09-834-975-29	Sequence 29, Appl
c	147	7	4.7	488	5	US-10-027-632-73197	Sequence 73197, A
c	148	7	4.7	488	5	US-10-027-632-73198	Sequence 73198, A
c	149	7	4.7	488	5	US-10-027-632-73199	Sequence 73199, A
c	150	7	4.7	488	5	US-10-027-632-91923	Sequence 91923, A
c	151	7	4.7	488	5	US-10-027-632-317857	Sequence 317857,
c	152	7	4.7	488	6	US-10-027-632-73197	Sequence 73197, A
c	153	7	4.7	488	6	US-10-027-632-73198	Sequence 73198, A
c	154	7	4.7	488	6	US-10-027-632-73199	Sequence 73199, A
c	155	7	4.7	488	6	US-10-027-632-91923	Sequence 91923, A
c	156	7	4.7	488	6	US-10-027-632-317857	Sequence 317857,
c	157	7	4.7	489	7	US-10-621-901-987	Sequence 987, App
	158	7	4.7	496	3	US-09-918-995-14903	Sequence 14903, A
c	159	7	4.7	498	7	US-10-621-901-50	Sequence 50, Appl
c	160	7	4.7	498	8	US-10-357-930-48164	Sequence 48164, A
	161	7	4.7	506	8	US-10-425-115-124636	Sequence 124636,
	162	7	4.7	507	6	US-10-029-386-11098	Sequence 11098, A
c	163	7	4.7	509	4	US-09-925-065A-304102	Sequence 304102,
c	164	7	4.7	509	4	US-09-925-065A-304103	Sequence 304103,
	165	7	4.7	512	3	US-09-864-761-14788	Sequence 14788, A
c	166	7	4.7	512	6	US-10-146-860-11	Sequence 11, Appl
	167	7	4.7	513	3	US-09-834-975-641	Sequence 641, App
	168	7	4.7	513	9	US-10-450-763-10148	Sequence 10148, A
	169	7	4.7	515	4	US-09-925-065A-787865	Sequence 787865,
c	170	7	4.7	515	5	US-10-027-632-86496	Sequence 86496, A
c	171	7	4.7	515	6	US-10-027-632-86496	Sequence 86496, A
	172	7	4.7	516	5	US-10-060-036-1051	Sequence 1051, Ap
c	173	7	4.7	516	6	US-10-125-968-362	Sequence 362, App
c	174	7	4.7	522	8	US-10-363-345A-25921	Sequence 25921, A
	175	7	4.7	522	8	US-10-363-345A-25922	Sequence 25922, A
c	176	7	4.7	522	9	US-10-363-483A-25921	Sequence 25921, A
	177	7	4.7	522	9	US-10-363-483A-25922	Sequence 25922, A
	178	7	4.7	524	4	US-09-925-065A-455365	Sequence 455365,
	179	7	4.7	526	4	US-09-925-065A-435174	Sequence 435174,
	180	7	4.7	528	3	US-09-918-995-22303	Sequence 22303, A
c	181	7	4.7	528	9	US-10-487-901-6913	Sequence 6913, Ap
	182	7	4.7	530	4	US-09-925-065A-623014	Sequence 623014,
	183	7	4.7	530	7	US-10-437-963-32360	Sequence 32360, A
c	184	7	4.7	534	4	US-09-925-065A-51074	Sequence 51074, A
	185	7	4.7	539	4	US-09-925-065A-766112	Sequence 766112,
	186	7	4.7	539	4	US-09-925-065A-766113	Sequence 766113,
c	187	7	4.7	539	5	US-10-027-632-4919	Sequence 4919, Ap
c	188	7	4.7	539	6	US-10-027-632-4919	Sequence 4919, Ap
c	189	7	4.7	540	4	US-09-925-065A-752884	Sequence 752884,
c	190	7	4.7	541	4	US-09-925-065A-205681	Sequence 205681,
c	191	7	4.7	543	3	US-09-814-353-13970	Sequence 13970, A
	192	7	4.7	545	3	US-09-864-408A-1719	Sequence 1719, Ap
c	193	7	4.7	545	5	US-10-027-632-47754	Sequence 47754, A
c	194	7	4.7	545	6	US-10-027-632-47754	Sequence 47754, A
	195	7	4.7	548	4	US-09-925-065A-810826	Sequence 810826,
	196	7	4.7	549	7	US-10-282-122A-41913	Sequence 41913, A
	197	7	4.7	550	4	US-09-925-065A-137135	Sequence 137135,
	198	7	4.7	551	4	US-09-925-065A-123248	Sequence 123248,
c	199	7	4.7	552	8	US-10-363-345A-29547	Sequence 29547, A
	200	7	4.7	552	8	US-10-363-345A-29548	Sequence 29548, A
c	201	7	4.7	552	9	US-10-363-483A-29547	Sequence 29547, A
	202	7	4.7	552	9	US-10-363-483A-29548	Sequence 29548, A
c	203	7	4.7	555	3	US-09-918-995-26126	Sequence 26126, A
c	204	7	4.7	555	4	US-09-925-065A-643449	Sequence 643449,
	205	7	4.7	557	3	US-09-814-353-2660	Sequence 2660, Ap
	206	7	4.7	557	3	US-09-814-353-8993	Sequence 8993, Ap
	207	7	4.7	557	5	US-10-201-310-17	Sequence 17, Appl
	208	7	4.7	559	4	US-09-925-065A-846418	Sequence 846418,
c	209	7	4.7	561	4	US-09-925-065A-760512	Sequence 760512,
c	210	7	4.7	562	4	US-09-925-065A-124610	Sequence 124610,
	211	7	4.7	565	4	US-09-925-065A-761519	Sequence 761519,
c	212	7	4.7	566	3	US-09-864-761-13345	Sequence 13345, A
	213	7	4.7	566	4	US-09-925-065A-771199	Sequence 771199,
	214	7	4.7	566	6	US-10-029-386-3932	Sequence 3932, Ap
	215	7	4.7	567	8	US-10-363-345A-9993	Sequence 9993, Ap
c	216	7	4.7	567	8	US-10-363-345A-9994	Sequence 9994, Ap
	217	7	4.7	567	9	US-10-363-483A-9993	Sequence 9993, Ap
c	218	7	4.7	567	9	US-10-363-483A-9994	Sequence 9994, Ap
	219	7	4.7	568	4	US-09-925-065A-17111	Sequence 17111, A
c	220	7	4.7	568	4	US-09-925-065A-441555	Sequence 441555,
c	221	7	4.7	568	7	US-10-021-323-11217	Sequence 11217, A
	222	7	4.7	571	4	US-09-925-065A-762385	Sequence 762385,
	223	7	4.7	572	5	US-10-027-632-233101	Sequence 233101,
	224	7	4.7	572	6	US-10-027-632-233101	Sequence 233101,
	225	7	4.7	573	3	US-09-974-300-7366	Sequence 7366, Ap
c	226	7	4.7	574	3	US-09-864-761-9340	Sequence 9340, Ap

c 227	7	4.7	575	4	US-09-925-065A-603977	Sequence 603977,
c 228	7	4.7	575	4	US-09-925-065A-603978	Sequence 603978,
c 229	7	4.7	576	4	US-09-925-065A-883897	Sequence 883897,
c 230	7	4.7	577	5	US-10-027-632-15207	Sequence 15207, A
c 231	7	4.7	577	6	US-10-027-632-15207	Sequence 15207, A
232	7	4.7	580	4	US-09-925-065A-791073	Sequence 791073,
233	7	4.7	580	4	US-09-925-065A-848338	Sequence 848338,
c 234	7	4.7	583	4	US-09-925-065A-244461	Sequence 244461,
c 235	7	4.7	583	4	US-09-925-065A-244462	Sequence 244462,
c 236	7	4.7	583	4	US-09-925-065A-244463	Sequence 244463,
237	7	4.7	586	3	US-09-864-761-7177	Sequence 7177, Ap
c 238	7	4.7	586	4	US-09-925-065A-739320	Sequence 739320,
239	7	4.7	586	6	US-10-029-386-8028	Sequence 8028, Ap
240	7	4.7	588	3	US-09-974-300-4903	Sequence 4903, Ap
c 241	7	4.7	588	4	US-09-925-065A-21277	Sequence 21277, A
242	7	4.7	588	8	US-10-357-930-55024	Sequence 55024, A
c 243	7	4.7	593	4	US-09-925-065A-461621	Sequence 461621,
c 244	7	4.7	593	5	US-10-027-632-259943	Sequence 259943,
c 245	7	4.7	593	6	US-10-027-632-259943	Sequence 259943,
246	7	4.7	595	4	US-09-925-065A-383360	Sequence 383360,
c 247	7	4.7	598	4	US-09-925-065A-739079	Sequence 739079,
c 248	7	4.7	598	5	US-10-027-632-243386	Sequence 243386,
c 249	7	4.7	598	6	US-10-027-632-243386	Sequence 243386,
c 250	7	4.7	599	4	US-09-925-065A-304104	Sequence 304104,
251	7	4.7	600	3	US-09-864-761-14723	Sequence 14723, A
252	7	4.7	600	4	US-09-925-065A-297159	Sequence 297159,
253	7	4.7	600	4	US-09-925-065A-297160	Sequence 297160,
254	7	4.7	600	4	US-09-925-065A-770636	Sequence 770636,
255	7	4.7	600	6	US-10-029-386-8013	Sequence 8013, Ap
c 256	7	4.7	600	9	US-10-972-079-881	Sequence 881, App
c 257	7	4.7	600	9	US-10-972-079-882	Sequence 882, App
c 258	7	4.7	600	9	US-10-972-079-1411	Sequence 1411, Ap
c 259	7	4.7	600	9	US-10-972-079-5779	Sequence 5779, Ap
260	7	4.7	600	9	US-10-972-079-21980	Sequence 21980, A
261	7	4.7	600	9	US-10-972-079-34817	Sequence 34817, A
c 262	7	4.7	600	9	US-10-972-079-35091	Sequence 35091, A
c 263	7	4.7	600	9	US-10-972-079-41484	Sequence 41484, A
c 264	7	4.7	600	9	US-10-972-079-53221	Sequence 53221, A
265	7	4.7	600	9	US-10-972-079-76991	Sequence 76991, A
266	7	4.7	600	9	US-10-972-079-76992	Sequence 76992, A
c 267	7	4.7	606	4	US-09-925-065A-930991	Sequence 930991,
c 268	7	4.7	611	8	US-10-363-345A-22637	Sequence 22637, A
269	7	4.7	611	8	US-10-363-345A-22638	Sequence 22638, A
c 270	7	4.7	611	9	US-10-363-483A-22637	Sequence 22637, A
271	7	4.7	611	9	US-10-363-483A-22638	Sequence 22638, A
c 272	7	4.7	613	4	US-09-925-065A-528146	Sequence 528146,
273	7	4.7	614	4	US-09-925-065A-819222	Sequence 819222,
274	7	4.7	615	3	US-09-814-353-15377	Sequence 15377, A
275	7	4.7	615	4	US-09-925-065A-420204	Sequence 420204,
276	7	4.7	615	4	US-09-925-065A-420205	Sequence 420205,
c 277	7	4.7	616	4	US-09-925-065A-259258	Sequence 259258,
278	7	4.7	617	4	US-09-925-065A-305608	Sequence 305608,
279	7	4.7	617	4	US-09-925-065A-305609	Sequence 305609,
280	7	4.7	621	5	US-10-027-632-220213	Sequence 220213,
281	7	4.7	621	6	US-10-027-632-220213	Sequence 220213,
282	7	4.7	624	4	US-09-925-065A-196365	Sequence 196365,
c 283	7	4.7	628	4	US-09-925-065A-754136	Sequence 754136,
c 284	7	4.7	628	4	US-09-925-065A-754137	Sequence 754137,
c 285	7	4.7	634	4	US-09-925-065A-933392	Sequence 933392,
286	7	4.7	635	4	US-09-925-065A-731743	Sequence 731743,
287	7	4.7	635	4	US-09-925-065A-731744	Sequence 731744,
288	7	4.7	637	4	US-09-925-065A-774082	Sequence 774082,
289	7	4.7	637	4	US-09-925-065A-774083	Sequence 774083,
290	7	4.7	637	4	US-09-925-065A-837178	Sequence 837178,
291	7	4.7	637	9	US-10-450-763-10151	Sequence 10151, A
c 292	7	4.7	639	4	US-09-925-065A-123750	Sequence 123750,
c 293	7	4.7	639	4	US-09-925-065A-749343	Sequence 749343,
c 294	7	4.7	639	4	US-09-925-065A-749344	Sequence 749344,
c 295	7	4.7	640	4	US-09-925-065A-941724	Sequence 941724,
296	7	4.7	641	4	US-09-925-065A-885409	Sequence 885409,
297	7	4.7	641	4	US-09-925-065A-885410	Sequence 885410,
c 298	7	4.7	643	4	US-09-925-065A-796338	Sequence 796338,
c 299	7	4.7	643	4	US-09-925-065A-796339	Sequence 796339,
c 300	7	4.7	654	4	US-09-925-065A-849878	Sequence 849878,
c 301	7	4.7	658	5	US-10-027-632-137750	Sequence 137750,
c 302	7	4.7	658	5	US-10-027-632-137751	Sequence 137751,
c 303	7	4.7	658	5	US-10-027-632-137752	Sequence 137752,
c 304	7	4.7	658	6	US-10-027-632-137750	Sequence 137750,
c 305	7	4.7	658	6	US-10-027-632-137751	Sequence 137751,
c 306	7	4.7	658	6	US-10-027-632-137752	Sequence 137752,
c 307	7	4.7	659	6	US-10-146-860-12	Sequence 12, Appl
c 308	7	4.7	662	8	US-10-363-345A-40703	Sequence 40703, A
309	7	4.7	662	8	US-10-363-345A-40704	Sequence 40704, A
c 310	7	4.7	662	9	US-10-363-483A-40703	Sequence 40703, A
311	7	4.7	662	9	US-10-363-483A-40704	Sequence 40704, A
c 312	7	4.7	664	8	US-10-363-345A-615	Sequence 615, App
313	7	4.7	664	8	US-10-363-345A-616	Sequence 616, App
c 314	7	4.7	664	9	US-10-363-483A-615	Sequence 615, App
315	7	4.7	664	9	US-10-363-483A-616	Sequence 616, App
c 316	7	4.7	666	8	US-10-363-345A-13239	Sequence 13239, A
317	7	4.7	666	8	US-10-363-345A-13240	Sequence 13240, A
c 318	7	4.7	666	9	US-10-363-483A-13239	Sequence 13239, A
319	7	4.7	666	9	US-10-363-483A-13240	Sequence 13240, A
c 320	7	4.7	667	5	US-10-027-632-202790	Sequence 202790,
c 321	7	4.7	667	6	US-10-027-632-202790	Sequence 202790,
322	7	4.7	676	7	US-10-437-963-70958	Sequence 70958, A
c 323	7	4.7	677	4	US-09-925-065A-199686	Sequence 199686,
c 324	7	4.7	677	4	US-09-925-065A-199687	Sequence 199687,
325	7	4.7	679	7	US-10-767-701-13556	Sequence 13556, A
326	7	4.7	688	5	US-10-027-632-147761	Sequence 147761,
327	7	4.7	688	6	US-10-027-632-147761	Sequence 147761,
328	7	4.7	693	3	US-09-974-300-4910	Sequence 4910, Ap
c 329	7	4.7	704	8	US-10-363-345A-23747	Sequence 23747, A
330	7	4.7	704	8	US-10-363-345A-23748	Sequence 23748, A
c 331	7	4.7	704	9	US-10-363-483A-23747	Sequence 23747, A
332	7	4.7	704	9	US-10-363-483A-23748	Sequence 23748, A
333	7	4.7	708	8	US-10-425-115-139165	Sequence 139165,
c 334	7	4.7	710	4	US-09-925-065A-908064	Sequence 908064,
335	7	4.7	711	7	US-10-437-963-62073	Sequence 62073, A
336	7	4.7	712	4	US-09-925-065A-58956	Sequence 58956, A
c 337	7	4.7	712	8	US-10-363-345A-9527	Sequence 9527, Ap
338	7	4.7	712	8	US-10-363-345A-9528	Sequence 9528, Ap
c 339	7	4.7	712	9	US-10-363-483A-9527	Sequence 9527, Ap
340	7	4.7	712	9	US-10-363-483A-9528	Sequence 9528, Ap
c 341	7	4.7	721	4	US-09-925-065A-668638	Sequence 668638,
c 342	7	4.7	723	5	US-10-027-632-13885	Sequence 13885, A
c 343	7	4.7	723	6	US-10-027-632-13885	Sequence 13885, A
c 344	7	4.7	726	5	US-10-027-632-149055	Sequence 149055,
c 345	7	4.7	726	6	US-10-027-632-149055	Sequence 149055,
c 346	7	4.7	726	7	US-10-424-599-95499	Sequence 95499, A
347	7	4.7	727	3	US-09-834-975-770	Sequence 770, App
348	7	4.7	727	3	US-09-814-353-20527	Sequence 20527, A
349	7	4.7	727	8	US-10-357-930-21436	Sequence 21436, A
350	7	4.7	727	8	US-10-357-930-22434	Sequence 22434, A
351	7	4.7	727	8	US-10-357-930-24727	Sequence 24727, A
352	7	4.7	727	8	US-10-357-930-25606	Sequence 25606, A
353	7	4.7	727	8	US-10-357-930-27277	Sequence 27277, A
354	7	4.7	727	8	US-10-357-930-28268	Sequence 28268, A
c 355	7	4.7	728	4	US-09-925-065A-693874	Sequence 693874,
356	7	4.7	742	6	US-10-211-160-13	Sequence 13, Appl
357	7	4.7	742	6	US-10-051-681A-13	Sequence 13, Appl
358	7	4.7	742	6	US-10-147-603-19	Sequence 19, Appl
359	7	4.7	755	5	US-10-027-632-18840	Sequence 18840, A
360	7	4.7	755	6	US-10-027-632-18840	Sequence 18840, A
361	7	4.7	760	5	US-10-027-632-149789	Sequence 149789,
362	7	4.7	760	6	US-10-027-632-149789	Sequence 149789,
c 363	7	4.7	760	8	US-10-425-115-115517	Sequence 115517,
364	7	4.7	775	7	US-10-282-122A-9780	Sequence 9780, Ap
365	7	4.7	776	6	US-10-147-603-25	Sequence 25, Appl
366	7	4.7	777	6	US-10-147-603-13	Sequence 13, Appl
367	7	4.7	790	5	US-10-208-018-117	Sequence 117, App
368	7	4.7	807	4	US-09-925-065A-28987	Sequence 28987, A
369	7	4.7	807	6	US-10-257-826A-212	Sequence 212, App
370	7	4.7	809	5	US-10-121-857-61	Sequence 61, Appl
371	7	4.7	809	5	US-10-208-018-61	Sequence 61, Appl
372	7	4.7	811	6	US-10-147-603-21	Sequence 21, Appl

373	7	4.7	813	3	US-09-765-527-246	Sequence 246, App
374	7	4.7	813	6	US-10-127-890-11	Sequence 11, Appl
375	7	4.7	813	9	US-10-717-243-11	Sequence 11, Appl
376	7	4.7	814	4	US-09-925-065A-923844	Sequence 923844,
377	7	4.7	822	6	US-10-147-603-24	Sequence 24, Appl
378	7	4.7	823	6	US-10-147-603-14	Sequence 14, Appl
c 379	7	4.7	823	8	US-10-363-345A-18413	Sequence 18413, A
380	7	4.7	823	8	US-10-363-345A-18414	Sequence 18414, A
c 381	7	4.7	823	9	US-10-363-483A-18413	Sequence 18413, A
382	7	4.7	823	9	US-10-363-483A-18414	Sequence 18414, A
c 383	7	4.7	826	7	US-10-425-114-34025	Sequence 34025, A
384	7	4.7	836	6	US-10-147-603-15	Sequence 15, Appl
385	7	4.7	851	6	US-10-147-603-18	Sequence 18, Appl
c 386	7	4.7	855	3	US-09-938-842A-561	Sequence 561, App
c 387	7	4.7	855	3	US-09-938-842A-561	Sequence 561, App
c 388	7	4.7	855	7	US-10-424-599-74345	Sequence 74345, A
389	7	4.7	857	5	US-10-027-632-152637	Sequence 152637,
390	7	4.7	857	5	US-10-027-632-152638	Sequence 152638,
391	7	4.7	857	5	US-10-027-632-152639	Sequence 152639,
392	7	4.7	857	6	US-10-027-632-152637	Sequence 152637,
393	7	4.7	857	6	US-10-027-632-152638	Sequence 152638,
394	7	4.7	857	6	US-10-027-632-152639	Sequence 152639,
395	7	4.7	860	4	US-09-925-065A-90376	Sequence 90376, A
396	7	4.7	860	4	US-09-925-065A-90377	Sequence 90377, A
c 397	7	4.7	863	4	US-09-925-065A-719979	Sequence 719979,
398	7	4.7	863	6	US-10-147-603-6	Sequence 6, Appli
399	7	4.7	882	6	US-10-147-603-16	Sequence 16, Appl
c 400	7	4.7	897	6	US-10-365-742-59	Sequence 59, Appl
401	7	4.7	897	6	US-10-147-603-12	Sequence 12, Appl
c 402	7	4.7	899	8	US-10-363-345A-24779	Sequence 24779, A
403	7	4.7	899	8	US-10-363-345A-24780	Sequence 24780, A
c 404	7	4.7	899	9	US-10-363-483A-24779	Sequence 24779, A
405	7	4.7	899	9	US-10-363-483A-24780	Sequence 24780, A
c 406	7	4.7	914	9	US-10-486-977-50	Sequence 50, Appl
407	7	4.7	915	5	US-10-027-632-121253	Sequence 121253,
408	7	4.7	915	6	US-10-027-632-121253	Sequence 121253,
409	7	4.7	920	6	US-10-147-603-20	Sequence 20, Appl
410	7	4.7	925	4	US-09-925-065A-32187	Sequence 32187, A
c 411	7	4.7	935	8	US-10-363-345A-4993	Sequence 4993, Ap
412	7	4.7	935	8	US-10-363-345A-4994	Sequence 4994, Ap
c 413	7	4.7	935	9	US-10-363-483A-4993	Sequence 4993, Ap
414	7	4.7	935	9	US-10-363-483A-4994	Sequence 4994, Ap
415	7	4.7	947	6	US-10-147-603-26	Sequence 26, Appl
416	7	4.7	955	3	US-09-765-527-258	Sequence 258, App
417	7	4.7	955	6	US-10-147-603-17	Sequence 17, Appl
418	7	4.7	964	5	US-10-027-632-100968	Sequence 100968,
419	7	4.7	964	5	US-10-027-632-100969	Sequence 100969,
420	7	4.7	964	6	US-10-027-632-100968	Sequence 100968,
421	7	4.7	964	6	US-10-027-632-100969	Sequence 100969,
422	7	4.7	978	6	US-10-147-603-22	Sequence 22, Appl
423	7	4.7	984	7	US-10-437-963-73549	Sequence 73549, A
424	7	4.7	993	6	US-10-147-603-23	Sequence 23, Appl
425	7	4.7	995	6	US-10-147-603-2	Sequence 2, Appli
426	7	4.7	1003	3	US-09-765-527-252	Sequence 252, App
427	7	4.7	1009	6	US-10-147-603-11	Sequence 11, Appl
c 428	7	4.7	1010	4	US-09-925-065A-27118	Sequence 27118, A
c 429	7	4.7	1010	4	US-09-925-065A-27119	Sequence 27119, A
c 430	7	4.7	1010	4	US-09-925-065A-27120	Sequence 27120, A
c 431	7	4.7	1010	4	US-09-925-065A-27121	Sequence 27121, A
432	7	4.7	1010	5	US-10-027-632-30760	Sequence 30760, A
433	7	4.7	1010	6	US-10-027-632-30760	Sequence 30760, A
434	7	4.7	1011	9	US-10-450-763-10153	Sequence 10153, A
c 435	7	4.7	1014	3	US-09-770-445-216	Sequence 216, App
c 436	7	4.7	1020	8	US-10-363-345A-14107	Sequence 14107, A
437	7	4.7	1020	8	US-10-363-345A-14108	Sequence 14108, A
c 438	7	4.7	1020	9	US-10-363-483A-14107	Sequence 14107, A
439	7	4.7	1020	9	US-10-363-483A-14108	Sequence 14108, A
c 440	7	4.7	1040	6	US-10-146-860-13	Sequence 13, Appl
441	7	4.7	1050	3	US-09-972-473-3	Sequence 3, Appli
442	7	4.7	1050	3	US-09-972-473-3	Sequence 3, Appli
443	7	4.7	1050	9	US-10-819-054-3	Sequence 3, Appli
444	7	4.7	1053	3	US-09-976-736-2	Sequence 2, Appli
445	7	4.7	1053	9	US-10-998-271-2	Sequence 2, Appli
c 446	7	4.7	1070	7	US-10-437-963-72870	Sequence 72870, A
447	7	4.7	1072	3	US-09-765-527-250	Sequence 250, App
c 448	7	4.7	1074	6	US-10-174-693-54	Sequence 54, Appl
c 449	7	4.7	1075	6	US-10-174-693-55	Sequence 55, Appl
450	7	4.7	1077	5	US-10-027-632-31305	Sequence 31305, A
451	7	4.7	1077	6	US-10-027-632-31305	Sequence 31305, A
c 452	7	4.7	1077	9	US-10-501-282-3199	Sequence 3199, Ap
c 453	7	4.7	1077	9	US-10-501-282-3201	Sequence 3201, Ap
c 454	7	4.7	1077	9	US-10-501-282-3203	Sequence 3203, Ap
c 455	7	4.7	1089	6	US-10-369-493-34806	Sequence 34806, A
456	7	4.7	1089	7	US-10-724-972A-2364	Sequence 2364, Ap
c 457	7	4.7	1097	7	US-10-437-963-19862	Sequence 19862, A
458	7	4.7	1105	9	US-10-450-763-10154	Sequence 10154, A
c 459	7	4.7	1140	8	US-10-425-115-120994	Sequence 120994,
c 460	7	4.7	1141	5	US-10-226-715-9	Sequence 9, Appli
c 461	7	4.7	1143	6	US-10-412-222-4	Sequence 4, Appli
c 462	7	4.7	1143	6	US-10-412-233-4	Sequence 4, Appli
463	7	4.7	1143	7	US-10-451-168-9	Sequence 9, Appli
464	7	4.7	1143	7	US-10-451-168-10	Sequence 10, Appl
465	7	4.7	1143	9	US-10-980-387-9	Sequence 9, Appli
466	7	4.7	1143	9	US-10-980-387-10	Sequence 10, Appl
c 467	7	4.7	1161	6	US-10-369-493-44223	Sequence 44223, A
c 468	7	4.7	1167	7	US-10-282-122A-36977	Sequence 36977, A
469	7	4.7	1176	6	US-10-074-596-2	Sequence 2, Appli
470	7	4.7	1178	8	US-10-757-356-7	Sequence 7, Appli
471	7	4.7	1179	8	US-10-363-345A-4907	Sequence 4907, Ap
c 472	7	4.7	1179	8	US-10-363-345A-4908	Sequence 4908, Ap
473	7	4.7	1179	9	US-10-363-483A-4907	Sequence 4907, Ap
c 474	7	4.7	1179	9	US-10-363-483A-4908	Sequence 4908, Ap
c 475	7	4.7	1182	10	US-11-097-143-22640	Sequence 22640, A
c 476	7	4.7	1185	3	US-09-364-847-52	Sequence 52, Appl
c 477	7	4.7	1185	3	US-09-942-891-9	Sequence 9, Appli
478	7	4.7	1199	8	US-10-425-115-90023	Sequence 90023, A
479	7	4.7	1201	7	US-10-425-114-4193	Sequence 4193, Ap
480	7	4.7	1205	9	US-10-450-763-5720	Sequence 5720, Ap
481	7	4.7	1206	9	US-10-501-282-4319	Sequence 4319, Ap
482	7	4.7	1206	9	US-10-501-282-4321	Sequence 4321, Ap
483	7	4.7	1206	9	US-10-501-282-4323	Sequence 4323, Ap
484	7	4.7	1227	9	US-10-450-763-17208	Sequence 17208, A
c 485	7	4.7	1228	8	US-10-363-345A-2971	Sequence 2971, Ap
486	7	4.7	1228	8	US-10-363-345A-2972	Sequence 2972, Ap
c 487	7	4.7	1228	9	US-10-363-483A-2971	Sequence 2971, Ap
488	7	4.7	1228	9	US-10-363-483A-2972	Sequence 2972, Ap
489	7	4.7	1229	9	US-10-450-763-16606	Sequence 16606, A
c 490	7	4.7	1252	5	US-10-027-632-76104	Sequence 76104, A
c 491	7	4.7	1252	6	US-10-027-632-76104	Sequence 76104, A
c 492	7	4.7	1277	9	US-10-492-835-3	Sequence 3, Appli
c 493	7	4.7	1283	4	US-09-925-065A-710488	Sequence 710488,
494	7	4.7	1297	3	US-09-822-846-264	Sequence 264, App
c 495	7	4.7	1317	7	US-10-767-701-12901	Sequence 12901, A
c 496	7	4.7	1320	7	US-10-282-122A-26804	Sequence 26804, A
497	7	4.7	1328	8	US-10-425-115-98008	Sequence 98008, A
498	7	4.7	1331	8	US-10-737-450-97	Sequence 97, Appl
499	7	4.7	1335	7	US-10-641-643-1010	Sequence 1010, Ap
c 500	7	4.7	1339	7	US-10-398-221-3062	Sequence 3062, Ap
c 501	7	4.7	1360	3	US-09-880-107-2269	Sequence 2269, Ap
c 502	7	4.7	1360	3	US-09-873-367C-707	Sequence 707, App
c 503	7	4.7	1360	9	US-10-843-641A-707	Sequence 707, App
504	7	4.7	1367	3	US-09-864-864-332	Sequence 332, App
505	7	4.7	1367	5	US-10-171-581-1	Sequence 1, Appli
506	7	4.7	1367	6	US-10-172-118-641	Sequence 641, App
507	7	4.7	1367	7	US-10-342-887-641	Sequence 641, App
508	7	4.7	1367	7	US-10-717-597-289	Sequence 289, App
c 509	7	4.7	1367	7	US-10-437-963-28238	Sequence 28238, A
510	7	4.7	1368	8	US-10-416-330-21	Sequence 21, Appl
511	7	4.7	1380	9	US-10-450-763-11677	Sequence 11677, A
512	7	4.7	1390	6	US-10-264-049-261	Sequence 261, App
c 513	7	4.7	1390	10	US-11-097-143-41228	Sequence 41228, A
c 514	7	4.7	1395	8	US-10-363-345A-525	Sequence 525, App
515	7	4.7	1395	8	US-10-363-345A-526	Sequence 526, App
c 516	7	4.7	1395	9	US-10-363-483A-525	Sequence 525, App
517	7	4.7	1395	9	US-10-363-483A-526	Sequence 526, App
518	7	4.7	1403	9	US-10-450-763-11678	Sequence 11678, A

c 519	7	4.7	1413	7	US-10-437-963-77367	Sequence 77367, A
520	7	4.7	1416	9	US-10-887-553A-128	Sequence 128, App
c 521	7	4.7	1417	8	US-10-425-115-18342	Sequence 18342, A
c 522	7	4.7	1431	7	US-10-764-425-7	Sequence 7, Appli
c 523	7	4.7	1431	9	US-10-887-553A-184	Sequence 184, App
c 524	7	4.7	1431	10	US-11-019-829-5	Sequence 5, Appli
c 525	7	4.7	1432	6	US-10-133-937-3	Sequence 3, Appli
c 526	7	4.7	1432	6	US-10-159-563-3	Sequence 3, Appli
c 527	7	4.7	1432	6	US-10-159-563-191	Sequence 191, App
c 528	7	4.7	1432	7	US-10-755-889-271	Sequence 271, App
c 529	7	4.7	1433	7	US-10-437-963-73456	Sequence 73456, A
c 530	7	4.7	1498	8	US-10-425-115-1871	Sequence 1871, Ap
531	7	4.7	1500	9	US-10-964-195-12	Sequence 12, Appl
532	7	4.7	1517	9	US-10-964-195-10	Sequence 10, Appl
533	7	4.7	1527	6	US-10-074-596-10	Sequence 10, Appl
c 534	7	4.7	1539	7	US-10-282-122A-39529	Sequence 39529, A
535	7	4.7	1542	9	US-10-926-731A-11	Sequence 11, Appl
536	7	4.7	1554	7	US-10-398-221-3281	Sequence 3281, Ap
537	7	4.7	1593	7	US-10-641-643-1498	Sequence 1498, Ap
538	7	4.7	1596	7	US-10-641-643-1476	Sequence 1476, Ap
539	7	4.7	1596	9	US-10-450-763-10159	Sequence 10159, A
540	7	4.7	1612	9	US-10-450-763-19364	Sequence 19364, A
541	7	4.7	1623	7	US-10-437-963-66305	Sequence 66305, A
c 542	7	4.7	1659	3	US-09-815-242-9963	Sequence 9963, Ap
543	7	4.7	1686	6	US-10-369-493-40606	Sequence 40606, A
544	7	4.7	1686	7	US-10-424-599-68454	Sequence 68454, A
545	7	4.7	1708	9	US-10-795-159-207	Sequence 207, App
546	7	4.7	1779	6	US-10-071-645-4	Sequence 4, Appli
c 547	7	4.7	1803	4	US-09-925-065A-726953	Sequence 726953,
548	7	4.7	1818	6	US-10-369-493-42594	Sequence 42594, A
549	7	4.7	1822	5	US-10-027-632-97167	Sequence 97167, A
550	7	4.7	1822	5	US-10-027-632-97168	Sequence 97168, A
551	7	4.7	1822	6	US-10-027-632-97167	Sequence 97167, A
552	7	4.7	1822	6	US-10-027-632-97168	Sequence 97168, A
553	7	4.7	1849	7	US-10-296-115-414	Sequence 414, App
554	7	4.7	1849	9	US-10-450-763-10160	Sequence 10160, A
c 555	7	4.7	1869	8	US-10-472-928-3179	Sequence 3179, Ap
c 556	7	4.7	1872	3	US-09-815-242-9401	Sequence 9401, Ap
c 557	7	4.7	1872	7	US-10-282-122A-37901	Sequence 37901, A
c 558	7	4.7	1902	7	US-10-474-776-137	Sequence 137, App
c 559	7	4.7	1902	9	US-10-617-320-1488	Sequence 1488, Ap
c 560	7	4.7	1925	4	US-09-925-065A-71070	Sequence 71070, A
c 561	7	4.7	1929	3	US-09-364-847-58	Sequence 58, Appl
c 562	7	4.7	1929	3	US-09-364-847-60	Sequence 60, Appl
c 563	7	4.7	1929	7	US-10-282-122A-15416	Sequence 15416, A
c 564	7	4.7	1974	9	US-10-735-973-8	Sequence 8, Appli
c 565	7	4.7	1983	9	US-10-450-763-5686	Sequence 5686, Ap
c 566	7	4.7	1996	6	US-10-104-047-219	Sequence 219, App
c 567	7	4.7	2000	3	US-09-938-842A-4006	Sequence 4006, Ap
c 568	7	4.7	2000	3	US-09-938-842A-4006	Sequence 4006, Ap
c 569	7	4.7	2024	3	US-09-919-039-168	Sequence 168, App
c 570	7	4.7	2024	6	US-10-252-157-26	Sequence 26, Appl
c 571	7	4.7	2025	6	US-10-146-860-100	Sequence 100, App
c 572	7	4.7	2062	8	US-10-739-930-762	Sequence 762, App
c 573	7	4.7	2064	7	US-10-282-122A-13230	Sequence 13230, A
c 574	7	4.7	2082	8	US-10-739-930-1804	Sequence 1804, Ap
575	7	4.7	2098	8	US-10-425-115-169657	Sequence 169657,
576	7	4.7	2102	3	US-09-822-830A-71	Sequence 71, Appl
c 577	7	4.7	2107	5	US-10-213-791-29	Sequence 29, Appl
578	7	4.7	2124	9	US-10-504-173-36	Sequence 36, Appl
579	7	4.7	2190	6	US-10-104-047-226	Sequence 226, App
580	7	4.7	2229	8	US-10-741-849-6274	Sequence 6274, Ap
581	7	4.7	2337	7	US-10-282-122A-11610	Sequence 11610, A
c 582	7	4.7	2371	7	US-10-437-963-58240	Sequence 58240, A
c 583	7	4.7	2371	9	US-10-492-835-7	Sequence 7, Appli
584	7	4.7	2378	10	US-11-097-143-39418	Sequence 39418, A
c 585	7	4.7	2391	6	US-10-320-800-5	Sequence 5, Appli
c 586	7	4.7	2394	3	US-09-994-192-3	Sequence 3, Appli
c 587	7	4.7	2394	5	US-10-181-660-2	Sequence 2, Appli
c 588	7	4.7	2394	5	US-10-181-660-10	Sequence 10, Appl
c 589	7	4.7	2394	8	US-10-181-600-2	Sequence 2, Appli
c 590	7	4.7	2394	8	US-10-181-600-10	Sequence 10, Appl
c 591	7	4.7	2394	9	US-10-606-618-3	Sequence 3, Appli
592	7	4.7	2407	10	US-11-084-080-25	Sequence 25, Appl
c 593	7	4.7	2419	9	US-10-492-835-11	Sequence 11, Appl
c 594	7	4.7	2435	7	US-10-239-439-3	Sequence 3, Appli
c 595	7	4.7	2436	5	US-10-213-791-31	Sequence 31, Appl
596	7	4.7	2452	6	US-10-172-118-1577	Sequence 1577, Ap
597	7	4.7	2452	7	US-10-342-887-1577	Sequence 1577, Ap
c 598	7	4.7	2456	7	US-10-433-793-134	Sequence 134, App
599	7	4.7	2468	7	US-10-619-685-1	Sequence 1, Appli
600	7	4.7	2479	3	US-09-972-473-1	Sequence 1, Appli
601	7	4.7	2479	3	US-09-972-473-1	Sequence 1, Appli
602	7	4.7	2479	6	US-10-051-618A-1	Sequence 1, Appli
603	7	4.7	2479	6	US-10-172-118-1422	Sequence 1422, Ap
604	7	4.7	2479	6	US-10-159-563-187	Sequence 187, App
605	7	4.7	2479	7	US-10-342-887-1422	Sequence 1422, Ap
606	7	4.7	2479	9	US-10-819-054-1	Sequence 1, Appli
607	7	4.7	2479	9	US-10-956-157-1820	Sequence 1820, Ap
608	7	4.7	2479	9	US-10-287-436A-91	Sequence 91, Appl
609	7	4.7	2479	9	US-10-287-436A-715	Sequence 715, App
610	7	4.7	2479	9	US-10-287-436A-979	Sequence 979, App
611	7	4.7	2490	5	US-10-201-310-1	Sequence 1, Appli
612	7	4.7	2493	7	US-10-437-963-95638	Sequence 95638, A
613	7	4.7	2502	5	US-10-084-817-29	Sequence 29, Appl
614	7	4.7	2523	7	US-10-437-963-95641	Sequence 95641, A
c 615	7	4.7	2534	5	US-10-027-632-102790	Sequence 102790,
c 616	7	4.7	2534	6	US-10-027-632-102790	Sequence 102790,
617	7	4.7	2586	3	US-09-909-320-235	Sequence 235, App
618	7	4.7	2586	3	US-09-909-088B-235	Sequence 235, App
619	7	4.7	2586	3	US-09-905-291A-235	Sequence 235, App
620	7	4.7	2586	3	US-09-902-853-235	Sequence 235, App
621	7	4.7	2586	3	US-09-907-824-235	Sequence 235, App
622	7	4.7	2586	3	US-09-907-841-235	Sequence 235, App
623	7	4.7	2586	3	US-09-904-011-235	Sequence 235, App
624	7	4.7	2586	3	US-09-903-640-235	Sequence 235, App
625	7	4.7	2586	3	US-09-908-093-235	Sequence 235, App
626	7	4.7	2586	3	US-09-906-742-235	Sequence 235, App
627	7	4.7	2586	3	US-09-906-838-235	Sequence 235, App
628	7	4.7	2586	3	US-09-907-613-235	Sequence 235, App
629	7	4.7	2586	3	US-09-907-942-235	Sequence 235, App
630	7	4.7	2586	3	US-09-904-859-235	Sequence 235, App
631	7	4.7	2586	3	US-09-909-204-235	Sequence 235, App
632	7	4.7	2586	3	US-09-904-820-235	Sequence 235, App
633	7	4.7	2586	3	US-09-904-786-235	Sequence 235, App
634	7	4.7	2586	3	US-09-906-646-235	Sequence 235, App
635	7	4.7	2586	3	US-09-906-700-235	Sequence 235, App
636	7	4.7	2586	3	US-09-903-786-235	Sequence 235, App
637	7	4.7	2586	3	US-09-902-903-235	Sequence 235, App
638	7	4.7	2586	3	US-09-903-749A-235	Sequence 235, App
639	7	4.7	2586	3	US-09-904-119-235	Sequence 235, App
640	7	4.7	2586	3	US-09-904-956-235	Sequence 235, App
641	7	4.7	2586	3	US-09-902-736-235	Sequence 235, App
642	7	4.7	2586	3	US-09-907-794-235	Sequence 235, App
643	7	4.7	2586	3	US-09-903-943-235	Sequence 235, App
644	7	4.7	2586	3	US-09-904-462-235	Sequence 235, App
645	7	4.7	2586	3	US-09-907-925-235	Sequence 235, App
646	7	4.7	2586	3	US-09-902-692-235	Sequence 235, App
647	7	4.7	2586	3	US-09-903-520-235	Sequence 235, App
648	7	4.7	2586	3	US-09-905-056-235	Sequence 235, App
649	7	4.7	2586	3	US-09-909-064-235	Sequence 235, App
650	7	4.7	2586	3	US-09-904-553-235	Sequence 235, App
651	7	4.7	2586	3	US-09-905-381-235	Sequence 235, App
652	7	4.7	2586	3	US-09-904-485-235	Sequence 235, App
653	7	4.7	2586	3	US-09-905-348-235	Sequence 235, App
654	7	4.7	2586	3	US-09-905-088-235	Sequence 235, App
655	7	4.7	2586	3	US-09-907-575-235	Sequence 235, App
656	7	4.7	2586	3	US-09-905-075-235	Sequence 235, App
657	7	4.7	2586	3	US-09-902-759-235	Sequence 235, App
658	7	4.7	2586	3	US-09-902-634-235	Sequence 235, App
659	7	4.7	2586	3	US-09-902-713-235	Sequence 235, App
660	7	4.7	2586	3	US-09-907-979-235	Sequence 235, App
661	7	4.7	2586	3	US-09-902-615-235	Sequence 235, App
662	7	4.7	2586	3	US-09-903-925-235	Sequence 235, App
663	7	4.7	2586	3	US-09-906-760A-235	Sequence 235, App
664	7	4.7	2586	3	US-09-903-823-235	Sequence 235, App

665	7	4.7	2586	3	US-09-907-652-235	Sequence 235, App
666	7	4.7	2586	3	US-09-902-572A-235	Sequence 235, App
667	7	4.7	2586	3	US-09-902-979-235	Sequence 235, App
668	7	4.7	2586	3	US-09-905-125-235	Sequence 235, App
669	7	4.7	2586	3	US-09-906-815A-235	Sequence 235, App
670	7	4.7	2586	3	US-09-905-449-235	Sequence 235, App
671	7	4.7	2586	3	US-09-903-806-235	Sequence 235, App
672	7	4.7	2586	3	US-09-904-992-235	Sequence 235, App
673	7	4.7	2586	3	US-09-904-838-235	Sequence 235, App
674	7	4.7	2586	3	US-09-906-777-235	Sequence 235, App
675	7	4.7	2586	3	US-09-903-603A-235	Sequence 235, App
676	7	4.7	2586	3	US-09-904-532-235	Sequence 235, App
677	7	4.7	2586	3	US-09-904-766-235	Sequence 235, App
678	7	4.7	2586	3	US-09-904-920A-235	Sequence 235, App
679	7	4.7	2586	3	US-09-904-877A-235	Sequence 235, App
680	7	4.7	2586	3	US-09-903-562-235	Sequence 235, App
681	7	4.7	2586	3	US-09-906-618-235	Sequence 235, App
682	7	4.7	2586	3	US-09-907-728-235	Sequence 235, App
683	7	4.7	2586	3	US-09-904-805-235	Sequence 235, App
684	7	4.7	2586	3	US-09-904-938A-235	Sequence 235, App
685	7	4.7	2586	3	US-09-906-722A-235	Sequence 235, App
686	7	4.7	2586	3	US-09-908-576-235	Sequence 235, App
687	7	4.7	2586	5	US-10-006-867-7	Sequence 7, Appli
688	7	4.7	2586	5	US-10-063-547-7	Sequence 7, Appli
689	7	4.7	2586	5	US-10-063-551-7	Sequence 7, Appli
690	7	4.7	2586	5	US-10-063-616-7	Sequence 7, Appli
691	7	4.7	2586	5	US-10-063-569-7	Sequence 7, Appli
692	7	4.7	2586	5	US-10-063-513-7	Sequence 7, Appli
693	7	4.7	2586	5	US-10-063-515-7	Sequence 7, Appli
694	7	4.7	2586	5	US-10-063-512-7	Sequence 7, Appli
695	7	4.7	2586	5	US-10-063-502-7	Sequence 7, Appli
696	7	4.7	2586	5	US-10-063-549-7	Sequence 7, Appli
697	7	4.7	2586	5	US-10-063-554-7	Sequence 7, Appli
698	7	4.7	2586	5	US-10-063-553-7	Sequence 7, Appli
699	7	4.7	2586	5	US-10-063-518-7	Sequence 7, Appli
700	7	4.7	2586	5	US-10-063-598-7	Sequence 7, Appli
701	7	4.7	2586	5	US-10-227-693-7	Sequence 7, Appli
702	7	4.7	2586	5	US-10-063-563-7	Sequence 7, Appli
703	7	4.7	2586	5	US-10-063-555-7	Sequence 7, Appli
704	7	4.7	2586	5	US-10-063-594-7	Sequence 7, Appli
705	7	4.7	2586	5	US-10-063-567-7	Sequence 7, Appli
706	7	4.7	2586	5	US-10-063-599-7	Sequence 7, Appli
707	7	4.7	2586	5	US-10-063-595-7	Sequence 7, Appli
708	7	4.7	2586	5	US-10-223-085-49	Sequence 49, Appl
709	7	4.7	2586	5	US-10-223-084-49	Sequence 49, Appl
710	7	4.7	2586	5	US-10-223-088-49	Sequence 49, Appl
711	7	4.7	2586	5	US-10-223-090-49	Sequence 49, Appl
712	7	4.7	2586	5	US-10-063-580-7	Sequence 7, Appli
713	7	4.7	2586	5	US-10-223-087-49	Sequence 49, Appl
714	7	4.7	2586	5	US-10-063-557-7	Sequence 7, Appli
715	7	4.7	2586	5	US-10-063-585-7	Sequence 7, Appli
716	7	4.7	2586	6	US-10-223-083-49	Sequence 49, Appl
717	7	4.7	2586	6	US-10-223-089-49	Sequence 49, Appl
718	7	4.7	2586	6	US-10-063-588-7	Sequence 7, Appli
719	7	4.7	2586	6	US-10-063-735-7	Sequence 7, Appli
720	7	4.7	2586	6	US-10-063-526-7	Sequence 7, Appli
721	7	4.7	2586	6	US-10-063-586-7	Sequence 7, Appli
722	7	4.7	2586	6	US-10-299-976-235	Sequence 235, App
723	7	4.7	2586	6	US-10-063-546-7	Sequence 7, Appli
724	7	4.7	2586	6	US-10-063-564-7	Sequence 7, Appli
725	7	4.7	2586	6	US-10-063-662-7	Sequence 7, Appli
726	7	4.7	2586	6	US-10-063-510-7	Sequence 7, Appli
727	7	4.7	2586	6	US-10-063-669-7	Sequence 7, Appli
728	7	4.7	2586	6	US-10-063-670-7	Sequence 7, Appli
729	7	4.7	2586	6	US-10-063-671-7	Sequence 7, Appli
730	7	4.7	2586	6	US-10-063-674-7	Sequence 7, Appli
731	7	4.7	2586	6	US-10-063-675-7	Sequence 7, Appli
732	7	4.7	2586	6	US-10-063-676-7	Sequence 7, Appli
733	7	4.7	2586	6	US-10-063-686-7	Sequence 7, Appli
734	7	4.7	2586	6	US-10-063-689-7	Sequence 7, Appli
735	7	4.7	2586	6	US-10-063-692-7	Sequence 7, Appli
736	7	4.7	2586	6	US-10-063-693-7	Sequence 7, Appli
737	7	4.7	2586	6	US-10-063-694-7	Sequence 7, Appli
738	7	4.7	2586	6	US-10-063-698-7	Sequence 7, Appli
739	7	4.7	2586	6	US-10-063-699-7	Sequence 7, Appli
740	7	4.7	2586	6	US-10-063-702-7	Sequence 7, Appli
741	7	4.7	2586	6	US-10-063-705-7	Sequence 7, Appli
742	7	4.7	2586	6	US-10-063-707-7	Sequence 7, Appli
743	7	4.7	2586	6	US-10-063-709-7	Sequence 7, Appli
744	7	4.7	2586	6	US-10-063-713-7	Sequence 7, Appli
745	7	4.7	2586	6	US-10-063-724-7	Sequence 7, Appli
746	7	4.7	2586	6	US-10-063-727-7	Sequence 7, Appli
747	7	4.7	2586	6	US-10-063-730-7	Sequence 7, Appli
748	7	4.7	2586	6	US-10-063-734-7	Sequence 7, Appli
749	7	4.7	2586	6	US-10-063-736-7	Sequence 7, Appli
750	7	4.7	2586	6	US-10-063-742-7	Sequence 7, Appli
751	7	4.7	2586	6	US-10-063-743-7	Sequence 7, Appli
752	7	4.7	2586	6	US-10-063-744-7	Sequence 7, Appli
753	7	4.7	2586	6	US-10-063-565-7	Sequence 7, Appli
754	7	4.7	2586	6	US-10-063-577-7	Sequence 7, Appli
755	7	4.7	2586	6	US-10-063-591-7	Sequence 7, Appli
756	7	4.7	2586	6	US-10-063-610-7	Sequence 7, Appli
757	7	4.7	2586	6	US-10-063-673-7	Sequence 7, Appli
758	7	4.7	2586	6	US-10-063-710-7	Sequence 7, Appli
759	7	4.7	2586	6	US-10-063-711-7	Sequence 7, Appli
760	7	4.7	2586	6	US-10-063-712-7	Sequence 7, Appli
761	7	4.7	2586	6	US-10-063-714-7	Sequence 7, Appli
762	7	4.7	2586	6	US-10-063-715-7	Sequence 7, Appli
763	7	4.7	2586	6	US-10-063-716-7	Sequence 7, Appli
764	7	4.7	2586	6	US-10-063-717-7	Sequence 7, Appli
765	7	4.7	2586	6	US-10-063-720-7	Sequence 7, Appli
766	7	4.7	2586	6	US-10-063-722-7	Sequence 7, Appli
767	7	4.7	2586	6	US-10-063-726-7	Sequence 7, Appli
768	7	4.7	2586	6	US-10-063-728-7	Sequence 7, Appli
769	7	4.7	2586	6	US-10-063-731-7	Sequence 7, Appli
770	7	4.7	2586	6	US-10-063-732-7	Sequence 7, Appli
771	7	4.7	2586	6	US-10-063-523-7	Sequence 7, Appli
772	7	4.7	2586	6	US-10-063-527-7	Sequence 7, Appli
773	7	4.7	2586	6	US-10-063-579-7	Sequence 7, Appli
774	7	4.7	2586	6	US-10-063-581-7	Sequence 7, Appli
775	7	4.7	2586	6	US-10-063-583-7	Sequence 7, Appli
776	7	4.7	2586	6	US-10-063-589-7	Sequence 7, Appli
777	7	4.7	2586	6	US-10-063-593-7	Sequence 7, Appli
778	7	4.7	2586	6	US-10-063-596-7	Sequence 7, Appli
779	7	4.7	2586	6	US-10-063-600-7	Sequence 7, Appli
780	7	4.7	2586	6	US-10-063-604-7	Sequence 7, Appli
781	7	4.7	2586	6	US-10-063-607-7	Sequence 7, Appli
782	7	4.7	2586	6	US-10-063-612-7	Sequence 7, Appli
783	7	4.7	2586	6	US-10-063-615-7	Sequence 7, Appli
784	7	4.7	2586	6	US-10-063-640-7	Sequence 7, Appli
785	7	4.7	2586	6	US-10-063-642-7	Sequence 7, Appli
786	7	4.7	2586	6	US-10-063-644-7	Sequence 7, Appli
787	7	4.7	2586	6	US-10-063-649-7	Sequence 7, Appli
788	7	4.7	2586	6	US-10-063-650-7	Sequence 7, Appli
789	7	4.7	2586	6	US-10-063-652-7	Sequence 7, Appli
790	7	4.7	2586	6	US-10-063-654-7	Sequence 7, Appli
791	7	4.7	2586	6	US-10-063-659-7	Sequence 7, Appli
792	7	4.7	2586	6	US-10-063-661-7	Sequence 7, Appli
793	7	4.7	2586	6	US-10-063-528-7	Sequence 7, Appli
794	7	4.7	2586	6	US-10-063-540-7	Sequence 7, Appli
795	7	4.7	2586	6	US-10-063-568-7	Sequence 7, Appli
796	7	4.7	2586	6	US-10-063-570-7	Sequence 7, Appli
797	7	4.7	2586	6	US-10-063-582-7	Sequence 7, Appli
798	7	4.7	2586	6	US-10-063-587-7	Sequence 7, Appli
799	7	4.7	2586	6	US-10-063-592-7	Sequence 7, Appli
800	7	4.7	2586	6	US-10-063-597-7	Sequence 7, Appli
801	7	4.7	2586	6	US-10-063-602-7	Sequence 7, Appli
802	7	4.7	2586	6	US-10-063-606-7	Sequence 7, Appli
803	7	4.7	2586	6	US-10-063-609-7	Sequence 7, Appli
804	7	4.7	2586	6	US-10-063-611-7	Sequence 7, Appli
805	7	4.7	2586	6	US-10-063-614-7	Sequence 7, Appli
806	7	4.7	2586	6	US-10-063-639-7	Sequence 7, Appli
807	7	4.7	2586	6	US-10-063-643-7	Sequence 7, Appli
808	7	4.7	2586	6	US-10-063-646-7	Sequence 7, Appli
809	7	4.7	2586	6	US-10-063-651-7	Sequence 7, Appli
810	7	4.7	2586	6	US-10-063-653-7	Sequence 7, Appli

	811	7	4.7	2586	6	US-10-063-660-7	Sequence 7, Appli
	812	7	4.7	2586	6	US-10-063-665-7	Sequence 7, Appli
	813	7	4.7	2586	6	US-10-063-584-7	Sequence 7, Appli
	814	7	4.7	2586	6	US-10-063-536-7	Sequence 7, Appli
	815	7	4.7	2586	6	US-10-063-562-7	Sequence 7, Appli
	816	7	4.7	2586	6	US-10-063-638-7	Sequence 7, Appli
	817	7	4.7	2586	6	US-10-063-666-7	Sequence 7, Appli
	818	7	4.7	2586	6	US-10-063-672-7	Sequence 7, Appli
	819	7	4.7	2586	6	US-10-063-682-7	Sequence 7, Appli
	820	7	4.7	2586	6	US-10-063-721-7	Sequence 7, Appli
	821	7	4.7	2586	6	US-10-063-723-7	Sequence 7, Appli
	822	7	4.7	2586	6	US-10-063-514-7	Sequence 7, Appli
	823	7	4.7	2586	6	US-10-063-516-7	Sequence 7, Appli
	824	7	4.7	2586	6	US-10-063-529-7	Sequence 7, Appli
	825	7	4.7	2586	6	US-10-299-937-235	Sequence 235, App
	826	7	4.7	2586	6	US-10-063-684-7	Sequence 7, Appli
	827	7	4.7	2586	6	US-10-063-688-7	Sequence 7, Appli
	828	7	4.7	2586	6	US-10-223-081-49	Sequence 49, Appl
	829	7	4.7	2586	6	US-10-063-520-7	Sequence 7, Appli
	830	7	4.7	2586	6	US-10-063-647-7	Sequence 7, Appli
	831	7	4.7	2586	6	US-10-063-548-7	Sequence 7, Appli
	832	7	4.7	2586	6	US-10-063-578-7	Sequence 7, Appli
	833	7	4.7	2586	6	US-10-063-648-7	Sequence 7, Appli
	834	7	4.7	2586	6	US-10-063-677-7	Sequence 7, Appli
	835	7	4.7	2586	6	US-10-063-718-7	Sequence 7, Appli
	836	7	4.7	2586	6	US-10-063-741-7	Sequence 7, Appli
	837	7	4.7	2586	6	US-10-063-617-7	Sequence 7, Appli
	838	7	4.7	2586	6	US-10-223-082-49	Sequence 49, Appl
	839	7	4.7	2586	6	US-10-063-664-7	Sequence 7, Appli
	840	7	4.7	2586	6	US-10-063-561-7	Sequence 7, Appli
	841	7	4.7	2586	6	US-10-063-618-7	Sequence 7, Appli
	842	7	4.7	2586	6	US-10-063-657-7	Sequence 7, Appli
	843	7	4.7	2586	6	US-10-063-668-7	Sequence 7, Appli
	844	7	4.7	2586	6	US-10-298-993-235	Sequence 235, App
	845	7	4.7	2586	6	US-10-305-654-49	Sequence 49, Appl
	846	7	4.7	2586	6	US-10-448-923-235	Sequence 235, App
	847	7	4.7	2586	6	US-10-449-656-235	Sequence 235, App
	848	7	4.7	2586	6	US-10-448-713-235	Sequence 235, App
	849	7	4.7	2586	7	US-10-425-447-235	Sequence 235, App
	850	7	4.7	2586	7	US-10-081-056-49	Sequence 49, Appl
	851	7	4.7	2586	7	US-10-063-745-7	Sequence 7, Appli
	852	7	4.7	2586	7	US-10-215-371-235	Sequence 235, App
	853	7	4.7	2586	7	US-10-797-366-235	Sequence 235, App
	854	7	4.7	2586	8	US-10-771-187-235	Sequence 235, App
	855	7	4.7	2586	9	US-10-972-317-7	Sequence 7, Appli
	856	7	4.7	2586	9	US-10-963-467-235	Sequence 235, App
	857	7	4.7	2586	9	US-10-978-255-235	Sequence 235, App
	858	7	4.7	2586	9	US-10-970-823-235	Sequence 235, App
	859	7	4.7	2608	3	US-09-918-715-201	Sequence 201, App
	860	7	4.7	2608	8	US-10-474-794-201	Sequence 201, App
	861	7	4.7	2608	9	US-10-979-159-201	Sequence 201, App
	862	7	4.7	2619	8	US-10-723-940-122	Sequence 122, App
	863	7	4.7	2645	4	US-09-925-065A-89593	Sequence 89593, A
c	864	7	4.7	2657	7	US-10-424-599-10475	Sequence 10475, A
	865	7	4.7	2679	6	US-10-104-047-1168	Sequence 1168, Ap
c	866	7	4.7	2728	8	US-10-602-494-317	Sequence 317, App
c	867	7	4.7	2728	8	US-10-602-494-319	Sequence 319, App
c	868	7	4.7	2728	8	US-10-602-494-321	Sequence 321, App
	869	7	4.7	2735	5	US-10-168-066-18	Sequence 18, Appl
	870	7	4.7	2744	7	US-10-152-319A-1838	Sequence 1838, Ap
	871	7	4.7	2744	9	US-10-764-420-1225	Sequence 1225, Ap
	872	7	4.7	2744	9	US-10-887-553A-110	Sequence 110, App
c	873	7	4.7	2790	6	US-10-257-909A-25	Sequence 25, Appl
	874	7	4.7	2803	9	US-10-764-420-1429	Sequence 1429, Ap
	875	7	4.7	2880	7	US-10-191-803-192	Sequence 192, App
	876	7	4.7	2920	5	US-10-128-714-249	Sequence 249, App
	877	7	4.7	2943	8	US-10-739-930-1215	Sequence 1215, Ap
	878	7	4.7	2987	5	US-10-128-714-5249	Sequence 5249, Ap
c	879	7	4.7	3016	7	US-10-641-643-259	Sequence 259, App
c	880	7	4.7	3039	5	US-10-232-665-19	Sequence 19, Appl
c	881	7	4.7	3039	5	US-10-232-665-21	Sequence 21, Appl
c	882	7	4.7	3041	10	US-11-097-143-7666	Sequence 7666, Ap
c	883	7	4.7	3044	5	US-10-232-665-38	Sequence 38, Appl
c	884	7	4.7	3051	9	US-10-486-319A-7	Sequence 7, Appli
c	885	7	4.7	3083	3	US-09-814-353-19945	Sequence 19945, A
c	886	7	4.7	3130	6	US-10-146-860-16	Sequence 16, Appl
c	887	7	4.7	3130	8	US-10-684-206-35	Sequence 35, Appl
c	888	7	4.7	3130	9	US-10-450-763-6955	Sequence 6955, Ap
c	889	7	4.7	3182	10	US-11-097-143-22639	Sequence 22639, A
c	890	7	4.7	3222	6	US-10-369-493-33817	Sequence 33817, A
c	891	7	4.7	3233	10	US-11-097-143-22648	Sequence 22648, A
c	892	7	4.7	3332	6	US-10-146-860-10	Sequence 10, Appl
	893	7	4.7	3367	7	US-10-276-774-811	Sequence 811, App
c	894	7	4.7	3411	7	US-10-437-963-72157	Sequence 72157, A
c	895	7	4.7	3450	5	US-10-232-665-17	Sequence 17, Appl
c	896	7	4.7	3455	5	US-10-232-665-36	Sequence 36, Appl
c	897	7	4.7	3469	5	US-10-232-665-23	Sequence 23, Appl
	898	7	4.7	3693	9	US-10-450-763-19220	Sequence 19220, A
c	899	7	4.7	3754	5	US-10-232-665-15	Sequence 15, Appl
	900	7	4.7	3767	9	US-10-887-553A-691	Sequence 691, App
	901	7	4.7	3786	6	US-10-245-802-7	Sequence 7, Appli
c	902	7	4.7	3829	6	US-10-146-860-15	Sequence 15, Appl
c	903	7	4.7	3850	8	US-10-723-860-5749	Sequence 5749, Ap
c	904	7	4.7	3995	10	US-11-097-143-41227	Sequence 41227, A
	905	7	4.7	4032	9	US-10-450-763-22289	Sequence 22289, A
	906	7	4.7	4080	7	US-10-473-574-34	Sequence 34, Appl
c	907	7	4.7	4110	8	US-10-473-126-341	Sequence 341, App
	908	7	4.7	4131	7	US-10-161-493-59	Sequence 59, Appl
c	909	7	4.7	4149	5	US-10-232-665-13	Sequence 13, Appl
	910	7	4.7	4215	3	US-09-835-976B-3	Sequence 3, Appli
	911	7	4.7	4260	3	US-09-835-976B-15	Sequence 15, Appl
	912	7	4.7	4267	3	US-09-948-002-47	Sequence 47, Appl
	913	7	4.7	4267	6	US-10-189-267-11	Sequence 11, Appl
	914	7	4.7	4267	7	US-10-633-163-47	Sequence 47, Appl
	915	7	4.7	4267	9	US-10-631-467-963	Sequence 963, App
	916	7	4.7	4345	8	US-10-357-930-23329	Sequence 23329, A
	917	7	4.7	4345	8	US-10-357-930-29211	Sequence 29211, A
	918	7	4.7	4345	10	US-11-019-005-1	Sequence 1, Appli
	919	7	4.7	4345	10	US-11-019-005-3	Sequence 3, Appli
	920	7	4.7	4345	10	US-11-019-005-5	Sequence 5, Appli
	921	7	4.7	4345	10	US-11-019-005-7	Sequence 7, Appli
c	922	7	4.7	4350	10	US-11-097-143-41215	Sequence 41215, A
	923	7	4.7	4360	7	US-10-473-574-35	Sequence 35, Appl
	924	7	4.7	4417	3	US-09-796-753-23	Sequence 23, Appl
	925	7	4.7	4417	6	US-10-038-307-3	Sequence 3, Appli
	926	7	4.7	4417	6	US-10-201-292-3	Sequence 3, Appli
	927	7	4.7	4574	7	US-10-619-685-3	Sequence 3, Appli
c	928	7	4.7	4805	3	US-09-754-831A-40	Sequence 40, Appl
c	929	7	4.7	4805	9	US-10-671-317-40	Sequence 40, Appl
	930	7	4.7	4955	8	US-10-723-860-1682	Sequence 1682, Ap
	931	7	4.7	4962	10	US-11-097-143-25819	Sequence 25819, A
	932	7	4.7	4995	10	US-11-097-143-25816	Sequence 25816, A
c	933	7	4.7	5059	10	US-11-056-409-1	Sequence 1, Appli
	934	7	4.7	5220	3	US-09-918-715-186	Sequence 186, App
	935	7	4.7	5220	3	US-09-918-715-300	Sequence 300, App
	936	7	4.7	5220	8	US-10-474-794-186	Sequence 186, App
	937	7	4.7	5220	8	US-10-474-794-300	Sequence 300, App
	938	7	4.7	5220	9	US-10-979-159-186	Sequence 186, App
	939	7	4.7	5220	9	US-10-979-159-300	Sequence 300, App
c	940	7	4.7	5706	6	US-10-146-860-3	Sequence 3, Appli
c	941	7	4.7	5856	6	US-10-311-455-541	Sequence 541, App
	942	7	4.7	5862	3	US-09-764-891-7363	Sequence 7363, Ap
c	943	7	4.7	5876	9	US-10-895-225A-19	Sequence 19, Appl
c	944	7	4.7	6226	10	US-11-097-143-4852	Sequence 4852, Ap
	945	7	4.7	6228	3	US-09-815-242-4760	Sequence 4760, Ap
	946	7	4.7	6330	9	US-10-499-353A-31	Sequence 31, Appl
c	947	7	4.7	6361	6	US-10-311-455-1114	Sequence 1114, Ap
c	948	7	4.7	6521	6	US-10-311-455-1929	Sequence 1929, Ap
	949	7	4.7	6561	3	US-09-815-242-8815	Sequence 8815, Ap
c	950	7	4.7	6694	7	US-10-221-613-273	Sequence 273, App
	951	7	4.7	6736	8	US-10-798-941-1	Sequence 1, Appli
	952	7	4.7	6736	8	US-10-798-941-5	Sequence 5, Appli
	953	7	4.7	7004	8	US-10-798-941-3	Sequence 3, Appli
c	954	7	4.7	7146	8	US-10-357-930-24946	Sequence 24946, A
c	955	7	4.7	7893	3	US-09-070-927A-228	Sequence 228, App
c	956	7	4.7	7966	5	US-10-116-802-115	Sequence 115, App

c 957	7	4.7	8349	6	US-10-198-478-16	Sequence 16, Appl
958	7	4.7	8463	7	US-10-263-929-92	Sequence 92, Appl
c 959	7	4.7	8553	7	US-10-152-319A-1523	Sequence 1523, Ap
960	7	4.7	8865	10	US-11-097-143-16679	Sequence 16679, A
c 961	7	4.7	8946	6	US-10-311-455-883	Sequence 883, App
962	7	4.7	9390	5	US-10-205-823-263	Sequence 263, App
963	7	4.7	9390	6	US-10-172-118-1220	Sequence 1220, Ap
964	7	4.7	9390	7	US-10-342-887-1220	Sequence 1220, Ap
965	7	4.7	9390	9	US-10-504-173-91	Sequence 91, Appl
966	7	4.7	9390	10	US-11-051-454-263	Sequence 263, App
c 967	7	4.7	9591	3	US-09-764-891-6043	Sequence 6043, Ap
c 968	7	4.7	9591	5	US-10-091-438-268	Sequence 268, App
969	7	4.7	9804	10	US-11-097-143-25813	Sequence 25813, A
c 970	7	4.7	10048	7	US-10-433-793-45	Sequence 45, Appl
c 971	7	4.7	10476	3	US-09-964-824A-98	Sequence 98, Appl
c 972	7	4.7	10476	3	US-09-964-824A-552	Sequence 552, App
c 973	7	4.7	10476	9	US-10-843-641A-5401	Sequence 5401, Ap
c 974	7	4.7	10476	9	US-10-843-641A-5855	Sequence 5855, Ap
c 975	7	4.7	10476	9	US-10-756-149-839	Sequence 839, App
976	7	4.7	11502	10	US-11-097-143-16678	Sequence 16678, A
c 977	7	4.7	12415	3	US-09-764-891-6044	Sequence 6044, Ap
c 978	7	4.7	12415	5	US-10-091-438-269	Sequence 269, App
c 979	7	4.7	12669	7	US-10-221-613-411	Sequence 411, App
980	7	4.7	13365	9	US-10-499-353A-26	Sequence 26, Appl
c 981	7	4.7	15606	10	US-11-097-143-22562	Sequence 22562, A
982	7	4.7	15613	9	US-10-499-353A-23	Sequence 23, Appl
983	7	4.7	16161	3	US-09-957-956-8	Sequence 8, Appli
984	7	4.7	16161	9	US-10-642-946-8	Sequence 8, Appli
985	7	4.7	16309	9	US-10-499-353A-24	Sequence 24, Appl
986	7	4.7	16387	9	US-10-499-353A-25	Sequence 25, Appl
987	7	4.7	16854	9	US-10-499-353A-22	Sequence 22, Appl
c 988	7	4.7	17410	2	US-08-957-425-3	Sequence 3, Appli
c 989	7	4.7	17410	6	US-10-321-799-3	Sequence 3, Appli
c 990	7	4.7	17410	7	US-10-428-997A-3	Sequence 3, Appli
c 991	7	4.7	17415	10	US-11-005-197-1	Sequence 1, Appli
992	7	4.7	18795	9	US-10-499-353A-16	Sequence 16, Appl
993	7	4.7	19027	9	US-10-499-353A-13	Sequence 13, Appl
994	7	4.7	19181	9	US-10-499-353A-21	Sequence 21, Appl
995	7	4.7	19242	9	US-10-499-353A-20	Sequence 20, Appl
996	7	4.7	19247	9	US-10-499-353A-14	Sequence 14, Appl
997	7	4.7	19267	9	US-10-499-353A-15	Sequence 15, Appl
998	7	4.7	19344	9	US-10-499-353A-17	Sequence 17, Appl
999	7	4.7	19707	9	US-10-499-353A-18	Sequence 18, Appl
1000	7	4.7	20017	9	US-10-499-353A-19	Sequence 19, Appl

ALIGNMENTS

```
RESULT 1
US-11-084-080-15
; Sequence 15, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-15

Alignment Scores:
Pred. No.:                4.16e-124      Length:          2404
Score:                    122.00         Matches:         122
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              81.9%          Indels:          0
DB:                       10             Gaps:            0

US-10-758-902-9 (1-149) x US-11-084-080-15 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 884

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 944

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1004

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1064

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1124

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1184

Qy        121 AlaLys 122
              ||||||
Db       1185 GCCAAA 1190

RESULT 2
US-11-084-080-19
; Sequence 19, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Alignment Scores:
Pred. No.:              4.16e-124       Length:         2404
Score:                  122.00          Matches:        122
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            81.9%           Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-9 (1-149) x US-11-084-080-19 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1643 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1702

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1703 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 1762

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1763 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1822

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1823 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1882

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1883 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1942

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1943 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 2002

Qy        121 AlaLys 122
              ||||||
Db       2003 GCCAAA 2008

RESULT 3
US-11-084-080-21
; Sequence 21, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-21

Alignment Scores:
Pred. No.:              4.16e-124       Length:         2404
Score:                  122.00          Matches:        122
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            81.9%           Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-9 (1-149) x US-11-084-080-21 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 191

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 251

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 311

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 371

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 431

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 491

Qy        121 AlaLys 122
              ||||||
Db        492 GCCAAA 497

RESULT 4
US-11-084-080-23
; Sequence 23, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Alignment Scores:
Pred. No.:              4.16e-124       Length:         2404
```

```
Score:                 122.00        Matches:       122
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           81.9%         Indels:        0
DB:                    10            Gaps:          0

US-10-758-902-9 (1-149) x US-11-084-080-23 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        950 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1009

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1010 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 1069

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1129

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1130 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1189

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1190 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1249

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1250 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1309

Qy        121 AlaLys 122
              ||||||
Db       1310 GCCAAA 1315

RESULT 5
US-11-084-080-27
; Sequence 27, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 2431
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-011
US-11-084-080-27

Alignment Scores:
Pred. No.:             4.2e-124      Length:        2431
Score:                 122.00        Matches:       122
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           81.9%         Indels:        0
DB:                    10            Gaps:          0

US-10-758-902-9 (1-149) x US-11-084-080-27 (1-2431)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 911

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        912 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 971

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1031

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1091

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1092 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1151

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1152 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1211

Qy        121 AlaLys 122
              ||||||
Db       1212 GCCAAA 1217

RESULT 6
US-10-758-902-8
; Sequence 8, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)...(361)
US-10-758-902-8

Alignment Scores:
Pred. No.:             1.12e-122     Length:        363
Score:                 120.00        Matches:       120
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           80.5%         Indels:        0
DB:                    8             Gaps:          0

US-10-758-902-9 (1-149) x US-10-758-902-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361

RESULT 7
US-10-758-902-5
; Sequence 5, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-5

Alignment Scores:
Pred. No.:              5.75e-14        Length:         65
Score:                  21.00           Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.1%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-9 (1-149) x US-10-758-902-5 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 8
US-10-322-281-115/c
; Sequence 115, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc S. Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: 529452001000
;  CURRENT APPLICATION NUMBER: US/10/322,281
;  CURRENT FILING DATE:  2002-12-17
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 115
;   LENGTH: 289190
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(289190)
;   OTHER INFORMATION: n = A,T,C or G
US-10-322-281-115

Alignment Scores:
Pred. No.:              3.06e+03        Length:         289190
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.0%            Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-9 (1-149) x US-10-322-281-115 (1-289190)

Qy         56 SerLysLysThrValLysValAlaIle 64
              |||||||||||||||||||||||||||
Db     104584 AGCAAGAAAACTGTCAAGGTTGCCATC 104558

RESULT 9
US-10-741-601-14447
; Sequence 14447, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14447
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-14447

Alignment Scores:
Pred. No.:              39.2            Length:         201
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-9 (1-149) x US-10-741-601-14447 (1-201)

Qy         55 ThrSerLysLysThrValLysVal 62
              ||||||||||||||||||||||||
Db         43 ACAAGCAAAAAAACAGTAAAGGTC 66

RESULT 10
US-09-925-065A-47024
; Sequence 47024, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
```

```
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47024
;   LENGTH: 416
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-47024

Alignment Scores:
Pred. No.:              78.1          Length:         416
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-47024 (1-416)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        303 ACAGTGTCATTTAATTTGGGAGAG 326

RESULT 11
US-09-925-065A-630179/c
; Sequence 630179, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 630179
;   LENGTH: 487
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-630179

Alignment Scores:
Pred. No.:              90.7          Length:         487
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-630179 (1-487)

Qy        136 GluPheSerIleGluAlaIleTrp 143
              |||||||||||||||||||||||
Db        481 GAATTCAGCATTGAAGCCATCTGG 458

RESULT 12
US-10-027-632-281750/c
; Sequence 281750, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 281750
;   LENGTH: 524
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-281750

Alignment Scores:
Pred. No.:              97.3          Length:         524
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     5             Gaps:           0

US-10-758-902-9 (1-149) x US-10-027-632-281750 (1-524)

Qy          97 LysLeuProGlyValThrAsn 104
               ||||||||||||||||||||||
Db        172 AAACTATTTCCAGGGGTAACTAAT 149

RESULT 13
US-10-027-632-281750/c
; Sequence 281750, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
```

```
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 281750
;   LENGTH: 524
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-281750

Alignment Scores:
Pred. No.:              97.3          Length:         524
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-9 (1-149) x US-10-027-632-281750 (1-524)

Qy         97 LysLeuPheProGlyValThrAsn 104
              ||||||||||||||||||||||
Db        172 AAACTATTTCCAGGGGTAACTAAT 149

RESULT 14
US-09-925-065A-325312
; Sequence 325312, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 325312
;   LENGTH: 565
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-325312

Alignment Scores:
Pred. No.:              104           Length:         565
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-325312 (1-565)

Qy         29 ThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||
Db        145 ACTCCAGTTTGCCAGCTTCCAGTT 168

RESULT 15
US-09-925-065A-787599
; Sequence 787599, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 787599
;   LENGTH: 622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-787599

Alignment Scores:
Pred. No.:              114           Length:         622
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-787599 (1-622)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db         17 ACAGTGTCATTTAATTTGGGAGAG 40

RESULT 16
US-10-767-795-223
; Sequence 223, Application US/10767795
; Publication No. US20040181830A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Zhou, Yihua
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53534)B
;  CURRENT APPLICATION NUMBER: US/10/767,795
;  CURRENT FILING DATE:  2004-01-30
;  NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 223
;   LENGTH: 759
;   TYPE: DNA
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
;   OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C47653_1
US-10-767-795-223

Alignment Scores:
Pred. No.:              138           Length:         759
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-9 (1-149) x US-10-767-795-223 (1-759)

Qy         91 ProThrValAlaThrSerLysLeu 98
              |||||||||||||||||||||||
Db         91 CCCACAGTGGCCACTTCCAAGCTC 114

RESULT 17
```

```
US-10-619-761-71/c
; Sequence 71, Application US/10619761
; Publication No. US20050059010A1
; GENERAL INFORMATION:
;  APPLICANT: STONE, EDWIN M.
;  APPLICANT:  SHEFFIELD, VAL C.
;  TITLE OF INVENTION: MACULAR DEGENERATION DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: UIA-018.03
;  CURRENT APPLICATION NUMBER: US/10/619,761
;  CURRENT FILING DATE:  2003-07-14
;  PRIOR APPLICATION NUMBER: US/09/322,357
;  PRIOR FILING DATE: 1999-05-28
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
;   LENGTH: 979
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence may
;   OTHER INFORMATION: be a, t, c, g, other or unknown
US-10-619-761-71

Alignment Scores:
Pred. No.:              176           Length:        979
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     9             Gaps:          0

US-10-758-902-9 (1-149) x US-10-619-761-71 (1-979)

Qy         33 GlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||
Db        947 CAGTTACCGGTAACTCTGCAAACT 924

RESULT 18
US-10-437-963-47027
; Sequence 47027, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 47027
;   LENGTH: 1549
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_49836C.1
US-10-437-963-47027

Alignment Scores:
Pred. No.:              272           Length:        1549
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     7             Gaps:          0

US-10-758-902-9 (1-149) x US-10-437-963-47027 (1-1549)

Qy         29 ThrProValCysGlnLeuProVal 36
              |||||||||||||||||||||||||
Db        724 ACTCCGGTATGTCAACTACCTGTC 747

RESULT 19
US-10-425-115-183970/c
; Sequence 183970, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 183970
;   LENGTH: 1560
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_99368C.1
US-10-425-115-183970

Alignment Scores:
Pred. No.:              274           Length:        1560
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-9 (1-149) x US-10-425-115-183970 (1-1560)

Qy         52 IleThrThrThrSerLysLysThr 59
              |||||||||||||||||||||||||
Db        669 ATTACTACAACAAGCAAGAAGACC 646

RESULT 20
US-10-425-114-32782/c
; Sequence 32782, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32782
;   LENGTH: 1686
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLMO17021G08_FLI
US-10-425-114-32782

Alignment Scores:
Pred. No.:              295           Length:        1686
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
```

```
DB:                    7             Gaps:          0

US-10-758-902-9 (1-149) x US-10-425-114-32782 (1-1686)

Qy         96 SerLysLeuPheProGlyValThr 103
              |||||||||||||||||||||||
Db        112 TCTAAGTTGTTCCCAGGGGTTACC 89

RESULT 21
US-10-425-114-32261/c
; Sequence 32261, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32261
;   LENGTH: 1879
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLB73280B05_FLI
US-10-425-114-32261

Alignment Scores:
Pred. No.:              327           Length:        1879
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     7             Gaps:          0

US-10-758-902-9 (1-149) x US-10-425-114-32261 (1-1879)

Qy         96 SerLysLeuPheProGlyValThr 103
              |||||||||||||||||||||||
Db        382 TCTAAGTTGTTCCCAGGGGTTACC 359

RESULT 22
US-09-938-842A-5069/c
; Sequence 5069, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 5069
;   LENGTH: 2000
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-5069

Alignment Scores:
Pred. No.:              347           Length:        2000
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-9 (1-149) x US-09-938-842A-5069 (1-2000)

Qy        134 LysLeuGluPheSerIleGluAla 141
              |||||||||||||||||||||||
Db        819 AAACTTGAATTTTCAATCGAAGCA 796

RESULT 23
US-09-938-842A-5069/c
; Sequence 5069, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 5069
;   LENGTH: 2000
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-5069

Alignment Scores:
Pred. No.:              347           Length:        2000
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-9 (1-149) x US-09-938-842A-5069 (1-2000)

Qy        134 LysLeuGluPheSerIleGluAla 141
              |||||||||||||||||||||||
Db        819 AAACTTGAATTTTCAATCGAAGCA 796

RESULT 24
US-10-425-114-30640/c
; Sequence 30640, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
```

; SEQ ID NO 30640
; LENGTH: 2187
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73052H05_FLI
US-10-425-114-30640

Alignment Scores:

Pred. No.:	378	Length:	2187
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	7	Gaps:	0

US-10-758-902-9 (1-149) x US-10-425-114-30640 (1-2187)

```
Qy         96 SerLysLeuPheProGlyValThr 103
              ||||||||||||||||||||||
Db        689 TCTAAGTTGTTCCCAGGGGTTACC 666
```

RESULT 25
US-09-925-065A-694362/c
; Sequence 694362, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 694362
; LENGTH: 2443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352,
; LOCATION: 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362,
; LOCATION: 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372,
; LOCATION: 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391,
; LOCATION: 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401,
; LOCATION: 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411,
; LOCATION: 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430,
; LOCATION: 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440,
; LOCATION: 2441, 2442
; OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-694362

Alignment Scores:

Pred. No.:	419	Length:	2443
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-9 (1-149) x US-09-925-065A-694362 (1-2443)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db       2040 ACAGTGTCATTTAATTTGGGAGAG 2017
```

RESULT 26
US-10-252-157-398
; Sequence 398, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Pearson, Cecelia I.
; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: PA-0027-1 US
; CURRENT APPLICATION NUMBER: US/10/252,157
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,048
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: PERL Program
; SEQ ID NO 398
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030190640A1 040057.2
US-10-252-157-398

Alignment Scores:

Pred. No.:	473	Length:	2772
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-9 (1-149) x US-10-252-157-398 (1-2772)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db       2634 ACAGTGTCATTTAATTTGGGAGAG 2657
```

RESULT 27
US-10-425-115-87686/c
; Sequence 87686, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 87686
; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_179970C.1
US-10-425-115-87686

```
Alignment Scores:
Pred. No.:                477             Length:         2797
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       8               Gaps:           0

US-10-758-902-9 (1-149) x US-10-425-115-87686 (1-2797)

Qy          96 SerLysLeuPheProGlyValThr 103
               ||||||||||||||||||||||||
Db        1204 TCTAAGTTGTTCCCAGGGGTTACC 1181

RESULT 28
US-10-221-714A-84/c
; Sequence 84, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with
;  TITLE OF INVENTION:  tumor suppressor genes and oncogenes
;  FILE REFERENCE: 5013.1005
;  CURRENT APPLICATION NUMBER: US/10/221,714A
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: PCT/EP01/02955
;  PRIOR FILING DATE: 2001-03-15
;  PRIOR APPLICATION NUMBER: DE 10013847.0
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: DE 10019058.8
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 84
;   LENGTH: 6413
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 3770, 4027
;   OTHER INFORMATION: n is a or g or c or t
US-10-221-714A-84

Alignment Scores:
Pred. No.:                1.05e+03        Length:         6413
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       7               Gaps:           0

US-10-758-902-9 (1-149) x US-10-221-714A-84 (1-6413)

Qy          52 IleThrThrThrSerLysLysThr 59
               |||||||||||||||||||||||
Db          87 ATAACAACTACCTCAAAAAAAACT 64

RESULT 29
US-10-433-793-30/c
; Sequence 30, Application US/10433793
; Publication No. US20040142334A1
; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/433,793
;  CURRENT FILING DATE:  2003-06-06
;  NUMBER OF SEQ ID NOS: 212
; SEQ ID NO 30
;   LENGTH: 6413
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (3770, 4027)
;   OTHER INFORMATION: unknown base
US-10-433-793-30

Alignment Scores:
Pred. No.:                1.05e+03        Length:         6413
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       7               Gaps:           0

US-10-758-902-9 (1-149) x US-10-433-793-30 (1-6413)

Qy          52 IleThrThrThrSerLysLysThr 59
               |||||||||||||||||||||||
Db          87 ATAACAACTACCTCAAAAAAAACT 64

RESULT 30
US-10-741-601-5652/c
; Sequence 5652, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5652
;   LENGTH: 12648
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5652

Alignment Scores:
Pred. No.:                2e+03           Length:         12648
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       7               Gaps:           0

US-10-758-902-9 (1-149) x US-10-741-601-5652 (1-12648)

Qy           3 ThrValSerPheAsnLeuGlyGlu 10
               |||||||||||||||||||||||
Db       12509 ACAGTGTCATTTAATTTGGGAGAG 12486

RESULT 31
US-10-668-767-9/c
; Sequence 9, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
```

```
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 16363
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15890)..(15890)
;   OTHER INFORMATION: n = a, c, g, or t
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(15327)
;   OTHER INFORMATION:
US-10-668-767-9

Alignment Scores:
Pred. No.:              2.55e+03      Length:         16363
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     7             Gaps:           0

US-10-758-902-9 (1-149) x US-10-668-767-9 (1-16363)

Qy       105 ArgValThrLeuThrPheAspGly 112
             ||||||||||||||||||||||||
Db      7218 CGGGTAACGCTCACCTTCGACGGG 7195

RESULT 32
US-10-741-601-5690
; Sequence 5690, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5690
;   LENGTH: 31657
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5690

Alignment Scores:
Pred. No.:              4.77e+03      Length:         31657
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     7             Gaps:           0

US-10-758-902-9 (1-149) x US-10-741-601-5690 (1-31657)

Qy         3 ThrValSerPheAsnLeuGlyGlu 10
             |||||||||||||||||||||||
Db       190 ACAGTGTCATTTAATTTGGGAGAG 213

RESULT 33
US-10-087-192-1261
; Sequence 1261, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1261
;   LENGTH: 35076
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(35076)
;   OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1261

Alignment Scores:
Pred. No.:              5.26e+03      Length:         35076
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     5             Gaps:           0

US-10-758-902-9 (1-149) x US-10-087-192-1261 (1-35076)

Qy          30 ProValCysGlnLeuProValThr 37
               |||||||||||||||||||||||
Db       31394 CCTGTTTGTCAGCTTCCTGTTACT 31417

RESULT 34
US-10-741-601-5771
; Sequence 5771, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5771
;   LENGTH: 41309
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5771

Alignment Scores:
Pred. No.:              6.14e+03      Length:         41309
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     7             Gaps:           0

US-10-758-902-9 (1-149) x US-10-741-601-5771 (1-41309)

Qy         3 ThrValSerPheAsnLeuGlyGlu 10
             |||||||||||||||||||||||
```

```
Db      34625 ACAGTGTCATTTAATTTGGGAGAG 34648

RESULT 35
US-10-085-117-133/c
; Sequence 133, Application US/10085117
; Publication No. US20030232334A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: 529452000121
;  CURRENT APPLICATION NUMBER: US/10/085,117
;  CURRENT FILING DATE:  2002-02-27
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 361
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
;   LENGTH: 55606
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: (1)...(55606)
;   OTHER INFORMATION: n = any nucleotide
US-10-085-117-133

Alignment Scores:
Pred. No.:              8.15e+03        Length:         55606
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x US-10-085-117-133 (1-55606)

Qy         31 ValCysGlnLeuProValThrLeu 38
              |||||||||||||||||||||||
Db      54784 GTTTGCCAGTTGCCAGTGACCCTG 54761

RESULT 36
US-10-741-601-5650
; Sequence 5650, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5650
;   LENGTH: 63693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5650

Alignment Scores:
Pred. No.:              9.27e+03        Length:         63693
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-9 (1-149) x US-10-741-601-5650 (1-63693)

Qy         55 ThrSerLysLysThrValLysVal 62
              |||||||||||||||||||||||
Db      50804 ACAAGCAAAAAAACAGTAAAGGTC 50827

RESULT 37
US-10-085-117-151/c
; Sequence 151, Application US/10085117
; Publication No. US20030232334A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: 529452000121
;  CURRENT APPLICATION NUMBER: US/10/085,117
;  CURRENT FILING DATE:  2002-02-27
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 361
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151
;   LENGTH: 77038
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: (1)...(77038)
;   OTHER INFORMATION: n = any nucleotide
US-10-085-117-151

Alignment Scores:
Pred. No.:              1.11e+04        Length:         77038
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x US-10-085-117-151 (1-77038)

Qy         57 LysLysThrValLysValAlaIle 64
              |||||||||||||||||||||||
Db      6193 AAGAAAACAGTCAAGGTTGCTATC 6170

RESULT 38
US-10-087-192-628/c
; Sequence 628, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 628
;   LENGTH: 92247
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(92247)
;   OTHER INFORMATION: n = A,T,C or G
US-10-087-192-628

Alignment Scores:
Pred. No.:              1.32e+04        Length:         92247
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
```

```
Query Match:            5.4%          Indels:        0
DB:                     5             Gaps:          0

US-10-758-902-9 (1-149) x US-10-087-192-628 (1-92247)

Qy        101 GlyValThrAsnArgValThrLeu 108
              ||||||||||||||||||||||||
Db      10645 GGAGTCACAAACCGGGTCACCCTA 10622

RESULT 39
US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
;  FILE REFERENCE: E01/1208/WO
;  CURRENT APPLICATION NUMBER: US/10/312,841
;  CURRENT FILING DATE:  2002-12-30
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
;   LENGTH: 3673778
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (3294164)
US-10-312-841-1

Alignment Scores:
Pred. No.:              4.3e+05       Length:        3673778
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-9 (1-149) x US-10-312-841-1 (1-3673778)

Qy        131 GlyValTyrLysLeuGluPheSer 138
              ||||||||||||||||||||||||
Db    2971742 GGGGTTTATAAGTTAGAATTTAGT 2971765

RESULT 40
US-10-758-902-3/c
; Sequence 3, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR primer 116 for Ribosome-inactivating protein,
;   OTHER INFORMATION: bouganin.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 3, 6, 12, 15
;   OTHER INFORMATION: n = A,T,C or G
US-10-758-902-3

Alignment Scores:
Pred. No.:              63.8          Length:        23
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.7%          Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-9 (1-149) x US-10-758-902-3 (1-23)

Qy         23 AsnGluLeuAlaLysGlyThr 29
              |||||||||||||||||||||
Db         23 AAYGARCTNGCNAARGGNACN 3


Search completed: February 20, 2006, 03:26:02
Job time : 1786.59 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 02:03:29 ; Search time 522.749 Seconds
(without alignments)
605.048 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 149
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7204252 seqs, 1061369211 residues

Word size: 1

Total number of hits satisfying chosen parameters: 14406942

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160842_4223/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=oligo.rnpbn
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
-USER=US10758902_@CGN_1_1_380_@runat_17022006_160842_4223 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	8	5.4	201	8	US-10-995-561-34779	Sequence 34779, A
	2	8	5.4	416	6	US-09-925-065A-47024	Sequence 47024, A
c	3	8	5.4	487	6	US-09-925-065A-630179	Sequence 630179,
	4	8	5.4	565	6	US-09-925-065A-325312	Sequence 325312,
	5	8	5.4	622	6	US-09-925-065A-787599	Sequence 787599,
	6	8	5.4	631	8	US-10-750-185-28892	Sequence 28892, A
	7	8	5.4	631	8	US-10-750-623-28892	Sequence 28892, A
c	8	8	5.4	2443	6	US-09-925-065A-694362	Sequence 694362,
c	9	8	5.4	12648	8	US-10-995-561-13271	Sequence 13271, A
c	10	8	5.4	31130	12	US-11-124-367A-5063	Sequence 5063, Ap
	11	8	5.4	31657	8	US-10-995-561-13334	Sequence 13334, A
	12	8	5.4	41309	8	US-10-995-561-13487	Sequence 13487, A
	13	8	5.4	63693	8	US-10-995-561-13269	Sequence 13269, A
	14	7	4.7	25	12	US-11-136-527-329283	Sequence 329283,
c	15	7	4.7	50	12	US-11-175-859-100900	Sequence 100900,
	16	7	4.7	63	8	US-10-310-914A-13009	Sequence 13009, A
c	17	7	4.7	201	8	US-10-995-561-18821	Sequence 18821, A
c	18	7	4.7	201	8	US-10-995-561-19052	Sequence 19052, A
c	19	7	4.7	201	12	US-11-124-368A-10188	Sequence 10188, A
	20	7	4.7	279	12	US-11-145-703-62	Sequence 62, Appl
	21	7	4.7	279	12	US-11-145-703-85	Sequence 85, Appl
	22	7	4.7	280	12	US-11-145-703-74	Sequence 74, Appl
	23	7	4.7	280	12	US-11-145-703-97	Sequence 97, Appl
	24	7	4.7	280	12	US-11-145-703-109	Sequence 109, App
c	25	7	4.7	297	8	US-10-467-657-4591	Sequence 4591, Ap
	26	7	4.7	297	8	US-10-467-657-8599	Sequence 8599, Ap
	27	7	4.7	336	6	US-09-925-065A-350812	Sequence 350812,
	28	7	4.7	388	12	US-11-145-703-60	Sequence 60, Appl
	29	7	4.7	388	12	US-11-145-703-83	Sequence 83, Appl
	30	7	4.7	389	12	US-11-145-703-72	Sequence 72, Appl
	31	7	4.7	389	12	US-11-145-703-95	Sequence 95, Appl
	32	7	4.7	389	12	US-11-145-703-107	Sequence 107, App
c	33	7	4.7	410	6	US-09-925-065A-367811	Sequence 367811,
	34	7	4.7	439	8	US-10-802-796-98	Sequence 98, Appl
c	35	7	4.7	509	6	US-09-925-065A-304102	Sequence 304102,
c	36	7	4.7	509	6	US-09-925-065A-304103	Sequence 304103,
	37	7	4.7	515	6	US-09-925-065A-787865	Sequence 787865,
	38	7	4.7	524	6	US-09-925-065A-455365	Sequence 455365,
	39	7	4.7	526	6	US-09-925-065A-435174	Sequence 435174,
	40	7	4.7	530	6	US-09-925-065A-623014	Sequence 623014,
c	41	7	4.7	534	6	US-09-925-065A-51074	Sequence 51074, A
	42	7	4.7	539	6	US-09-925-065A-766112	Sequence 766112,
	43	7	4.7	539	6	US-09-925-065A-766113	Sequence 766113,
c	44	7	4.7	540	6	US-09-925-065A-752884	Sequence 752884,
c	45	7	4.7	541	6	US-09-925-065A-205681	Sequence 205681,
	46	7	4.7	548	6	US-09-925-065A-810826	Sequence 810826,
	47	7	4.7	550	6	US-09-925-065A-137135	Sequence 137135,
	48	7	4.7	551	6	US-09-925-065A-123248	Sequence 123248,
c	49	7	4.7	555	6	US-09-925-065A-643449	Sequence 643449,
	50	7	4.7	559	6	US-09-925-065A-846418	Sequence 846418,
c	51	7	4.7	561	6	US-09-925-065A-760512	Sequence 760512,
c	52	7	4.7	562	6	US-09-925-065A-124610	Sequence 124610,
	53	7	4.7	565	6	US-09-925-065A-761519	Sequence 761519,
	54	7	4.7	566	6	US-09-925-065A-771199	Sequence 771199,
	55	7	4.7	568	6	US-09-925-065A-17111	Sequence 17111, A
c	56	7	4.7	568	6	US-09-925-065A-441555	Sequence 441555,
	57	7	4.7	571	6	US-09-925-065A-762385	Sequence 762385,
c	58	7	4.7	575	6	US-09-925-065A-603977	Sequence 603977,
c	59	7	4.7	575	6	US-09-925-065A-603978	Sequence 603978,
c	60	7	4.7	576	6	US-09-925-065A-883897	Sequence 883897,
	61	7	4.7	580	6	US-09-925-065A-791073	Sequence 791073,
	62	7	4.7	580	6	US-09-925-065A-848338	Sequence 848338,
c	63	7	4.7	583	6	US-09-925-065A-244461	Sequence 244461,
c	64	7	4.7	583	6	US-09-925-065A-244462	Sequence 244462,
c	65	7	4.7	583	6	US-09-925-065A-244463	Sequence 244463,
c	66	7	4.7	586	6	US-09-925-065A-739320	Sequence 739320,
c	67	7	4.7	588	6	US-09-925-065A-21277	Sequence 21277, A
c	68	7	4.7	593	6	US-09-925-065A-461621	Sequence 461621,
	69	7	4.7	595	6	US-09-925-065A-383360	Sequence 383360,
c	70	7	4.7	598	6	US-09-925-065A-739079	Sequence 739079,
c	71	7	4.7	599	6	US-09-925-065A-304104	Sequence 304104,
	72	7	4.7	600	6	US-09-925-065A-297159	Sequence 297159,
	73	7	4.7	600	6	US-09-925-065A-297160	Sequence 297160,
	74	7	4.7	600	6	US-09-925-065A-770636	Sequence 770636,
c	75	7	4.7	600	8	US-10-750-185-157	Sequence 157, App
	76	7	4.7	600	8	US-10-750-185-20576	Sequence 20576, A
c	77	7	4.7	600	8	US-10-750-185-21085	Sequence 21085, A

c 78	7	4.7	600	8	US-10-750-623-157	Sequence 157, App
79	7	4.7	600	8	US-10-750-623-20576	Sequence 20576, A
c 80	7	4.7	600	8	US-10-750-623-21085	Sequence 21085, A
c 81	7	4.7	601	8	US-10-750-185-193	Sequence 193, App
c 82	7	4.7	601	8	US-10-750-623-193	Sequence 193, App
c 83	7	4.7	606	6	US-09-925-065A-930991	Sequence 930991,
c 84	7	4.7	613	6	US-09-925-065A-528146	Sequence 528146,
85	7	4.7	614	6	US-09-925-065A-819222	Sequence 819222,
86	7	4.7	615	6	US-09-925-065A-420204	Sequence 420204,
87	7	4.7	615	6	US-09-925-065A-420205	Sequence 420205,
c 88	7	4.7	616	6	US-09-925-065A-259258	Sequence 259258,
89	7	4.7	617	6	US-09-925-065A-305608	Sequence 305608,
90	7	4.7	617	6	US-09-925-065A-305609	Sequence 305609,
91	7	4.7	624	6	US-09-925-065A-196365	Sequence 196365,
c 92	7	4.7	628	6	US-09-925-065A-754136	Sequence 754136,
c 93	7	4.7	628	6	US-09-925-065A-754137	Sequence 754137,
c 94	7	4.7	634	6	US-09-925-065A-933392	Sequence 933392,
95	7	4.7	635	6	US-09-925-065A-731743	Sequence 731743,
96	7	4.7	635	6	US-09-925-065A-731744	Sequence 731744,
97	7	4.7	637	6	US-09-925-065A-774082	Sequence 774082,
98	7	4.7	637	6	US-09-925-065A-774083	Sequence 774083,
99	7	4.7	637	6	US-09-925-065A-837178	Sequence 837178,
c 100	7	4.7	639	6	US-09-925-065A-123750	Sequence 123750,
c 101	7	4.7	639	6	US-09-925-065A-749343	Sequence 749343,
c 102	7	4.7	639	6	US-09-925-065A-749344	Sequence 749344,
c 103	7	4.7	640	6	US-09-925-065A-941724	Sequence 941724,
104	7	4.7	641	6	US-09-925-065A-885409	Sequence 885409,
105	7	4.7	641	6	US-09-925-065A-885410	Sequence 885410,
c 106	7	4.7	643	6	US-09-925-065A-796338	Sequence 796338,
c 107	7	4.7	643	6	US-09-925-065A-796339	Sequence 796339,
c 108	7	4.7	654	6	US-09-925-065A-849878	Sequence 849878,
c 109	7	4.7	677	6	US-09-925-065A-199686	Sequence 199686,
c 110	7	4.7	677	6	US-09-925-065A-199687	Sequence 199687,
c 111	7	4.7	710	6	US-09-925-065A-908064	Sequence 908064,
112	7	4.7	712	6	US-09-925-065A-58956	Sequence 58956, A
c 113	7	4.7	721	6	US-09-925-065A-668638	Sequence 668638,
c 114	7	4.7	728	6	US-09-925-065A-693874	Sequence 693874,
c 115	7	4.7	736	8	US-10-750-185-34696	Sequence 34696, A
c 116	7	4.7	736	8	US-10-750-623-34696	Sequence 34696, A
117	7	4.7	742	12	US-11-145-703-19	Sequence 19, Appl
118	7	4.7	776	12	US-11-145-703-25	Sequence 25, Appl
119	7	4.7	777	12	US-11-145-703-13	Sequence 13, Appl
c 120	7	4.7	805	8	US-10-750-185-38510	Sequence 38510, A
c 121	7	4.7	805	8	US-10-750-623-38510	Sequence 38510, A
122	7	4.7	807	6	US-09-925-065A-28987	Sequence 28987, A
123	7	4.7	811	12	US-11-145-703-21	Sequence 21, Appl
124	7	4.7	814	6	US-09-925-065A-923844	Sequence 923844,
125	7	4.7	822	12	US-11-145-703-24	Sequence 24, Appl
126	7	4.7	823	12	US-11-145-703-14	Sequence 14, Appl
c 127	7	4.7	830	8	US-10-750-185-41214	Sequence 41214, A
c 128	7	4.7	830	8	US-10-750-623-41214	Sequence 41214, A
129	7	4.7	836	12	US-11-145-703-15	Sequence 15, Appl
130	7	4.7	851	12	US-11-145-703-18	Sequence 18, Appl
131	7	4.7	860	6	US-09-925-065A-90376	Sequence 90376, A
132	7	4.7	860	6	US-09-925-065A-90377	Sequence 90377, A
c 133	7	4.7	863	6	US-09-925-065A-719979	Sequence 719979,
134	7	4.7	863	12	US-11-145-703-6	Sequence 6, Appli
135	7	4.7	882	12	US-11-145-703-16	Sequence 16, Appl
136	7	4.7	897	12	US-11-145-703-12	Sequence 12, Appl
137	7	4.7	920	12	US-11-145-703-20	Sequence 20, Appl
138	7	4.7	925	6	US-09-925-065A-32187	Sequence 32187, A
139	7	4.7	947	12	US-11-145-703-26	Sequence 26, Appl
140	7	4.7	951	8	US-10-821-234-674	Sequence 674, App
141	7	4.7	955	12	US-11-145-703-17	Sequence 17, Appl
142	7	4.7	960	8	US-10-793-626-791	Sequence 791, App
143	7	4.7	960	8	US-10-793-626-2007	Sequence 2007, Ap
144	7	4.7	978	12	US-11-145-703-22	Sequence 22, Appl
145	7	4.7	993	12	US-11-145-703-23	Sequence 23, Appl
146	7	4.7	995	12	US-11-145-703-2	Sequence 2, Appli
147	7	4.7	1009	12	US-11-145-703-11	Sequence 11, Appl
c 148	7	4.7	1010	6	US-09-925-065A-27118	Sequence 27118, A
c 149	7	4.7	1010	6	US-09-925-065A-27119	Sequence 27119, A
c 150	7	4.7	1010	6	US-09-925-065A-27120	Sequence 27120, A
c 151	7	4.7	1010	6	US-09-925-065A-27121	Sequence 27121, A
c 152	7	4.7	1152	8	US-10-750-185-43523	Sequence 43523, A
c 153	7	4.7	1152	8	US-10-750-623-43523	Sequence 43523, A
c 154	7	4.7	1185	12	US-11-169-096-9	Sequence 9, Appli
155	7	4.7	1195	8	US-10-750-185-38487	Sequence 38487, A
156	7	4.7	1195	8	US-10-750-623-38487	Sequence 38487, A
157	7	4.7	1202	8	US-10-750-185-46068	Sequence 46068, A
158	7	4.7	1202	8	US-10-750-623-46068	Sequence 46068, A
c 159	7	4.7	1277	8	US-10-492-835-3	Sequence 3, Appli
c 160	7	4.7	1283	6	US-09-925-065A-710488	Sequence 710488,
161	7	4.7	1400	12	US-11-136-527-6993	Sequence 6993, Ap
c 162	7	4.7	1432	12	US-11-000-688-1223	Sequence 1223, Ap
c 163	7	4.7	1722	8	US-10-750-185-42577	Sequence 42577, A
c 164	7	4.7	1722	8	US-10-750-623-42577	Sequence 42577, A
c 165	7	4.7	1761	8	US-10-750-185-34496	Sequence 34496, A
c 166	7	4.7	1761	8	US-10-750-623-34496	Sequence 34496, A
c 167	7	4.7	1803	6	US-09-925-065A-726953	Sequence 726953,
168	7	4.7	1824	8	US-10-750-185-37184	Sequence 37184, A
169	7	4.7	1824	8	US-10-750-623-37184	Sequence 37184, A
c 170	7	4.7	1925	6	US-09-925-065A-71070	Sequence 71070, A
171	7	4.7	1959	8	US-10-750-185-46514	Sequence 46514, A
172	7	4.7	1959	8	US-10-750-623-46514	Sequence 46514, A
c 173	7	4.7	1996	9	US-11-072-512-219	Sequence 219, App
c 174	7	4.7	2081	8	US-10-750-185-62534	Sequence 62534, A
c 175	7	4.7	2081	8	US-10-750-623-62534	Sequence 62534, A
c 176	7	4.7	2162	8	US-10-750-185-43351	Sequence 43351, A
c 177	7	4.7	2162	8	US-10-750-623-43351	Sequence 43351, A
178	7	4.7	2190	9	US-11-072-512-226	Sequence 226, App
179	7	4.7	2296	8	US-10-750-185-62004	Sequence 62004, A
180	7	4.7	2296	8	US-10-750-623-62004	Sequence 62004, A
c 181	7	4.7	2371	8	US-10-492-835-7	Sequence 7, Appli
c 182	7	4.7	2419	8	US-10-492-835-11	Sequence 11, Appl
183	7	4.7	2586	7	US-10-063-703-7	Sequence 7, Appli
184	7	4.7	2586	12	US-11-102-240-7	Sequence 7, Appli
185	7	4.7	2631	8	US-10-793-626-3760	Sequence 3760, Ap
186	7	4.7	2645	6	US-09-925-065A-89593	Sequence 89593, A
187	7	4.7	2679	9	US-11-072-512-1168	Sequence 1168, Ap
188	7	4.7	2738	12	US-11-122-329-66	Sequence 66, Appl
c 189	7	4.7	2850	8	US-10-750-185-27384	Sequence 27384, A
c 190	7	4.7	2850	8	US-10-750-623-27384	Sequence 27384, A
191	7	4.7	2880	12	US-11-136-527-2897	Sequence 2897, Ap
c 192	7	4.7	2883	8	US-10-793-626-4366	Sequence 4366, Ap
c 193	7	4.7	3039	12	US-11-192-801-19	Sequence 19, Appl
c 194	7	4.7	3039	12	US-11-192-801-21	Sequence 21, Appl
c 195	7	4.7	3044	12	US-11-192-801-38	Sequence 38, Appl
c 196	7	4.7	3130	12	US-11-169-041-89	Sequence 89, Appl
c 197	7	4.7	3450	12	US-11-192-801-17	Sequence 17, Appl
c 198	7	4.7	3455	12	US-11-192-801-36	Sequence 36, Appl
c 199	7	4.7	3469	12	US-11-192-801-23	Sequence 23, Appl
c 200	7	4.7	3712	12	US-11-136-527-2314	Sequence 2314, Ap
c 201	7	4.7	3754	12	US-11-192-801-15	Sequence 15, Appl
c 202	7	4.7	3885	8	US-10-793-626-3883	Sequence 3883, Ap
c 203	7	4.7	4149	12	US-11-192-801-13	Sequence 13, Appl
c 204	7	4.7	8553	12	US-11-136-527-229	Sequence 229, App
c 205	7	4.7	12968	8	US-10-995-561-13403	Sequence 13403, A
c 206	7	4.7	17410	12	US-11-051-568-3	Sequence 3, Appli
207	7	4.7	20304	12	US-11-124-367A-5051	Sequence 5051, Ap
c 208	7	4.7	21044	12	US-11-124-367A-5018	Sequence 5018, Ap
c 209	7	4.7	53328	8	US-10-995-561-13243	Sequence 13243, A
210	7	4.7	57303	12	US-11-124-367A-5032	Sequence 5032, Ap
211	7	4.7	63984	12	US-11-121-086-26	Sequence 26, Appl
c 212	7	4.7	77246	12	US-11-124-368A-2907	Sequence 2907, Ap
213	7	4.7	100000	12	US-11-124-367A-5004	Sequence 5004, Ap
214	7	4.7	137671	12	US-11-121-086-47	Sequence 47, Appl
215	7	4.7	151828	12	US-11-117-187-197	Sequence 197, App
216	7	4.7	159695	12	US-11-121-086-56	Sequence 56, Appl
c 217	7	4.7	162085	12	US-11-121-086-7	Sequence 7, Appli
218	7	4.7	168753	12	US-11-181-234-1	Sequence 1, Appli
c 219	7	4.7	241805	8	US-10-995-561-13215	Sequence 13215, A
c 220	7	4.7	319608	12	US-11-145-703-1	Sequence 1, Appli
c 221	7	4.7	380749	8	US-10-995-561-13216	Sequence 13216, A
c 222	7	4.7	394468	8	US-10-995-561-13473	Sequence 13473, A
223	7	4.7	1082144	12	US-11-117-187-211	Sequence 211, App

c 224	7	4.7	1691140	12	US-11-091-018-1	Sequence 1, Appli
c 225	6	4.0	18	8	US-10-310-914A-387011	Sequence 387011,
226	6	4.0	19	8	US-10-310-914A-195697	Sequence 195697,
227	6	4.0	19	8	US-10-310-914A-451683	Sequence 451683,
228	6	4.0	19	8	US-10-310-914A-480089	Sequence 480089,
229	6	4.0	19	8	US-10-310-914A-1352459	Sequence 1352459,
c 230	6	4.0	19	10	US-11-101-244-98592	Sequence 98592, A
c 231	6	4.0	19	10	US-11-101-244-364105	Sequence 364105,
232	6	4.0	19	10	US-11-101-244-492697	Sequence 492697,
233	6	4.0	19	10	US-11-101-244-819066	Sequence 819066,
234	6	4.0	19	10	US-11-101-244-1034469	Sequence 1034469,
c 235	6	4.0	19	10	US-11-101-244-1079085	Sequence 1079085,
c 236	6	4.0	19	10	US-11-101-244-1161544	Sequence 1161544,
237	6	4.0	19	10	US-11-101-244-1305795	Sequence 1305795,
c 238	6	4.0	19	10	US-11-101-244-1426012	Sequence 1426012,
239	6	4.0	19	10	US-11-101-244-1568607	Sequence 1568607,
c 240	6	4.0	19	11	US-11-083-784-98592	Sequence 98592, A
c 241	6	4.0	19	11	US-11-083-784-364105	Sequence 364105,
242	6	4.0	19	11	US-11-083-784-492697	Sequence 492697,
243	6	4.0	19	11	US-11-083-784-819066	Sequence 819066,
244	6	4.0	19	11	US-11-083-784-1034469	Sequence 1034469,
c 245	6	4.0	19	11	US-11-083-784-1079085	Sequence 1079085,
c 246	6	4.0	19	11	US-11-083-784-1161544	Sequence 1161544,
247	6	4.0	19	11	US-11-083-784-1305795	Sequence 1305795,
c 248	6	4.0	19	11	US-11-083-784-1426012	Sequence 1426012,
249	6	4.0	19	11	US-11-083-784-1568607	Sequence 1568607,
c 250	6	4.0	21	8	US-10-310-914A-475897	Sequence 475897,
251	6	4.0	22	8	US-10-857-780-4559	Sequence 4559, Ap
c 252	6	4.0	22	8	US-10-310-914A-676177	Sequence 676177,
253	6	4.0	22	8	US-10-310-914A-1135670	Sequence 1135670,
254	6	4.0	22	8	US-10-310-914A-1371121	Sequence 1371121,
c 255	6	4.0	23	8	US-10-310-914A-350649	Sequence 350649,
256	6	4.0	23	8	US-10-310-914A-480117	Sequence 480117,
257	6	4.0	23	8	US-10-310-914A-1352428	Sequence 1352428,
258	6	4.0	24	8	US-10-310-914A-723268	Sequence 723268,
c 259	6	4.0	25	8	US-10-750-185-6242	Sequence 6242, Ap
c 260	6	4.0	25	8	US-10-750-623-6242	Sequence 6242, Ap
c 261	6	4.0	25	8	US-10-310-914A-132117	Sequence 132117,
c 262	6	4.0	25	8	US-10-310-914A-424632	Sequence 424632,
263	6	4.0	25	12	US-11-121-849-28958	Sequence 28958, A
264	6	4.0	25	12	US-11-121-849-43082	Sequence 43082, A
265	6	4.0	25	12	US-11-121-849-43083	Sequence 43083, A
266	6	4.0	25	12	US-11-121-849-43733	Sequence 43733, A
267	6	4.0	25	12	US-11-121-849-147180	Sequence 147180,
268	6	4.0	25	12	US-11-121-849-153896	Sequence 153896,
c 269	6	4.0	25	12	US-11-121-849-195503	Sequence 195503,
270	6	4.0	25	12	US-11-121-849-244133	Sequence 244133,
c 271	6	4.0	25	12	US-11-121-849-253552	Sequence 253552,
c 272	6	4.0	25	12	US-11-121-849-255753	Sequence 255753,
273	6	4.0	25	12	US-11-121-849-287209	Sequence 287209,
274	6	4.0	25	12	US-11-121-849-306644	Sequence 306644,
275	6	4.0	25	12	US-11-121-849-306829	Sequence 306829,
276	6	4.0	25	12	US-11-121-849-310168	Sequence 310168,
277	6	4.0	25	12	US-11-121-849-315346	Sequence 315346,
c 278	6	4.0	25	12	US-11-121-849-348397	Sequence 348397,
c 279	6	4.0	25	12	US-11-121-849-360780	Sequence 360780,
280	6	4.0	25	12	US-11-121-849-376542	Sequence 376542,
281	6	4.0	25	12	US-11-121-849-438584	Sequence 438584,
282	6	4.0	25	12	US-11-121-849-465663	Sequence 465663,
283	6	4.0	25	12	US-11-121-849-466165	Sequence 466165,
284	6	4.0	25	12	US-11-121-849-466166	Sequence 466166,
285	6	4.0	25	12	US-11-121-849-470559	Sequence 470559,
c 286	6	4.0	25	12	US-11-121-849-492968	Sequence 492968,
c 287	6	4.0	25	12	US-11-121-849-500378	Sequence 500378,
288	6	4.0	25	12	US-11-121-849-547377	Sequence 547377,
c 289	6	4.0	25	12	US-11-121-849-580448	Sequence 580448,
c 290	6	4.0	25	12	US-11-121-849-590667	Sequence 590667,
c 291	6	4.0	25	12	US-11-121-849-599462	Sequence 599462,
292	6	4.0	25	12	US-11-121-849-612981	Sequence 612981,
c 293	6	4.0	25	12	US-11-121-849-664645	Sequence 664645,
294	6	4.0	25	12	US-11-121-849-671499	Sequence 671499,
295	6	4.0	25	12	US-11-121-849-671500	Sequence 671500,
296	6	4.0	25	12	US-11-121-849-671501	Sequence 671501,
297	6	4.0	25	12	US-11-121-849-671502	Sequence 671502,
c 298	6	4.0	25	12	US-11-136-527-15391	Sequence 15391, A
299	6	4.0	25	12	US-11-136-527-18521	Sequence 18521, A
300	6	4.0	25	12	US-11-136-527-18526	Sequence 18526, A
301	6	4.0	25	12	US-11-136-527-18530	Sequence 18530, A
302	6	4.0	25	12	US-11-136-527-18534	Sequence 18534, A
303	6	4.0	25	12	US-11-136-527-18535	Sequence 18535, A
c 304	6	4.0	25	12	US-11-136-527-47577	Sequence 47577, A
c 305	6	4.0	25	12	US-11-136-527-47578	Sequence 47578, A
c 306	6	4.0	25	12	US-11-136-527-47580	Sequence 47580, A
c 307	6	4.0	25	12	US-11-136-527-47583	Sequence 47583, A
c 308	6	4.0	25	12	US-11-136-527-47597	Sequence 47597, A
309	6	4.0	25	12	US-11-136-527-88836	Sequence 88836, A
310	6	4.0	25	12	US-11-136-527-88844	Sequence 88844, A
311	6	4.0	25	12	US-11-136-527-88848	Sequence 88848, A
312	6	4.0	25	12	US-11-136-527-88854	Sequence 88854, A
313	6	4.0	25	12	US-11-136-527-178680	Sequence 178680,
314	6	4.0	25	12	US-11-136-527-178697	Sequence 178697,
c 315	6	4.0	25	12	US-11-136-527-241927	Sequence 241927,
316	6	4.0	25	12	US-11-136-527-251139	Sequence 251139,
317	6	4.0	25	12	US-11-136-527-251147	Sequence 251147,
318	6	4.0	25	12	US-11-136-527-251168	Sequence 251168,
319	6	4.0	25	12	US-11-136-527-259415	Sequence 259415,
320	6	4.0	25	12	US-11-136-527-259428	Sequence 259428,
321	6	4.0	25	12	US-11-136-527-259443	Sequence 259443,
322	6	4.0	25	12	US-11-136-527-289898	Sequence 289898,
323	6	4.0	26	8	US-10-310-914A-331685	Sequence 331685,
324	6	4.0	26	8	US-10-310-914A-451685	Sequence 451685,
325	6	4.0	26	8	US-10-310-914A-451734	Sequence 451734,
326	6	4.0	26	8	US-10-310-914A-466509	Sequence 466509,
327	6	4.0	26	8	US-10-310-914A-903255	Sequence 903255,
c 328	6	4.0	26	8	US-10-310-914A-1229715	Sequence 1229715,
329	6	4.0	27	8	US-10-310-914A-331686	Sequence 331686,
c 330	6	4.0	27	8	US-10-310-914A-602017	Sequence 602017,
c 331	6	4.0	29	8	US-10-514-761-18	Sequence 18, Appl
332	6	4.0	40	12	US-11-107-335-30	Sequence 30, Appl
333	6	4.0	50	12	US-11-175-859-4867	Sequence 4867, Ap
334	6	4.0	50	12	US-11-175-859-6463	Sequence 6463, Ap
335	6	4.0	50	12	US-11-175-859-7898	Sequence 7898, Ap
336	6	4.0	50	12	US-11-175-859-11830	Sequence 11830, A
337	6	4.0	50	12	US-11-175-859-29350	Sequence 29350, A
c 338	6	4.0	50	12	US-11-175-859-33632	Sequence 33632, A
339	6	4.0	50	12	US-11-175-859-59519	Sequence 59519, A
c 340	6	4.0	50	12	US-11-175-859-63949	Sequence 63949, A
c 341	6	4.0	50	12	US-11-175-859-68407	Sequence 68407, A
342	6	4.0	50	12	US-11-175-859-71025	Sequence 71025, A
343	6	4.0	50	12	US-11-175-859-75692	Sequence 75692, A
c 344	6	4.0	50	12	US-11-175-859-75879	Sequence 75879, A
c 345	6	4.0	50	12	US-11-175-859-77817	Sequence 77817, A
346	6	4.0	50	12	US-11-175-859-99214	Sequence 99214, A
347	6	4.0	50	12	US-11-175-859-111533	Sequence 111533,
348	6	4.0	72	8	US-10-310-914A-16394	Sequence 16394, A
349	6	4.0	73	12	US-11-043-788-29	Sequence 29, Appl
350	6	4.0	77	8	US-10-310-914A-11339	Sequence 11339, A
c 351	6	4.0	80	12	US-11-120-543-38	Sequence 38, Appl
352	6	4.0	80	12	US-11-120-543-39	Sequence 39, Appl
353	6	4.0	91	12	US-11-114-879-59	Sequence 59, Appl
354	6	4.0	123	12	US-11-043-752-3342	Sequence 3342, Ap
355	6	4.0	124	8	US-10-310-914A-15440	Sequence 15440, A
356	6	4.0	131	8	US-10-310-914A-5657	Sequence 5657, Ap
c 357	6	4.0	171	6	US-09-925-065A-344456	Sequence 344456,
c 358	6	4.0	171	6	US-09-925-065A-344457	Sequence 344457,
c 359	6	4.0	171	6	US-09-925-065A-344458	Sequence 344458,
360	6	4.0	189	6	US-09-925-065A-634375	Sequence 634375,
361	6	4.0	200	12	US-11-098-686-452	Sequence 452, App
362	6	4.0	200	12	US-11-098-686-732	Sequence 732, App
363	6	4.0	200	12	US-11-098-686-1083	Sequence 1083, Ap
c 364	6	4.0	200	12	US-11-098-686-1919	Sequence 1919, Ap
365	6	4.0	200	12	US-11-098-686-2643	Sequence 2643, Ap
366	6	4.0	200	12	US-11-098-686-3798	Sequence 3798, Ap
c 367	6	4.0	200	12	US-11-098-686-4594	Sequence 4594, Ap
c 368	6	4.0	200	12	US-11-098-686-6077	Sequence 6077, Ap
c 369	6	4.0	200	12	US-11-098-686-6424	Sequence 6424, Ap

c 370	6	4.0	200	12	US-11-098-686-6654	Sequence 6654, Ap
c 371	6	4.0	200	12	US-11-098-686-6837	Sequence 6837, Ap
372	6	4.0	200	12	US-11-098-686-7963	Sequence 7963, Ap
c 373	6	4.0	201	8	US-10-995-561-8228	Sequence 8228, Ap
c 374	6	4.0	201	8	US-10-995-561-8237	Sequence 8237, Ap
c 375	6	4.0	201	8	US-10-995-561-8251	Sequence 8251, Ap
c 376	6	4.0	201	8	US-10-995-561-8282	Sequence 8282, Ap
c 377	6	4.0	201	8	US-10-995-561-16546	Sequence 16546, A
378	6	4.0	201	8	US-10-995-561-16555	Sequence 16555, A
379	6	4.0	201	8	US-10-995-561-16747	Sequence 16747, A
c 380	6	4.0	201	8	US-10-995-561-17140	Sequence 17140, A
381	6	4.0	201	8	US-10-995-561-17563	Sequence 17563, A
382	6	4.0	201	8	US-10-995-561-17564	Sequence 17564, A
c 383	6	4.0	201	8	US-10-995-561-18540	Sequence 18540, A
c 384	6	4.0	201	8	US-10-995-561-19238	Sequence 19238, A
c 385	6	4.0	201	8	US-10-995-561-26468	Sequence 26468, A
c 386	6	4.0	201	8	US-10-995-561-26794	Sequence 26794, A
c 387	6	4.0	201	8	US-10-995-561-26796	Sequence 26796, A
388	6	4.0	201	8	US-10-995-561-35953	Sequence 35953, A
c 389	6	4.0	201	8	US-10-995-561-36511	Sequence 36511, A
c 390	6	4.0	201	8	US-10-995-561-37270	Sequence 37270, A
c 391	6	4.0	201	8	US-10-995-561-37367	Sequence 37367, A
c 392	6	4.0	201	8	US-10-995-561-41655	Sequence 41655, A
393	6	4.0	201	8	US-10-995-561-42668	Sequence 42668, A
394	6	4.0	201	8	US-10-995-561-44017	Sequence 44017, A
c 395	6	4.0	201	8	US-10-995-561-44377	Sequence 44377, A
c 396	6	4.0	201	8	US-10-995-561-44667	Sequence 44667, A
397	6	4.0	201	8	US-10-995-561-46189	Sequence 46189, A
398	6	4.0	201	8	US-10-995-561-46326	Sequence 46326, A
c 399	6	4.0	201	8	US-10-995-561-47684	Sequence 47684, A
c 400	6	4.0	201	8	US-10-995-561-48762	Sequence 48762, A
c 401	6	4.0	201	8	US-10-995-561-48764	Sequence 48764, A
402	6	4.0	201	8	US-10-995-561-55290	Sequence 55290, A
403	6	4.0	201	8	US-10-995-561-55406	Sequence 55406, A
404	6	4.0	201	8	US-10-995-561-55677	Sequence 55677, A
405	6	4.0	201	8	US-10-995-561-55680	Sequence 55680, A
406	6	4.0	201	8	US-10-995-561-56499	Sequence 56499, A
407	6	4.0	201	8	US-10-995-561-56670	Sequence 56670, A
c 408	6	4.0	201	8	US-10-995-561-56764	Sequence 56764, A
409	6	4.0	201	8	US-10-995-561-68642	Sequence 68642, A
410	6	4.0	201	8	US-10-995-561-74132	Sequence 74132, A
411	6	4.0	201	8	US-10-995-561-74140	Sequence 74140, A
412	6	4.0	201	8	US-10-995-561-74199	Sequence 74199, A
413	6	4.0	201	8	US-10-995-561-74206	Sequence 74206, A
c 414	6	4.0	201	8	US-10-995-561-76515	Sequence 76515, A
415	6	4.0	201	8	US-10-995-561-77451	Sequence 77451, A
c 416	6	4.0	201	8	US-10-995-561-78328	Sequence 78328, A
417	6	4.0	201	8	US-10-995-561-79858	Sequence 79858, A
418	6	4.0	201	12	US-11-124-368A-3672	Sequence 3672, Ap
419	6	4.0	201	12	US-11-124-368A-4831	Sequence 4831, Ap
420	6	4.0	201	12	US-11-124-368A-6729	Sequence 6729, Ap
421	6	4.0	201	12	US-11-124-368A-9764	Sequence 9764, Ap
422	6	4.0	201	12	US-11-124-368A-9779	Sequence 9779, Ap
423	6	4.0	201	12	US-11-124-368A-15947	Sequence 15947, A
424	6	4.0	201	12	US-11-124-368A-19765	Sequence 19765, A
c 425	6	4.0	201	12	US-11-124-367A-6785	Sequence 6785, Ap
c 426	6	4.0	201	12	US-11-124-367A-6786	Sequence 6786, Ap
c 427	6	4.0	201	12	US-11-124-367A-6787	Sequence 6787, Ap
428	6	4.0	201	12	US-11-124-367A-6976	Sequence 6976, Ap
c 429	6	4.0	201	12	US-11-124-367A-9153	Sequence 9153, Ap
c 430	6	4.0	201	12	US-11-124-367A-9930	Sequence 9930, Ap
c 431	6	4.0	201	12	US-11-124-367A-10787	Sequence 10787, A
c 432	6	4.0	201	12	US-11-124-367A-11420	Sequence 11420, A
433	6	4.0	201	12	US-11-124-367A-11533	Sequence 11533, A
434	6	4.0	201	12	US-11-124-367A-13427	Sequence 13427, A
c 435	6	4.0	201	12	US-11-124-367A-13819	Sequence 13819, A
c 436	6	4.0	201	12	US-11-124-367A-19828	Sequence 19828, A
437	6	4.0	201	12	US-11-124-367A-25115	Sequence 25115, A
c 438	6	4.0	201	12	US-11-124-367A-26329	Sequence 26329, A
c 439	6	4.0	201	12	US-11-124-367A-26349	Sequence 26349, A
c 440	6	4.0	201	12	US-11-124-367A-26415	Sequence 26415, A
441	6	4.0	201	12	US-11-124-367A-29863	Sequence 29863, A
c 442	6	4.0	201	12	US-11-124-367A-30401	Sequence 30401, A
c 443	6	4.0	201	12	US-11-124-367A-32032	Sequence 32032, A
444	6	4.0	201	12	US-11-124-367A-33076	Sequence 33076, A
c 445	6	4.0	201	12	US-11-124-367A-33522	Sequence 33522, A
c 446	6	4.0	201	12	US-11-124-367A-33850	Sequence 33850, A
447	6	4.0	211	6	US-09-925-065A-149879	Sequence 149879,
448	6	4.0	211	6	US-09-925-065A-149880	Sequence 149880,
c 449	6	4.0	219	12	US-11-108-172-133	Sequence 133, App
450	6	4.0	236	6	US-09-925-065A-582513	Sequence 582513,
c 451	6	4.0	237	9	US-11-021-492-64	Sequence 64, Appl
c 452	6	4.0	248	12	US-11-224-076-11	Sequence 11, Appl
453	6	4.0	261	8	US-10-467-657-6745	Sequence 6745, Ap
c 454	6	4.0	261	8	US-10-467-657-7789	Sequence 7789, Ap
c 455	6	4.0	267	6	US-09-925-065A-207261	Sequence 207261,
456	6	4.0	276	6	US-09-925-065A-239750	Sequence 239750,
c 457	6	4.0	277	6	US-09-925-065A-113423	Sequence 113423,
c 458	6	4.0	277	6	US-09-925-065A-190950	Sequence 190950,
c 459	6	4.0	277	6	US-09-925-065A-190951	Sequence 190951,
c 460	6	4.0	277	6	US-09-925-065A-190952	Sequence 190952,
c 461	6	4.0	290	6	US-09-925-065A-10701	Sequence 10701, A
462	6	4.0	291	6	US-09-925-065A-842372	Sequence 842372,
c 463	6	4.0	318	6	US-09-925-065A-481926	Sequence 481926,
c 464	6	4.0	321	6	US-09-925-065A-99958	Sequence 99958, A
c 465	6	4.0	321	6	US-09-925-065A-99959	Sequence 99959, A
c 466	6	4.0	321	6	US-09-925-065A-99960	Sequence 99960, A
c 467	6	4.0	321	12	US-11-224-076-4	Sequence 4, Appli
468	6	4.0	323	6	US-09-925-065A-854820	Sequence 854820,
469	6	4.0	329	6	US-09-925-065A-138164	Sequence 138164,
470	6	4.0	329	6	US-09-925-065A-138165	Sequence 138165,
c 471	6	4.0	332	6	US-09-925-065A-560298	Sequence 560298,
c 472	6	4.0	332	6	US-09-925-065A-560299	Sequence 560299,
c 473	6	4.0	334	6	US-09-925-065A-182498	Sequence 182498,
474	6	4.0	334	6	US-09-925-065A-284904	Sequence 284904,
c 475	6	4.0	336	6	US-09-925-065A-222690	Sequence 222690,
476	6	4.0	337	6	US-09-925-065A-502416	Sequence 502416,
477	6	4.0	337	6	US-09-925-065A-581332	Sequence 581332,
478	6	4.0	345	8	US-10-793-626-2297	Sequence 2297, Ap
c 479	6	4.0	348	6	US-09-925-065A-525752	Sequence 525752,
480	6	4.0	349	6	US-09-925-065A-204502	Sequence 204502,
c 481	6	4.0	356	6	US-09-925-065A-361377	Sequence 361377,
c 482	6	4.0	359	6	US-09-925-065A-557801	Sequence 557801,
c 483	6	4.0	360	6	US-09-925-065A-829584	Sequence 829584,
c 484	6	4.0	364	6	US-09-925-065A-139444	Sequence 139444,
c 485	6	4.0	364	6	US-09-925-065A-139445	Sequence 139445,
486	6	4.0	366	6	US-09-925-065A-209076	Sequence 209076,
487	6	4.0	367	6	US-09-925-065A-156605	Sequence 156605,
488	6	4.0	373	6	US-09-925-065A-243393	Sequence 243393,
c 489	6	4.0	376	6	US-09-925-065A-140602	Sequence 140602,
c 490	6	4.0	376	6	US-09-925-065A-140603	Sequence 140603,
c 491	6	4.0	380	6	US-09-925-065A-228927	Sequence 228927,
492	6	4.0	382	6	US-09-925-065A-177369	Sequence 177369,
493	6	4.0	382	6	US-09-925-065A-177370	Sequence 177370,
494	6	4.0	382	6	US-09-925-065A-177371	Sequence 177371,
c 495	6	4.0	383	6	US-09-925-065A-441078	Sequence 441078,
496	6	4.0	383	6	US-09-925-065A-640444	Sequence 640444,
c 497	6	4.0	384	6	US-09-925-065A-257907	Sequence 257907,
c 498	6	4.0	384	6	US-09-925-065A-257908	Sequence 257908,
499	6	4.0	385	6	US-09-925-065A-206384	Sequence 206384,
500	6	4.0	385	6	US-09-925-065A-339217	Sequence 339217,
c 501	6	4.0	387	6	US-09-925-065A-337678	Sequence 337678,
c 502	6	4.0	387	12	US-11-224-076-9	Sequence 9, Appli
c 503	6	4.0	388	6	US-09-925-065A-247522	Sequence 247522,
c 504	6	4.0	388	6	US-09-925-065A-622007	Sequence 622007,
505	6	4.0	393	6	US-09-925-065A-262854	Sequence 262854,
c 506	6	4.0	394	6	US-09-925-065A-558619	Sequence 558619,
c 507	6	4.0	396	6	US-09-925-065A-182105	Sequence 182105,
c 508	6	4.0	396	6	US-09-925-065A-182106	Sequence 182106,
509	6	4.0	398	6	US-09-925-065A-124209	Sequence 124209,
c 510	6	4.0	398	6	US-09-925-065A-179024	Sequence 179024,
511	6	4.0	400	6	US-09-925-065A-469427	Sequence 469427,
512	6	4.0	400	6	US-09-925-065A-469428	Sequence 469428,
c 513	6	4.0	402	6	US-09-925-065A-585353	Sequence 585353,
514	6	4.0	402	6	US-09-925-065A-778927	Sequence 778927,
515	6	4.0	402	6	US-09-925-065A-778928	Sequence 778928,

	516	6	4.0	402	6	US-09-925-065A-840323	Sequence 840323,
	517	6	4.0	403	6	US-09-925-065A-471905	Sequence 471905,
c	518	6	4.0	404	6	US-09-925-065A-379589	Sequence 379589,
c	519	6	4.0	406	12	US-11-224-076-10	Sequence 10, Appl
c	520	6	4.0	407	6	US-09-925-065A-607552	Sequence 607552,
	521	6	4.0	407	6	US-09-925-065A-613438	Sequence 613438,
	522	6	4.0	407	6	US-09-925-065A-613439	Sequence 613439,
	523	6	4.0	410	6	US-09-925-065A-508381	Sequence 508381,
c	524	6	4.0	411	8	US-10-793-626-911	Sequence 911, App
	525	6	4.0	412	6	US-09-925-065A-226177	Sequence 226177,
c	526	6	4.0	413	6	US-09-925-065A-135985	Sequence 135985,
	527	6	4.0	413	6	US-09-925-065A-228467	Sequence 228467,
c	528	6	4.0	413	6	US-09-925-065A-274844	Sequence 274844,
c	529	6	4.0	413	6	US-09-925-065A-274845	Sequence 274845,
c	530	6	4.0	413	6	US-09-925-065A-274846	Sequence 274846,
c	531	6	4.0	413	6	US-09-925-065A-274847	Sequence 274847,
	532	6	4.0	413	6	US-09-925-065A-574298	Sequence 574298,
c	533	6	4.0	414	6	US-09-925-065A-125919	Sequence 125919,
	534	6	4.0	415	6	US-09-925-065A-439553	Sequence 439553,
	535	6	4.0	415	6	US-09-925-065A-439554	Sequence 439554,
	536	6	4.0	416	6	US-09-925-065A-912468	Sequence 912468,
c	537	6	4.0	417	6	US-09-925-065A-113088	Sequence 113088,
c	538	6	4.0	417	6	US-09-925-065A-113089	Sequence 113089,
	539	6	4.0	417	6	US-09-925-065A-191925	Sequence 191925,
	540	6	4.0	417	6	US-09-925-065A-646667	Sequence 646667,
c	541	6	4.0	419	6	US-09-925-065A-150920	Sequence 150920,
	542	6	4.0	420	6	US-09-925-065A-135499	Sequence 135499,
	543	6	4.0	420	6	US-09-925-065A-567637	Sequence 567637,
	544	6	4.0	420	6	US-09-925-065A-590250	Sequence 590250,
	545	6	4.0	421	6	US-09-925-065A-135496	Sequence 135496,
	546	6	4.0	422	6	US-09-925-065A-116233	Sequence 116233,
	547	6	4.0	422	6	US-09-925-065A-135495	Sequence 135495,
	548	6	4.0	422	6	US-09-925-065A-892649	Sequence 892649,
	549	6	4.0	422	6	US-09-925-065A-894930	Sequence 894930,
c	550	6	4.0	423	6	US-09-925-065A-95695	Sequence 95695, A
c	551	6	4.0	423	6	US-09-925-065A-130218	Sequence 130218,
	552	6	4.0	423	6	US-09-925-065A-824970	Sequence 824970,
c	553	6	4.0	424	6	US-09-925-065A-217393	Sequence 217393,
	554	6	4.0	424	6	US-09-925-065A-892505	Sequence 892505,
c	555	6	4.0	425	6	US-09-925-065A-204154	Sequence 204154,
c	556	6	4.0	425	6	US-09-925-065A-204155	Sequence 204155,
c	557	6	4.0	425	6	US-09-925-065A-459665	Sequence 459665,
	558	6	4.0	425	6	US-09-925-065A-892721	Sequence 892721,
	559	6	4.0	428	6	US-09-925-065A-237013	Sequence 237013,
	560	6	4.0	428	6	US-09-925-065A-646530	Sequence 646530,
c	561	6	4.0	429	6	US-09-925-065A-130219	Sequence 130219,
c	562	6	4.0	429	12	US-11-136-527-1391	Sequence 1391, Ap
	563	6	4.0	429	12	US-11-136-527-5487	Sequence 5487, Ap
c	564	6	4.0	430	6	US-09-925-065A-214164	Sequence 214164,
c	565	6	4.0	431	6	US-09-925-065A-214161	Sequence 214161,
	566	6	4.0	431	6	US-09-925-065A-348585	Sequence 348585,
c	567	6	4.0	433	6	US-09-925-065A-508144	Sequence 508144,
c	568	6	4.0	433	6	US-09-925-065A-508145	Sequence 508145,
	569	6	4.0	433	6	US-09-925-065A-639620	Sequence 639620,
	570	6	4.0	433	6	US-09-925-065A-639621	Sequence 639621,
c	571	6	4.0	434	6	US-09-925-065A-610211	Sequence 610211,
	572	6	4.0	435	6	US-09-925-065A-952914	Sequence 952914,
c	573	6	4.0	436	6	US-09-925-065A-195643	Sequence 195643,
c	574	6	4.0	438	6	US-09-925-065A-214162	Sequence 214162,
c	575	6	4.0	438	6	US-09-925-065A-214163	Sequence 214163,
c	576	6	4.0	439	6	US-09-925-065A-917848	Sequence 917848,
c	577	6	4.0	440	12	US-11-043-752-765	Sequence 765, App
c	578	6	4.0	441	6	US-09-925-065A-142089	Sequence 142089,
c	579	6	4.0	441	6	US-09-925-065A-233531	Sequence 233531,
c	580	6	4.0	441	6	US-09-925-065A-479193	Sequence 479193,
	581	6	4.0	442	6	US-09-925-065A-662831	Sequence 662831,
c	582	6	4.0	447	6	US-09-925-065A-200046	Sequence 200046,
	583	6	4.0	447	6	US-09-925-065A-217798	Sequence 217798,
c	584	6	4.0	447	6	US-09-925-065A-929791	Sequence 929791,
c	585	6	4.0	447	6	US-09-925-065A-950383	Sequence 950383,
c	586	6	4.0	449	6	US-09-925-065A-172316	Sequence 172316,
c	587	6	4.0	449	6	US-09-925-065A-259269	Sequence 259269,
	588	6	4.0	449	6	US-09-925-065A-381889	Sequence 381889,
c	589	6	4.0	449	6	US-09-925-065A-928120	Sequence 928120,
	590	6	4.0	450	6	US-09-925-065A-222394	Sequence 222394,
	591	6	4.0	450	6	US-09-925-065A-521460	Sequence 521460,
	592	6	4.0	450	6	US-09-925-065A-521461	Sequence 521461,
c	593	6	4.0	451	6	US-09-925-065A-927385	Sequence 927385,
	594	6	4.0	453	8	US-10-750-185-32400	Sequence 32400, A
	595	6	4.0	453	8	US-10-750-623-32400	Sequence 32400, A
c	596	6	4.0	454	6	US-09-925-065A-612109	Sequence 612109,
c	597	6	4.0	454	6	US-09-925-065A-637047	Sequence 637047,
c	598	6	4.0	454	6	US-09-925-065A-778596	Sequence 778596,
c	599	6	4.0	454	6	US-09-925-065A-840036	Sequence 840036,
c	600	6	4.0	454	12	US-11-000-688-1183	Sequence 1183, Ap
	601	6	4.0	457	6	US-09-925-065A-45347	Sequence 45347, A
	602	6	4.0	457	6	US-09-925-065A-233071	Sequence 233071,
c	603	6	4.0	458	6	US-09-925-065A-132265	Sequence 132265,
c	604	6	4.0	458	6	US-09-925-065A-414111	Sequence 414111,
c	605	6	4.0	458	9	US-11-031-206-153	Sequence 153, App
c	606	6	4.0	460	6	US-09-925-065A-106666	Sequence 106666,
	607	6	4.0	460	6	US-09-925-065A-117180	Sequence 117180,
	608	6	4.0	460	6	US-09-925-065A-153845	Sequence 153845,
c	609	6	4.0	460	6	US-09-925-065A-212964	Sequence 212964,
c	610	6	4.0	460	6	US-09-925-065A-506150	Sequence 506150,
c	611	6	4.0	460	6	US-09-925-065A-506151	Sequence 506151,
c	612	6	4.0	462	6	US-09-925-065A-222562	Sequence 222562,
	613	6	4.0	462	6	US-09-925-065A-443627	Sequence 443627,
	614	6	4.0	462	6	US-09-925-065A-443628	Sequence 443628,
	615	6	4.0	462	6	US-09-925-065A-443630	Sequence 443630,
	616	6	4.0	462	6	US-09-925-065A-738876	Sequence 738876,
	617	6	4.0	462	8	US-10-793-626-2825	Sequence 2825, Ap
c	618	6	4.0	462	9	US-11-021-492-176	Sequence 176, App
	619	6	4.0	463	6	US-09-925-065A-459907	Sequence 459907,
	620	6	4.0	463	6	US-09-925-065A-530430	Sequence 530430,
	621	6	4.0	464	6	US-09-925-065A-156965	Sequence 156965,
c	622	6	4.0	465	6	US-09-925-065A-311084	Sequence 311084,
c	623	6	4.0	465	6	US-09-925-065A-463972	Sequence 463972,
	624	6	4.0	465	6	US-09-925-065A-527888	Sequence 527888,
	625	6	4.0	465	6	US-09-925-065A-611477	Sequence 611477,
c	626	6	4.0	466	6	US-09-925-065A-400421	Sequence 400421,
c	627	6	4.0	466	6	US-09-925-065A-400422	Sequence 400422,
c	628	6	4.0	466	6	US-09-925-065A-472592	Sequence 472592,
c	629	6	4.0	467	6	US-09-925-065A-128009	Sequence 128009,
c	630	6	4.0	467	6	US-09-925-065A-128010	Sequence 128010,
	631	6	4.0	467	6	US-09-925-065A-545136	Sequence 545136,
	632	6	4.0	468	6	US-09-925-065A-244856	Sequence 244856,
	633	6	4.0	468	6	US-09-925-065A-244857	Sequence 244857,
	634	6	4.0	468	6	US-09-925-065A-244858	Sequence 244858,
c	635	6	4.0	469	6	US-09-925-065A-273942	Sequence 273942,
	636	6	4.0	469	6	US-09-925-065A-780197	Sequence 780197,
c	637	6	4.0	469	12	US-11-120-308-119	Sequence 119, App
c	638	6	4.0	470	6	US-09-925-065A-298509	Sequence 298509,
c	639	6	4.0	470	6	US-09-925-065A-483678	Sequence 483678,
c	640	6	4.0	471	6	US-09-925-065A-265327	Sequence 265327,
c	641	6	4.0	471	6	US-09-925-065A-265328	Sequence 265328,
c	642	6	4.0	471	6	US-09-925-065A-265329	Sequence 265329,
	643	6	4.0	471	6	US-09-925-065A-411002	Sequence 411002,
	644	6	4.0	471	6	US-09-925-065A-751736	Sequence 751736,
	645	6	4.0	472	6	US-09-925-065A-299401	Sequence 299401,
	646	6	4.0	473	6	US-09-925-065A-424848	Sequence 424848,
c	647	6	4.0	473	6	US-09-925-065A-482638	Sequence 482638,
c	648	6	4.0	473	6	US-09-925-065A-745194	Sequence 745194,
	649	6	4.0	474	6	US-09-925-065A-832500	Sequence 832500,
c	650	6	4.0	475	6	US-09-925-065A-113135	Sequence 113135,
c	651	6	4.0	475	6	US-09-925-065A-169703	Sequence 169703,
c	652	6	4.0	475	6	US-09-925-065A-280563	Sequence 280563,
	653	6	4.0	475	6	US-09-925-065A-956935	Sequence 956935,
c	654	6	4.0	475	12	US-11-123-896-391	Sequence 391, App
	655	6	4.0	476	6	US-09-925-065A-314097	Sequence 314097,
	656	6	4.0	477	6	US-09-925-065A-309723	Sequence 309723,
	657	6	4.0	477	6	US-09-925-065A-309724	Sequence 309724,
c	658	6	4.0	477	6	US-09-925-065A-576331	Sequence 576331,
c	659	6	4.0	477	12	US-11-098-686-8973	Sequence 8973, Ap
	660	6	4.0	478	6	US-09-925-065A-532007	Sequence 532007,
	661	6	4.0	478	6	US-09-925-065A-532008	Sequence 532008,

c 662	6	4.0	478	8	US-10-955-054A-20	Sequence 20, Appl
c 663	6	4.0	479	6	US-09-925-065A-606703	Sequence 606703,
c 664	6	4.0	479	6	US-09-925-065A-606704	Sequence 606704,
c 665	6	4.0	479	6	US-09-925-065A-606705	Sequence 606705,
c 666	6	4.0	479	6	US-09-925-065A-826095	Sequence 826095,
667	6	4.0	480	6	US-09-925-065A-196249	Sequence 196249,
668	6	4.0	480	6	US-09-925-065A-196250	Sequence 196250,
669	6	4.0	480	6	US-09-925-065A-203448	Sequence 203448,
670	6	4.0	480	6	US-09-925-065A-203449	Sequence 203449,
671	6	4.0	480	6	US-09-925-065A-203450	Sequence 203450,
672	6	4.0	480	6	US-09-925-065A-203451	Sequence 203451,
c 673	6	4.0	480	6	US-09-925-065A-440878	Sequence 440878,
674	6	4.0	480	6	US-09-925-065A-656380	Sequence 656380,
675	6	4.0	480	8	US-10-750-185-56571	Sequence 56571, A
676	6	4.0	480	8	US-10-750-623-56571	Sequence 56571, A
677	6	4.0	481	6	US-09-925-065A-337499	Sequence 337499,
c 678	6	4.0	482	6	US-09-925-065A-442678	Sequence 442678,
679	6	4.0	482	6	US-09-925-065A-443629	Sequence 443629,
680	6	4.0	482	6	US-09-925-065A-443631	Sequence 443631,
681	6	4.0	482	6	US-09-925-065A-443632	Sequence 443632,
682	6	4.0	482	6	US-09-925-065A-753423	Sequence 753423,
c 683	6	4.0	483	6	US-09-925-065A-398931	Sequence 398931,
c 684	6	4.0	483	7	US-10-943-015-1	Sequence 1, Appli
c 685	6	4.0	485	6	US-09-925-065A-542446	Sequence 542446,
686	6	4.0	485	6	US-09-925-065A-615799	Sequence 615799,
c 687	6	4.0	485	12	US-11-128-061-2355	Sequence 2355, Ap
c 688	6	4.0	485	12	US-11-128-061-5997	Sequence 5997, Ap
c 689	6	4.0	485	12	US-11-128-049-2355	Sequence 2355, Ap
c 690	6	4.0	485	12	US-11-128-049-5997	Sequence 5997, Ap
691	6	4.0	486	6	US-09-925-065A-240388	Sequence 240388,
c 692	6	4.0	486	6	US-09-925-065A-366255	Sequence 366255,
693	6	4.0	486	6	US-09-925-065A-823990	Sequence 823990,
694	6	4.0	486	6	US-09-925-065A-823991	Sequence 823991,
c 695	6	4.0	486	8	US-10-802-796-220	Sequence 220, App
696	6	4.0	487	6	US-09-925-065A-844720	Sequence 844720,
c 697	6	4.0	488	6	US-09-925-065A-191269	Sequence 191269,
698	6	4.0	488	6	US-09-925-065A-198231	Sequence 198231,
699	6	4.0	488	6	US-09-925-065A-198232	Sequence 198232,
700	6	4.0	488	6	US-09-925-065A-198233	Sequence 198233,
701	6	4.0	488	6	US-09-925-065A-237939	Sequence 237939,
702	6	4.0	488	6	US-09-925-065A-237940	Sequence 237940,
c 703	6	4.0	488	6	US-09-925-065A-319278	Sequence 319278,
704	6	4.0	488	6	US-09-925-065A-454998	Sequence 454998,
c 705	6	4.0	488	6	US-09-925-065A-514255	Sequence 514255,
c 706	6	4.0	488	6	US-09-925-065A-839633	Sequence 839633,
707	6	4.0	488	6	US-09-925-065A-939875	Sequence 939875,
708	6	4.0	488	6	US-09-925-065A-939876	Sequence 939876,
709	6	4.0	489	6	US-09-925-065A-140121	Sequence 140121,
710	6	4.0	489	6	US-09-925-065A-523005	Sequence 523005,
c 711	6	4.0	490	6	US-09-925-065A-599336	Sequence 599336,
c 712	6	4.0	490	6	US-09-925-065A-599337	Sequence 599337,
c 713	6	4.0	490	6	US-09-925-065A-599338	Sequence 599338,
c 714	6	4.0	490	6	US-09-925-065A-599339	Sequence 599339,
715	6	4.0	491	6	US-09-925-065A-371687	Sequence 371687,
716	6	4.0	491	6	US-09-925-065A-652768	Sequence 652768,
717	6	4.0	491	6	US-09-925-065A-778592	Sequence 778592,
c 718	6	4.0	492	6	US-09-925-065A-500374	Sequence 500374,
c 719	6	4.0	492	6	US-09-925-065A-500375	Sequence 500375,
c 720	6	4.0	492	6	US-09-925-065A-615386	Sequence 615386,
721	6	4.0	492	12	US-11-098-686-9740	Sequence 9740, Ap
722	6	4.0	493	6	US-09-925-065A-323291	Sequence 323291,
723	6	4.0	494	6	US-09-925-065A-192427	Sequence 192427,
c 724	6	4.0	494	6	US-09-925-065A-530134	Sequence 530134,
725	6	4.0	494	6	US-09-925-065A-654862	Sequence 654862,
c 726	6	4.0	495	6	US-09-925-065A-937590	Sequence 937590,
727	6	4.0	496	6	US-09-925-065A-319008	Sequence 319008,
c 728	6	4.0	496	6	US-09-925-065A-658401	Sequence 658401,
c 729	6	4.0	496	6	US-09-925-065A-833554	Sequence 833554,
c 730	6	4.0	497	6	US-09-925-065A-25589	Sequence 25589, A
c 731	6	4.0	497	6	US-09-925-065A-746410	Sequence 746410,
c 732	6	4.0	498	6	US-09-925-065A-152941	Sequence 152941,
c 733	6	4.0	498	6	US-09-925-065A-193666	Sequence 193666,
734	6	4.0	498	6	US-09-925-065A-652767	Sequence 652767,
c 735	6	4.0	499	6	US-09-925-065A-214368	Sequence 214368,
736	6	4.0	499	6	US-09-925-065A-568520	Sequence 568520,
737	6	4.0	500	6	US-09-925-065A-476530	Sequence 476530,
c 738	6	4.0	501	6	US-09-925-065A-473843	Sequence 473843,
c 739	6	4.0	501	6	US-09-925-065A-474749	Sequence 474749,
740	6	4.0	501	6	US-09-925-065A-577776	Sequence 577776,
c 741	6	4.0	501	6	US-09-925-065A-750263	Sequence 750263,
c 742	6	4.0	501	6	US-09-925-065A-855218	Sequence 855218,
c 743	6	4.0	501	6	US-09-925-065A-855219	Sequence 855219,
744	6	4.0	502	6	US-09-925-065A-279603	Sequence 279603,
c 745	6	4.0	502	6	US-09-925-065A-580052	Sequence 580052,
c 746	6	4.0	502	6	US-09-925-065A-580053	Sequence 580053,
747	6	4.0	502	6	US-09-925-065A-652766	Sequence 652766,
c 748	6	4.0	503	6	US-09-925-065A-222237	Sequence 222237,
c 749	6	4.0	503	6	US-09-925-065A-369773	Sequence 369773,
c 750	6	4.0	503	6	US-09-925-065A-404235	Sequence 404235,
751	6	4.0	503	6	US-09-925-065A-579244	Sequence 579244,
752	6	4.0	503	6	US-09-925-065A-579245	Sequence 579245,
753	6	4.0	503	6	US-09-925-065A-579246	Sequence 579246,
754	6	4.0	503	6	US-09-925-065A-579247	Sequence 579247,
c 755	6	4.0	503	6	US-09-925-065A-893208	Sequence 893208,
756	6	4.0	503	12	US-11-128-061-2734	Sequence 2734, Ap
757	6	4.0	503	12	US-11-128-061-6376	Sequence 6376, Ap
758	6	4.0	503	12	US-11-128-049-2734	Sequence 2734, Ap
759	6	4.0	503	12	US-11-128-049-6376	Sequence 6376, Ap
c 760	6	4.0	504	6	US-09-925-065A-405008	Sequence 405008,
761	6	4.0	504	6	US-09-925-065A-431795	Sequence 431795,
c 762	6	4.0	504	6	US-09-925-065A-468013	Sequence 468013,
c 763	6	4.0	505	6	US-09-925-065A-521624	Sequence 521624,
c 764	6	4.0	505	6	US-09-925-065A-601499	Sequence 601499,
765	6	4.0	506	6	US-09-925-065A-148583	Sequence 148583,
766	6	4.0	506	6	US-09-925-065A-148584	Sequence 148584,
c 767	6	4.0	506	6	US-09-925-065A-279293	Sequence 279293,
768	6	4.0	506	6	US-09-925-065A-939897	Sequence 939897,
769	6	4.0	506	6	US-09-925-065A-939899	Sequence 939899,
770	6	4.0	506	6	US-09-925-065A-939900	Sequence 939900,
771	6	4.0	507	6	US-09-925-065A-117701	Sequence 117701,
772	6	4.0	507	6	US-09-925-065A-226972	Sequence 226972,
773	6	4.0	507	6	US-09-925-065A-226973	Sequence 226973,
774	6	4.0	507	6	US-09-925-065A-251835	Sequence 251835,
c 775	6	4.0	507	6	US-09-925-065A-299274	Sequence 299274,
c 776	6	4.0	507	6	US-09-925-065A-299275	Sequence 299275,
777	6	4.0	507	6	US-09-925-065A-613237	Sequence 613237,
778	6	4.0	507	6	US-09-925-065A-838572	Sequence 838572,
779	6	4.0	507	6	US-09-925-065A-838573	Sequence 838573,
780	6	4.0	507	6	US-09-925-065A-838574	Sequence 838574,
c 781	6	4.0	508	6	US-09-925-065A-12440	Sequence 12440, A
c 782	6	4.0	508	6	US-09-925-065A-123603	Sequence 123603,
c 783	6	4.0	508	6	US-09-925-065A-123604	Sequence 123604,
c 784	6	4.0	508	6	US-09-925-065A-540587	Sequence 540587,
785	6	4.0	508	6	US-09-925-065A-815782	Sequence 815782,
c 786	6	4.0	508	6	US-09-925-065A-825502	Sequence 825502,
787	6	4.0	509	6	US-09-925-065A-38647	Sequence 38647, A
c 788	6	4.0	509	6	US-09-925-065A-176821	Sequence 176821,
c 789	6	4.0	509	6	US-09-925-065A-183736	Sequence 183736,
c 790	6	4.0	509	6	US-09-925-065A-234618	Sequence 234618,
791	6	4.0	509	6	US-09-925-065A-292199	Sequence 292199,
792	6	4.0	509	6	US-09-925-065A-664124	Sequence 664124,
793	6	4.0	510	6	US-09-925-065A-21274	Sequence 21274, A
794	6	4.0	510	6	US-09-925-065A-568674	Sequence 568674,
795	6	4.0	510	6	US-09-925-065A-650690	Sequence 650690,
796	6	4.0	510	6	US-09-925-065A-650691	Sequence 650691,
797	6	4.0	511	6	US-09-925-065A-145520	Sequence 145520,
c 798	6	4.0	511	6	US-09-925-065A-315422	Sequence 315422,
c 799	6	4.0	511	6	US-09-925-065A-500964	Sequence 500964,
800	6	4.0	511	6	US-09-925-065A-948313	Sequence 948313,
801	6	4.0	511	6	US-09-925-065A-948314	Sequence 948314,
802	6	4.0	511	6	US-09-925-065A-948315	Sequence 948315,
c 803	6	4.0	512	6	US-09-925-065A-32203	Sequence 32203, A
c 804	6	4.0	512	6	US-09-925-065A-36208	Sequence 36208, A
c 805	6	4.0	512	6	US-09-925-065A-468945	Sequence 468945,
806	6	4.0	513	6	US-09-925-065A-274974	Sequence 274974,
807	6	4.0	514	6	US-09-925-065A-279604	Sequence 279604,

	808	6	4.0	514	6	US-09-925-065A-350331	Sequence 350331,
	809	6	4.0	515	6	US-09-925-065A-148493	Sequence 148493,
c	810	6	4.0	515	6	US-09-925-065A-226819	Sequence 226819,
	811	6	4.0	515	6	US-09-925-065A-516567	Sequence 516567,
c	812	6	4.0	516	6	US-09-925-065A-186109	Sequence 186109,
c	813	6	4.0	516	6	US-09-925-065A-226820	Sequence 226820,
c	814	6	4.0	516	6	US-09-925-065A-640562	Sequence 640562,
c	815	6	4.0	516	6	US-09-925-065A-640563	Sequence 640563,
c	816	6	4.0	517	6	US-09-925-065A-202147	Sequence 202147,
c	817	6	4.0	517	6	US-09-925-065A-202148	Sequence 202148,
c	818	6	4.0	517	6	US-09-925-065A-266431	Sequence 266431,
c	819	6	4.0	517	6	US-09-925-065A-486275	Sequence 486275,
	820	6	4.0	517	6	US-09-925-065A-551046	Sequence 551046,
c	821	6	4.0	517	6	US-09-925-065A-616675	Sequence 616675,
c	822	6	4.0	517	6	US-09-925-065A-616676	Sequence 616676,
	823	6	4.0	518	6	US-09-925-065A-151680	Sequence 151680,
	824	6	4.0	518	6	US-09-925-065A-217859	Sequence 217859,
c	825	6	4.0	518	6	US-09-925-065A-481925	Sequence 481925,
c	826	6	4.0	519	6	US-09-925-065A-235762	Sequence 235762,
	827	6	4.0	519	6	US-09-925-065A-758150	Sequence 758150,
	828	6	4.0	519	9	US-11-021-492-18	Sequence 18, Appl
c	829	6	4.0	520	6	US-09-925-065A-334138	Sequence 334138,
c	830	6	4.0	520	6	US-09-925-065A-334139	Sequence 334139,
	831	6	4.0	520	6	US-09-925-065A-500721	Sequence 500721,
	832	6	4.0	520	6	US-09-925-065A-500722	Sequence 500722,
	833	6	4.0	520	6	US-09-925-065A-734423	Sequence 734423,
	834	6	4.0	522	6	US-09-925-065A-21879	Sequence 21879, A
	835	6	4.0	522	6	US-09-925-065A-141722	Sequence 141722,
c	836	6	4.0	522	6	US-09-925-065A-152275	Sequence 152275,
c	837	6	4.0	522	6	US-09-925-065A-152276	Sequence 152276,
c	838	6	4.0	522	6	US-09-925-065A-152277	Sequence 152277,
c	839	6	4.0	522	6	US-09-925-065A-367960	Sequence 367960,
	840	6	4.0	522	6	US-09-925-065A-551104	Sequence 551104,
c	841	6	4.0	522	6	US-09-925-065A-595744	Sequence 595744,
c	842	6	4.0	522	6	US-09-925-065A-734436	Sequence 734436,
	843	6	4.0	522	6	US-09-925-065A-873020	Sequence 873020,
	844	6	4.0	523	6	US-09-925-065A-98650	Sequence 98650, A
	845	6	4.0	523	6	US-09-925-065A-175228	Sequence 175228,
c	846	6	4.0	523	6	US-09-925-065A-178735	Sequence 178735,
	847	6	4.0	523	6	US-09-925-065A-194377	Sequence 194377,
	848	6	4.0	523	6	US-09-925-065A-361861	Sequence 361861,
	849	6	4.0	523	6	US-09-925-065A-361862	Sequence 361862,
	850	6	4.0	523	6	US-09-925-065A-601488	Sequence 601488,
	851	6	4.0	523	6	US-09-925-065A-760911	Sequence 760911,
	852	6	4.0	524	6	US-09-925-065A-16218	Sequence 16218, A
	853	6	4.0	524	6	US-09-925-065A-109534	Sequence 109534,
c	854	6	4.0	524	6	US-09-925-065A-214846	Sequence 214846,
	855	6	4.0	524	6	US-09-925-065A-551830	Sequence 551830,
c	856	6	4.0	524	6	US-09-925-065A-629842	Sequence 629842,
c	857	6	4.0	524	6	US-09-925-065A-858725	Sequence 858725,
	858	6	4.0	525	6	US-09-925-065A-150252	Sequence 150252,
	859	6	4.0	525	6	US-09-925-065A-164907	Sequence 164907,
	860	6	4.0	525	6	US-09-925-065A-164908	Sequence 164908,
	861	6	4.0	525	6	US-09-925-065A-164910	Sequence 164910,
c	862	6	4.0	525	6	US-09-925-065A-443905	Sequence 443905,
c	863	6	4.0	525	6	US-09-925-065A-493537	Sequence 493537,
c	864	6	4.0	526	6	US-09-925-065A-15858	Sequence 15858, A
c	865	6	4.0	526	6	US-09-925-065A-137362	Sequence 137362,
	866	6	4.0	526	6	US-09-925-065A-218110	Sequence 218110,
	867	6	4.0	526	6	US-09-925-065A-409267	Sequence 409267,
	868	6	4.0	526	6	US-09-925-065A-409268	Sequence 409268,
c	869	6	4.0	526	6	US-09-925-065A-514763	Sequence 514763,
c	870	6	4.0	526	6	US-09-925-065A-813340	Sequence 813340,
	871	6	4.0	527	6	US-09-925-065A-25482	Sequence 25482, A
	872	6	4.0	527	6	US-09-925-065A-259140	Sequence 259140,
	873	6	4.0	527	6	US-09-925-065A-259141	Sequence 259141,
c	874	6	4.0	527	6	US-09-925-065A-548699	Sequence 548699,
	875	6	4.0	527	6	US-09-925-065A-643862	Sequence 643862,
c	876	6	4.0	527	6	US-09-925-065A-782786	Sequence 782786,
c	877	6	4.0	527	6	US-09-925-065A-868619	Sequence 868619,
	878	6	4.0	528	6	US-09-925-065A-6037	Sequence 6037, Ap
	879	6	4.0	528	6	US-09-925-065A-116327	Sequence 116327,
c	880	6	4.0	528	6	US-09-925-065A-196318	Sequence 196318,
	881	6	4.0	528	6	US-09-925-065A-636079	Sequence 636079,
c	882	6	4.0	528	6	US-09-925-065A-662763	Sequence 662763,
	883	6	4.0	528	6	US-09-925-065A-933617	Sequence 933617,
c	884	6	4.0	529	6	US-09-925-065A-11267	Sequence 11267, A
c	885	6	4.0	529	6	US-09-925-065A-176620	Sequence 176620,
c	886	6	4.0	529	6	US-09-925-065A-219539	Sequence 219539,
c	887	6	4.0	529	6	US-09-925-065A-219540	Sequence 219540,
	888	6	4.0	529	6	US-09-925-065A-358936	Sequence 358936,
	889	6	4.0	529	6	US-09-925-065A-358937	Sequence 358937,
	890	6	4.0	529	6	US-09-925-065A-454445	Sequence 454445,
	891	6	4.0	529	6	US-09-925-065A-578278	Sequence 578278,
	892	6	4.0	529	6	US-09-925-065A-578279	Sequence 578279,
	893	6	4.0	529	6	US-09-925-065A-578280	Sequence 578280,
	894	6	4.0	529	6	US-09-925-065A-578281	Sequence 578281,
c	895	6	4.0	529	6	US-09-925-065A-599115	Sequence 599115,
	896	6	4.0	529	6	US-09-925-065A-638768	Sequence 638768,
c	897	6	4.0	529	6	US-09-925-065A-841645	Sequence 841645,
	898	6	4.0	530	6	US-09-925-065A-175824	Sequence 175824,
c	899	6	4.0	530	6	US-09-925-065A-377224	Sequence 377224,
c	900	6	4.0	530	6	US-09-925-065A-377225	Sequence 377225,
	901	6	4.0	530	6	US-09-925-065A-529713	Sequence 529713,
c	902	6	4.0	530	6	US-09-925-065A-553100	Sequence 553100,
	903	6	4.0	530	6	US-09-925-065A-580336	Sequence 580336,
c	904	6	4.0	531	6	US-09-925-065A-20278	Sequence 20278, A
	905	6	4.0	531	6	US-09-925-065A-192052	Sequence 192052,
	906	6	4.0	531	6	US-09-925-065A-270077	Sequence 270077,
	907	6	4.0	531	6	US-09-925-065A-356502	Sequence 356502,
c	908	6	4.0	531	6	US-09-925-065A-649229	Sequence 649229,
c	909	6	4.0	531	6	US-09-925-065A-649230	Sequence 649230,
c	910	6	4.0	532	6	US-09-925-065A-145318	Sequence 145318,
c	911	6	4.0	532	6	US-09-925-065A-145319	Sequence 145319,
c	912	6	4.0	532	6	US-09-925-065A-145320	Sequence 145320,
	913	6	4.0	532	6	US-09-925-065A-153827	Sequence 153827,
c	914	6	4.0	532	6	US-09-925-065A-548452	Sequence 548452,
c	915	6	4.0	532	6	US-09-925-065A-548453	Sequence 548453,
	916	6	4.0	532	6	US-09-925-065A-760842	Sequence 760842,
	917	6	4.0	532	6	US-09-925-065A-956909	Sequence 956909,
	918	6	4.0	533	6	US-09-925-065A-145705	Sequence 145705,
c	919	6	4.0	533	6	US-09-925-065A-372770	Sequence 372770,
c	920	6	4.0	533	6	US-09-925-065A-452772	Sequence 452772,
	921	6	4.0	533	6	US-09-925-065A-593647	Sequence 593647,
	922	6	4.0	533	6	US-09-925-065A-615298	Sequence 615298,
	923	6	4.0	533	6	US-09-925-065A-653939	Sequence 653939,
c	924	6	4.0	534	6	US-09-925-065A-255352	Sequence 255352,
c	925	6	4.0	534	6	US-09-925-065A-352079	Sequence 352079,
c	926	6	4.0	534	6	US-09-925-065A-754525	Sequence 754525,
c	927	6	4.0	535	6	US-09-925-065A-10037	Sequence 10037, A
	928	6	4.0	535	6	US-09-925-065A-189258	Sequence 189258,
c	929	6	4.0	535	6	US-09-925-065A-251850	Sequence 251850,
c	930	6	4.0	535	6	US-09-925-065A-251851	Sequence 251851,
c	931	6	4.0	535	6	US-09-925-065A-251852	Sequence 251852,
	932	6	4.0	535	6	US-09-925-065A-499886	Sequence 499886,
	933	6	4.0	535	6	US-09-925-065A-541534	Sequence 541534,
	934	6	4.0	535	6	US-09-925-065A-541535	Sequence 541535,
c	935	6	4.0	535	6	US-09-925-065A-587703	Sequence 587703,
	936	6	4.0	535	6	US-09-925-065A-647965	Sequence 647965,
	937	6	4.0	535	6	US-09-925-065A-758204	Sequence 758204,
	938	6	4.0	535	6	US-09-925-065A-845177	Sequence 845177,
	939	6	4.0	536	6	US-09-925-065A-30225	Sequence 30225, A
	940	6	4.0	536	6	US-09-925-065A-269398	Sequence 269398,
	941	6	4.0	536	6	US-09-925-065A-269400	Sequence 269400,
c	942	6	4.0	536	6	US-09-925-065A-540586	Sequence 540586,
c	943	6	4.0	536	6	US-09-925-065A-750752	Sequence 750752,
c	944	6	4.0	536	6	US-09-925-065A-803959	Sequence 803959,
c	945	6	4.0	536	6	US-09-925-065A-822987	Sequence 822987,
c	946	6	4.0	536	6	US-09-925-065A-822988	Sequence 822988,
c	947	6	4.0	536	6	US-09-925-065A-822989	Sequence 822989,
c	948	6	4.0	537	6	US-09-925-065A-106794	Sequence 106794,
	949	6	4.0	537	6	US-09-925-065A-157879	Sequence 157879,
c	950	6	4.0	537	6	US-09-925-065A-168163	Sequence 168163,
	951	6	4.0	537	6	US-09-925-065A-220036	Sequence 220036,
	952	6	4.0	537	6	US-09-925-065A-220037	Sequence 220037,
	953	6	4.0	537	6	US-09-925-065A-220038	Sequence 220038,

954	6	4.0	537	6	US-09-925-065A-285490	Sequence 285490,
955	6	4.0	537	6	US-09-925-065A-338232	Sequence 338232,
956	6	4.0	537	6	US-09-925-065A-768759	Sequence 768759,
957	6	4.0	537	6	US-09-925-065A-790763	Sequence 790763,
958	6	4.0	537	6	US-09-925-065A-790764	Sequence 790764,
959	6	4.0	537	6	US-09-925-065A-848118	Sequence 848118,
960	6	4.0	538	6	US-09-925-065A-31796	Sequence 31796, A
961	6	4.0	538	6	US-09-925-065A-238437	Sequence 238437,
962	6	4.0	538	6	US-09-925-065A-663712	Sequence 663712,
963	6	4.0	538	6	US-09-925-065A-663713	Sequence 663713,
c 964	6	4.0	538	6	US-09-925-065A-758323	Sequence 758323,
c 965	6	4.0	539	6	US-09-925-065A-467107	Sequence 467107,
c 966	6	4.0	539	6	US-09-925-065A-467108	Sequence 467108,
c 967	6	4.0	539	6	US-09-925-065A-467109	Sequence 467109,
c 968	6	4.0	539	6	US-09-925-065A-467110	Sequence 467110,
c 969	6	4.0	539	6	US-09-925-065A-626632	Sequence 626632,
c 970	6	4.0	540	6	US-09-925-065A-127763	Sequence 127763,
971	6	4.0	540	6	US-09-925-065A-424856	Sequence 424856,
c 972	6	4.0	540	6	US-09-925-065A-476154	Sequence 476154,
c 973	6	4.0	540	6	US-09-925-065A-476155	Sequence 476155,
c 974	6	4.0	540	6	US-09-925-065A-569621	Sequence 569621,
975	6	4.0	540	6	US-09-925-065A-859716	Sequence 859716,
976	6	4.0	541	6	US-09-925-065A-160757	Sequence 160757,
c 977	6	4.0	541	6	US-09-925-065A-261285	Sequence 261285,
c 978	6	4.0	541	6	US-09-925-065A-290519	Sequence 290519,
979	6	4.0	541	6	US-09-925-065A-326913	Sequence 326913,
c 980	6	4.0	541	6	US-09-925-065A-483873	Sequence 483873,
981	6	4.0	541	6	US-09-925-065A-766230	Sequence 766230,
c 982	6	4.0	542	6	US-09-925-065A-121890	Sequence 121890,
c 983	6	4.0	542	6	US-09-925-065A-140103	Sequence 140103,
c 984	6	4.0	542	6	US-09-925-065A-140104	Sequence 140104,
985	6	4.0	542	6	US-09-925-065A-291872	Sequence 291872,
986	6	4.0	542	6	US-09-925-065A-334236	Sequence 334236,
c 987	6	4.0	542	6	US-09-925-065A-496817	Sequence 496817,
c 988	6	4.0	542	6	US-09-925-065A-496818	Sequence 496818,
c 989	6	4.0	542	6	US-09-925-065A-511793	Sequence 511793,
c 990	6	4.0	543	6	US-09-925-065A-150015	Sequence 150015,
c 991	6	4.0	543	6	US-09-925-065A-150016	Sequence 150016,
c 992	6	4.0	543	6	US-09-925-065A-150017	Sequence 150017,
c 993	6	4.0	543	6	US-09-925-065A-150018	Sequence 150018,
c 994	6	4.0	543	6	US-09-925-065A-176891	Sequence 176891,
c 995	6	4.0	543	6	US-09-925-065A-176892	Sequence 176892,
c 996	6	4.0	543	6	US-09-925-065A-376881	Sequence 376881,
997	6	4.0	543	6	US-09-925-065A-517576	Sequence 517576,
998	6	4.0	543	6	US-09-925-065A-517577	Sequence 517577,
c 999	6	4.0	543	6	US-09-925-065A-570031	Sequence 570031,
c1000	6	4.0	543	6	US-09-925-065A-597844	Sequence 597844,

ALIGNMENTS

```
RESULT 1
US-10-995-561-34779
; Sequence 34779, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34779
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-34779

Alignment Scores:
Pred. No.:              77.6          Length:         201
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-9 (1-149) x US-10-995-561-34779 (1-201)

Qy         55 ThrSerLysLysThrValLysVal 62
              ||||||||||||||||||||||
Db         43 ACAAGCAAAAAAACAGTAAAGGTC 66

RESULT 2
US-09-925-065A-47024
; Sequence 47024, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47024
;   LENGTH: 416
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-47024

Alignment Scores:
Pred. No.:              147           Length:         416
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-47024 (1-416)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db        303 ACAGTGTCATTTAATTTGGGAGAG 326

RESULT 3
US-09-925-065A-630179/c
; Sequence 630179, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
```

```
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 630179
;   LENGTH: 487
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-630179

Alignment Scores:
Pred. No.:              169          Length:          487
Score:                  8.00         Matches:         8
Percent Similarity:     100.0%       Conservative:    0
Best Local Similarity:  100.0%       Mismatches:      0
Query Match:            5.4%         Indels:          0
DB:                     6            Gaps:            0

US-10-758-902-9 (1-149) x US-09-925-065A-630179 (1-487)

Qy        136 GluPheSerIleGluAlaIleTrp 143
              |||||||||||||||||||||||||
Db        481 GAATTCAGCATTGAAGCCATCTGG 458

RESULT 4
US-09-925-065A-325312
; Sequence 325312, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 325312
;   LENGTH: 565
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-325312

Alignment Scores:
Pred. No.:              192          Length:          565
Score:                  8.00         Matches:         8
Percent Similarity:     100.0%       Conservative:    0
Best Local Similarity:  100.0%       Mismatches:      0
Query Match:            5.4%         Indels:          0
DB:                     6            Gaps:            0

US-10-758-902-9 (1-149) x US-09-925-065A-325312 (1-565)

Qy         29 ThrProValCysGlnLeuProVal 36
              |||||||||||||||||||||||||
Db        145 ACTCCAGTTTGCCAGCTTCCAGTT 168

RESULT 5
US-09-925-065A-787599
; Sequence 787599, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 787599
;   LENGTH: 622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-787599

Alignment Scores:
Pred. No.:              209          Length:          622
Score:                  8.00         Matches:         8
Percent Similarity:     100.0%       Conservative:    0
Best Local Similarity:  100.0%       Mismatches:      0
Query Match:            5.4%         Indels:          0
DB:                     6            Gaps:            0

US-10-758-902-9 (1-149) x US-09-925-065A-787599 (1-622)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||||
Db         17 ACAGTGTCATTTAATTTGGGAGAG 40

RESULT 6
US-10-750-185-28892
; Sequence 28892, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 28892
;   LENGTH: 631
;   TYPE: DNA
;   ORGANISM: Bovine  19866882037319
US-10-750-185-28892

Alignment Scores:
Pred. No.:              212          Length:          631
Score:                  8.00         Matches:         8
Percent Similarity:     100.0%       Conservative:    0
Best Local Similarity:  100.0%       Mismatches:      0
Query Match:            5.4%         Indels:          0
DB:                     8            Gaps:            0

US-10-758-902-9 (1-149) x US-10-750-185-28892 (1-631)
```

```
Qy          94 AlaThrSerLysLeuPheProGly 101
               ||||||||||||||||||||||||
Db         403 GCAACTAGCAAACTGTTCCCAGGA 426

RESULT 7
US-10-750-623-28892
; Sequence 28892, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 28892
;   LENGTH: 631
;   TYPE: DNA
;   ORGANISM: Bovine  19866882037319
US-10-750-623-28892

Alignment Scores:
Pred. No.:              212           Length:         631
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-9 (1-149) x US-10-750-623-28892 (1-631)

Qy          94 AlaThrSerLysLeuPheProGly 101
               ||||||||||||||||||||||||
Db         403 GCAACTAGCAAACTGTTCCCAGGA 426

RESULT 8
US-09-925-065A-694362/c
; Sequence 694362, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 694362
;   LENGTH: 2443
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352,
;   LOCATION: 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362,
;   LOCATION: 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372,
;   LOCATION: 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391,
;   LOCATION: 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401,
;   LOCATION: 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411,
;   LOCATION: 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430,
;   LOCATION: 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440,
;   LOCATION: 2441, 2442
;   OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-694362

Alignment Scores:
Pred. No.:              695           Length:         2443
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-694362 (1-2443)

Qy           3 ThrValSerPheAsnLeuGlyGlu 10
               |||||||||||||||||||||||
Db        2040 ACAGTGTCATTTAATTTGGGAGAG 2017

RESULT 9
US-10-995-561-13271/c
; Sequence 13271, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13271
;   LENGTH: 12648
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13271

Alignment Scores:
Pred. No.:              2.94e+03      Length:         12648
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-9 (1-149) x US-10-995-561-13271 (1-12648)

Qy           3 ThrValSerPheAsnLeuGlyGlu 10
               |||||||||||||||||||||||
Db       12509 ACAGTGTCATTTAATTTGGGAGAG 12486

RESULT 10
US-11-124-367A-5063/c
; Sequence 5063, Application US/11124367A
; Publication No. US20060024700A1
```

; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5063
; LENGTH: 31130
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5063

Alignment Scores:

Pred. No.:	6.48e+03	Length:	31130
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	12	Gaps:	0

US-10-758-902-9 (1-149) x US-11-124-367A-5063 (1-31130)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db      30946 ACAGTGTCATTTAATTTGGGAGAG 30923
```

RESULT 11
US-10-995-561-13334
; Sequence 13334, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13334
; LENGTH: 31657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13334

Alignment Scores:

Pred. No.:	6.58e+03	Length:	31657
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-9 (1-149) x US-10-995-561-13334 (1-31657)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db        190 ACAGTGTCATTTAATTTGGGAGAG 213
```

RESULT 12
US-10-995-561-13487
; Sequence 13487, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13487
; LENGTH: 41309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13487

Alignment Scores:

Pred. No.:	8.31e+03	Length:	41309
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-9 (1-149) x US-10-995-561-13487 (1-41309)

```
Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db      34625 ACAGTGTCATTTAATTTGGGAGAG 34648
```

RESULT 13
US-10-995-561-13269
; Sequence 13269, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13269
; LENGTH: 63693
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13269

Alignment Scores:

Pred. No.:	1.21e+04	Length:	63693
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-9 (1-149) x US-10-995-561-13269 (1-63693)

```
Qy         55 ThrSerLysLysThrValLysVal 62
              ||||||||||||||||||||||
Db      50804 ACAAGCAAAAAAACAGTAAAGGTC 50827
```

RESULT 14
US-11-136-527-329283
; Sequence 329283, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

```
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 329283
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Probe
US-11-136-527-329283

Alignment Scores:
Pred. No.:                126             Length:         25
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.7%            Indels:         0
DB:                       12              Gaps:           0

US-10-758-902-9 (1-149) x US-11-136-527-329283 (1-25)

Qy        117 LeuValAsnAlaAlaLysVal 123
              |||||||||||||||||||||
Db          2 CTTGTAAATGCAGCTAAAGTC 22

RESULT 15
US-11-175-859-100900/c
; Sequence 100900, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
;  APPLICANT: Affymetrix, Inc.
;  APPLICANT:  Liu, Guoying et al.
;  TITLE OF INVENTION: Method of Analysis of Human Polymorphism
;  FILE REFERENCE: 3690.1
;  CURRENT APPLICATION NUMBER: US/11/175,859
;  CURRENT FILING DATE:  2005-07-05
;  PRIOR APPLICATION NUMBER: US 60/585,352
;  PRIOR FILING DATE: 2004-07-02
;  NUMBER OF SEQ ID NOS: 116251
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 100900
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: homo sapien
US-11-175-859-100900

Alignment Scores:
Pred. No.:                232             Length:         50
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.7%            Indels:         0
DB:                       12              Gaps:           0

US-10-758-902-9 (1-149) x US-11-175-859-100900 (1-50)

Qy         45 LysArgPheValLeuValAsp 51
              |||||||||||||||||||
Db         48 AAAAGGTTTGTGTTAGTTGAC 28

RESULT 16
US-10-310-914A-13009
; Sequence 13009, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13009
;   LENGTH: 63
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-13009

Alignment Scores:
Pred. No.:                284             Length:         63
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.7%            Indels:         0
DB:                       8               Gaps:           0

US-10-758-902-9 (1-149) x US-10-310-914A-13009 (1-63)

Qy         76 AspLysTrpAspGlyLysAsp 82
              |||||||||||||||||||
Db          7 GACAAGUGGGAUGGCAAGGAC 27

RESULT 17
US-10-995-561-18821/c
; Sequence 18821, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18821
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18821

Alignment Scores:
Pred. No.:                786             Length:         201
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.7%            Indels:         0
DB:                       8               Gaps:           0

US-10-758-902-9 (1-149) x US-10-995-561-18821 (1-201)

Qy         33 GlnLeuProValThrLeuGln 39
              |||||||||||||||||||
Db        166 CAATTACCTGTAACTTTGCAA 146

RESULT 18
US-10-995-561-19052/c
; Sequence 19052, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 19052
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-19052

Alignment Scores:
Pred. No.:              786          Length:         201
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            4.7%         Indels:         0
DB:                     8            Gaps:           0

US-10-758-902-9 (1-149) x US-10-995-561-19052 (1-201)

Qy         33 GlnLeuProValThrLeuGln 39
              |||||||||||||||||||||
Db         89 CAATTACCTGTAACTTTGCAA 69

RESULT 19
US-11-124-368A-10188/c
; Sequence 10188, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  James J. Devlin
;  APPLICANT:  May Luke
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Vascular Diseases, Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001524
;  CURRENT APPLICATION NUMBER: US/11/124,368A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,845
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/625,936
;  PRIOR FILING DATE: 2004-11-09
;  NUMBER OF SEQ ID NOS: 21112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10188
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-124-368A-10188

Alignment Scores:
Pred. No.:              786          Length:         201
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            4.7%         Indels:         0
DB:                     12           Gaps:           0

US-10-758-902-9 (1-149) x US-11-124-368A-10188 (1-201)

Qy         62 ValAlaIleAspValThrAsp 68
              |||||||||||||||||||||
Db         98 GTAGCAATTGATGTTACTGAT 78

RESULT 20
US-11-145-703-62
; Sequence 62, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 62
;   LENGTH: 279
;   TYPE: DNA
;   ORGANISM: Pan troglodytes
US-11-145-703-62

Alignment Scores:
Pred. No.:              1.05e+03     Length:         279
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            4.7%         Indels:         0
DB:                     12           Gaps:           0

US-10-758-902-9 (1-149) x US-11-145-703-62 (1-279)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||||
Db        104 ACTACAACCAGCAAAAAGACC 124

RESULT 21
US-11-145-703-85
; Sequence 85, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
```

```
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 85
;   LENGTH: 279
;   TYPE: DNA
;   ORGANISM: Gorilla gorilla
US-11-145-703-85

Alignment Scores:
Pred. No.:              1.05e+03       Length:        279
Score:                  7.00           Matches:       7
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.7%           Indels:        0
DB:                     12             Gaps:          0

US-10-758-902-9 (1-149) x US-11-145-703-85 (1-279)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        104 ACTACAACCAGCAAAAAGACC 124

RESULT 22
US-11-145-703-74
; Sequence 74, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 74
;   LENGTH: 280
;   TYPE: DNA
;   ORGANISM: Hylobates sp.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 256,260,263,267,272
;   OTHER INFORMATION: n=a, g, c or t
US-11-145-703-74

Alignment Scores:
Pred. No.:              1.05e+03       Length:        280
Score:                  7.00           Matches:       7
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.7%           Indels:        0
DB:                     12             Gaps:          0

US-10-758-902-9 (1-149) x US-11-145-703-74 (1-280)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        104 ACTACAACCAGCAAAAAGACC 124

RESULT 23
US-11-145-703-97
; Sequence 97, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 97
;   LENGTH: 280
;   TYPE: DNA
;   ORGANISM: Pongo pygmaeus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 267
;   OTHER INFORMATION: n=a, g, c or t
US-11-145-703-97

Alignment Scores:
Pred. No.:              1.05e+03       Length:        280
Score:                  7.00           Matches:       7
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.7%           Indels:        0
DB:                     12             Gaps:          0
```

```
US-10-758-902-9 (1-149) x US-11-145-703-97 (1-280)

Qy          53 ThrThrThrSerLysLysThr 59
               |||||||||||||||||||||
Db         104 ACTACAACCAGCAAAAAGACC 124

RESULT 24
US-11-145-703-109
; Sequence 109, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 109
;   LENGTH: 280
;   TYPE: DNA
;   ORGANISM: Macaca mulatta
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 268
;   OTHER INFORMATION: n=a, g, c or t
US-11-145-703-109

Alignment Scores:
Pred. No.:              1.05e+03       Length:         280
Score:                  7.00           Matches:        7
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            4.7%           Indels:         0
DB:                     12             Gaps:           0

US-10-758-902-9 (1-149) x US-11-145-703-109 (1-280)

Qy          53 ThrThrThrSerLysLysThr 59
               |||||||||||||||||||||
Db         104 ACTACAACCAGCAAAAAGACC 124

RESULT 25
US-10-467-657-4591/c
; Sequence 4591, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4591
;   LENGTH: 297
;   TYPE: DNA
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4591

Alignment Scores:
Pred. No.:              1.11e+03       Length:         297
Score:                  7.00           Matches:        7
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            4.7%           Indels:         0
DB:                     8              Gaps:           0

US-10-758-902-9 (1-149) x US-10-467-657-4591 (1-297)

Qy          34 LeuProValThrLeuGlnThr 40
               |||||||||||||||||||||
Db          95 TTACCGGTCACTTTGCAAACT 75

RESULT 26
US-10-467-657-8599
; Sequence 8599, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8599
;   LENGTH: 297
;   TYPE: DNA
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8599

Alignment Scores:
Pred. No.:              1.11e+03       Length:         297
Score:                  7.00           Matches:        7
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            4.7%           Indels:         0
DB:                     8              Gaps:           0

US-10-758-902-9 (1-149) x US-10-467-657-8599 (1-297)

Qy          34 LeuProValThrLeuGlnThr 40
               |||||||||||||||||||||
Db         203 TTACCGGTCACTTTGCAAACT 223

RESULT 27
```

```
US-09-925-065A-350812
; Sequence 350812, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 350812
;   LENGTH: 336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-350812

Alignment Scores:
Pred. No.:              1.23e+03        Length:         336
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-350812 (1-336)

Qy         30 ProValCysGlnLeuProVal 36
              |||||||||||||||||||
Db        212 CCTGTGTGTCAGTTACCAGTT 232

RESULT 28
US-11-145-703-60
; Sequence 60, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 60
;   LENGTH: 388
;   TYPE: DNA
;   ORGANISM: Pan troglodytes
US-11-145-703-60

Alignment Scores:
Pred. No.:              1.4e+03         Length:         388
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     12              Gaps:           0

US-10-758-902-9 (1-149) x US-11-145-703-60 (1-388)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 29
US-11-145-703-83
; Sequence 83, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 83
;   LENGTH: 388
;   TYPE: DNA
;   ORGANISM: Gorilla gorilla
US-11-145-703-83

Alignment Scores:
Pred. No.:              1.4e+03         Length:         388
```

```
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.7%          Indels:        0
DB:                     12            Gaps:          0

US-10-758-902-9 (1-149) x US-11-145-703-83 (1-388)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 30
US-11-145-703-72
; Sequence 72, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 72
;   LENGTH: 389
;   TYPE: DNA
;   ORGANISM: Hylobates sp.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 365,369,372,376,381
;   OTHER INFORMATION: n=a, g, c or t
US-11-145-703-72

Alignment Scores:
Pred. No.:              1.4e+03       Length:        389
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.7%          Indels:        0
DB:                     12            Gaps:          0

US-10-758-902-9 (1-149) x US-11-145-703-72 (1-389)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 31
US-11-145-703-95
; Sequence 95, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 95
;   LENGTH: 389
;   TYPE: DNA
;   ORGANISM: Pongo pygmaeus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 376
;   OTHER INFORMATION: n=a, g, c or t
US-11-145-703-95

Alignment Scores:
Pred. No.:              1.4e+03       Length:        389
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.7%          Indels:        0
DB:                     12            Gaps:          0

US-10-758-902-9 (1-149) x US-11-145-703-95 (1-389)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 32
US-11-145-703-107
; Sequence 107, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
```

```
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: 53.US16.DIV
;  CURRENT APPLICATION NUMBER: US/11/145,703
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US/10/147,603
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 09/539,333
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: Patent.pm
; SEQ ID NO 107
;   LENGTH: 389
;   TYPE: DNA
;   ORGANISM: Macaca mulatta
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 377
;   OTHER INFORMATION: n=a, g, c or t
US-11-145-703-107

Alignment Scores:
Pred. No.:              1.4e+03       Length:         389
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     12            Gaps:           0

US-10-758-902-9 (1-149) x US-11-145-703-107 (1-389)

Qy         53 ThrThrThrSerLysLysThr 59
              |||||||||||||||||||
Db        213 ACTACAACCAGCAAAAAGACC 233

RESULT 33
US-09-925-065A-367811/c
; Sequence 367811, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 367811
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-367811

Alignment Scores:
Pred. No.:              1.47e+03      Length:         410
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     6             Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-367811 (1-410)

Qy         94 AlaThrSerLysLeuPhePro 100
              |||||||||||||||||||||
Db        132 GCCACTTCCAAACTCTTTCCG 112

RESULT 34
US-10-802-796-98
; Sequence 98, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
;  APPLICANT: COLE, STEWART
;  APPLICANT:  BUCHRIESER-BROSCH, ROLAND
;  APPLICANT:  GORDON, STEPHEN
;  APPLICANT:  BILLAULT, ALAIN
;  TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
;  TITLE OF INVENTION:  FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
;  TITLE OF INVENTION:  DNA LIBRARY. APPLICATION TO THE DETECTION OF
;  TITLE OF INVENTION:  MYCOBACTERIA.
;  FILE REFERENCE: 05394.0011-00000
;  CURRENT APPLICATION NUMBER: US/10/802,796
;  CURRENT FILING DATE:  2004-03-18
;  PRIOR APPLICATION NUMBER: US/09/673,476
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/IB99/00740
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 09/060,756
;  PRIOR FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 743
;  SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 98
;   LENGTH: 439
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-10-802-796-98

Alignment Scores:
Pred. No.:              1.56e+03      Length:         439
Score:                  7.00          Matches:        7
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-9 (1-149) x US-10-802-796-98 (1-439)

Qy         19 GlnAspLeuArgAsnGluLeu 25
              |||||||||||||||||||||
Db        364 CAGGATCTCAGAAACGAGCTG 384

RESULT 35
US-09-925-065A-304102/c
; Sequence 304102, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
```

```
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 304102
;   LENGTH: 509
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-304102

Alignment Scores:
Pred. No.:              1.78e+03        Length:         509
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-304102 (1-509)

Qy         55 ThrSerLysLysThrValLys 61
              ||||||||||||||||||||
Db        432 ACATCAAAGAAAACAGTTAAG 412

RESULT 36
US-09-925-065A-304103/c
; Sequence 304103, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 304103
;   LENGTH: 509
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-304103

Alignment Scores:
Pred. No.:              1.78e+03        Length:         509
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-304103 (1-509)

Qy         55 ThrSerLysLysThrValLys 61
              ||||||||||||||||||||
Db        432 ACATCAAAGAAAACAGTTAAG 412

RESULT 37
US-09-925-065A-787865
; Sequence 787865, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 787865
;   LENGTH: 515
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-787865

Alignment Scores:
Pred. No.:              1.79e+03        Length:         515
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-787865 (1-515)

Qy         51 AspIleThrThrThrSerLys 57
              ||||||||||||||||||||
Db        183 GATATTACTACCACTTCTAAA 203

RESULT 38
US-09-925-065A-455365
; Sequence 455365, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 455365
```

```
;   LENGTH: 524
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-455365

Alignment Scores:
Pred. No.:              1.82e+03        Length:         524
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-455365 (1-524)

Qy          2 AsnThrValSerPheAsnLeu 8
              |||||||||||||||||||||
Db        247 AACACTGTTTCCTTCAATCTA 267

RESULT 39
US-09-925-065A-435174
; Sequence 435174, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 435174
;   LENGTH: 526
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-435174

Alignment Scores:
Pred. No.:              1.83e+03        Length:         526
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-435174 (1-526)

Qy        125 ArgLysAspLeuGluLeuGly 131
              |||||||||||||||||||||
Db        443 AGAAAGGACTTAGAACTTGGA 463

RESULT 40
US-09-925-065A-623014
; Sequence 623014, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 623014
;   LENGTH: 530
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-623014

Alignment Scores:
Pred. No.:              1.84e+03        Length:         530
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-9 (1-149) x US-09-925-065A-623014 (1-530)

Qy        136 GluPheSerIleGluAlaIle 142
              |||||||||||||||||||||
Db        159 GAATTTTCCATTGAAGCTATT 179


Search completed: February 20, 2006, 03:15:23
Job time : 554.749 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 00:56:48 ; Search time 5140.08 Seconds
(without alignments)
1356.257 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 149
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 1

Total number of hits satisfying chosen parameters: 82154958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10758902/runat_17022006_160835_4063/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=oligo.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US10758902_@CGN_1_1_10172_@runat_17022006_160835_4063 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	10	6.7	644	6	CA838401	CA838401 MCT016B04
	2	10	6.7	667	6	CA838446	CA838446 MCT016F04
	3	10	6.7	672	1	AW053585	AW053585 L30-2143T
	4	10	6.7	678	6	CA840373	CA840373 MCT036G03
	5	10	6.7	698	6	CA838926	CA838926 MCT021H09
	6	9	6.0	362	5	BY768107	BY768107 BY768107
c	7	9	6.0	371	4	AY067954	AY067954 Schmidtea
c	8	9	6.0	499	10	CZ581766	CZ581766 OA_BBa018
c	9	9	6.0	602	9	BZ494782	BZ494782 BONOG63TR
c	10	9	6.0	720	5	BX849231	BX849231 BX849231
	11	9	6.0	740	10	CL170043	CL170043 104_370_1
c	12	9	6.0	746	10	CW444509	CW444509 fsbb001f1
	13	9	6.0	756	10	CW431584	CW431584 fsbb001f1
c	14	9	6.0	909	5	BU911748	BU911748 AGENCOURT
	15	9	6.0	935	5	BU368460	BU368460 603789346
c	16	8	5.4	70	6	CD965140	CD965140 SEH_234 G
	17	8	5.4	84	3	BJ063727	BJ063727 BJ063727
c	18	8	5.4	103	3	BM417113	BM417113 952003H01
c	19	8	5.4	161	2	BF748333	BF748333 CM3-BN038
c	20	8	5.4	166	1	BB141468	BB141468 BB141468
c	21	8	5.4	210	1	AI784781	AI784781 SWAMCAC40
	22	8	5.4	225	1	AA328059	AA328059 EST31482
c	23	8	5.4	226	1	AU241088	AU241088 AU241088
c	24	8	5.4	233	10	CG689981	CG689981 ZMMBBc013
c	25	8	5.4	241	10	CL232182	CL232182 ZMMBBc018
c	26	8	5.4	246	2	BF352328	BF352328 RC6-HT059
c	27	8	5.4	258	7	CV372077	CV372077 PM3-CT080
c	28	8	5.4	259	2	BF929992	BF929992 CM4-NT021
	29	8	5.4	264	1	AW887063	AW887063 RC1-OT008
c	30	8	5.4	295	10	CL232378	CL232378 ZMMBBc019
c	31	8	5.4	299	10	CG834124	CG834124 ZMMBBc014
c	32	8	5.4	346	9	CC492594	CC492594 CH240_326
c	33	8	5.4	357	5	BY370947	BY370947 BY370947
	34	8	5.4	360	5	BY085125	BY085125 BY085125
	35	8	5.4	360	9	CC836296	CC836296 ZMMBBc048
c	36	8	5.4	362	3	BM953604	BM953604 952064C01
c	37	8	5.4	373	10	CG682026	CG682026 ZMMBBc014
c	38	8	5.4	378	1	AA561049	AA561049 vl40g06.r
c	39	8	5.4	380	10	CG700571	CG700571 ZMMBBc012
	40	8	5.4	391	3	BI976410	BI976410 485295 MA
	41	8	5.4	393	5	BY097645	BY097645 BY097645
c	42	8	5.4	395	10	CG743329	CG743329 ZMMBBc019
c	43	8	5.4	397	10	CG699158	CG699158 ZMMBBc012
c	44	8	5.4	401	1	AI643325	AI643325 vl40g06.y
c	45	8	5.4	402	2	BE652824	BE652824 UI-M-AO1-
c	46	8	5.4	402	5	BW918551	BW918551 BW918551
c	47	8	5.4	413	10	AG910167	AG910167 Drosophil
	48	8	5.4	415	5	BY550514	BY550514 BY550514
c	49	8	5.4	419	10	CL198527	CL198527 ZMMBBc025
	50	8	5.4	420	1	AI537655	AI537655 tp34a11.x
	51	8	5.4	420	8	DN507933	DN507933 HL0200030
c	52	8	5.4	422	1	AJ651621	AJ651621 AJ651621
c	53	8	5.4	432	8	DN170200	DN170200 LH_Ea06J
	54	8	5.4	434	3	BJ041197	BJ041197 BJ041197
c	55	8	5.4	442	3	BP380855	BP380855 BP380855
c	56	8	5.4	445	2	BF451736	BF451736 uz78f04.y
	57	8	5.4	452	2	BF807534	BF807534 RC2-CI009
	58	8	5.4	452	5	BQ594806	BQ594806 E012262-0
	59	8	5.4	454	1	AJ653060	AJ653060 AJ653060
	60	8	5.4	462	2	BE979588	BE979588 UI-M-BG2-
c	61	8	5.4	467	6	CB932256	CB932256 ri53f02.y
	62	8	5.4	471	1	AI845889	AI845889 UI-M-AO1-
	63	8	5.4	474	2	BE956461	BE956461 UI-M-BG2-
c	64	8	5.4	475	10	CG006677	CG006677 ZUAER57TH
c	65	8	5.4	476	1	AW467606	AW467606 he22c04.x
	66	8	5.4	482	7	CO044957	CO044957 UI-M-AO1-
	67	8	5.4	496	9	AQ399427	AQ399427 mgxb0018O
	68	8	5.4	499	1	AU087809	AU087809 AU087809
	69	8	5.4	501	1	AW748411	AW748411 RC4-BT025
	70	8	5.4	506	9	AZ400442	AZ400442 1M0166C15
c	71	8	5.4	506	9	CC383551	CC383551 PUHHN58TD
	72	8	5.4	506	10	CZ790592	CZ790592 OC_Ba015
c	73	8	5.4	507	10	CL534655	CL534655 trib012xf
c	74	8	5.4	511	9	AQ293712	AQ293712 HS_2267_A
	75	8	5.4	512	9	B76551	B76551 RPCI11-15L2
	76	8	5.4	517	2	BG037734	BG037734 dc67d08.y
	77	8	5.4	517	9	AQ428239	AQ428239 CITBI-E1-
c	78	8	5.4	520	1	AI035950	AI035950 ub50a10.r
	79	8	5.4	528	9	AQ333211	AQ333211 HS_5003_A
	80	8	5.4	541	10	AG955179	AG955179 Drosophil

	81	8	5.4	541	11	TA298D02Q AL489078 T. brucei
	82	8	5.4	547	9	AQ393377 CITBI-E1-
	83	8	5.4	553	9	AQ289856 AQ289856 nbxb0035H
	84	8	5.4	554	9	AQ398907 AQ398907 mgxb0014E
c	85	8	5.4	557	8	DR026138 Osmo00823
c	86	8	5.4	561	8	DN890586 DN890586 nag35e04.
c	87	8	5.4	567	7	CO640947 CO640947 USDA-FP_1
c	88	8	5.4	567	10	CZ658046 CZ658046 OM__Ba020
	89	8	5.4	569	9	AQ951919 AQ951919 Sheared D
c	90	8	5.4	569	11	DE070741 DE070741 Oryzias l
	91	8	5.4	571	9	AQ392863 AQ392863 CITBI-E1-
	92	8	5.4	572	6	CF789773 CF789773 867078 MA
	93	8	5.4	573	1	AL631729 AL631729 AL631729
c	94	8	5.4	573	5	BX926277 BX926277 BX926277
c	95	8	5.4	576	9	AY201067 AY201067 AY201067
	96	8	5.4	579	8	CX552120 CX552120 ydb19h12.
	97	8	5.4	581	3	BI402373 BI402373 MI-P-CP0-
	98	8	5.4	582	7	CN775134 CN775134 tae69h10.
	99	8	5.4	582	9	AQ448715 AQ448715 mgxb0021H
	100	8	5.4	584	8	CX680400 CX680400 ydb68h08.
	101	8	5.4	585	2	BE131785 BE131785 db38b02.y
	102	8	5.4	588	3	BM749169 BM749169 K-EST0024
c	103	8	5.4	588	6	CF790116 CF790116 867462 MA
	104	8	5.4	591	9	BH709841 BH709841 BOMKS83TF
	105	8	5.4	592	10	AG970100 AG970100 Drosophil
	106	8	5.4	594	5	BQ623082 BQ623082 USDA-FP_0
	107	8	5.4	597	10	AG950357 AG950357 Drosophil
	108	8	5.4	598	10	CG342562 CG342562 OG4AM87TC
	109	8	5.4	601	7	CN773487 CN773487 tae61d03.
c	110	8	5.4	601	9	AQ159380 AQ159380 nbxb0013F
	111	8	5.4	603	5	BX668613 BX668613 BX668613
c	112	8	5.4	606	9	AZ984687 AZ984687 2M0266J15
	113	8	5.4	607	6	CF180351 CF180351 815444 MA
c	114	8	5.4	607	10	CL532527 CL532527 trib007xj
	115	8	5.4	610	8	CX676781 CX676781 ydd23c04.
	116	8	5.4	612	2	BG924897 BG924897 HNC38-1-E
	117	8	5.4	616	5	BQ594721 BQ594721 E012441-0
c	118	8	5.4	617	5	BW750162 BW750162 BW750162
c	119	8	5.4	617	6	CD354962 CD354962 UI-M-GM0-
	120	8	5.4	623	10	CZ874300 CZ874300 OC__Ba027
	121	8	5.4	624	2	BB619249 BB619249 BB619249
c	122	8	5.4	625	10	CG763971 CG763971 ZMMBBc020
c	123	8	5.4	626	7	CN770424 CN770424 tae69h10.
c	124	8	5.4	627	8	DR708432 DR708432 Asn_09296
	125	8	5.4	628	5	BY718824 BY718824 BY718824
c	126	8	5.4	628	7	CN768873 CN768873 taf20d12.
	127	8	5.4	630	8	DN373796 DN373796 LIB38527_
c	128	8	5.4	637	1	AI394504 AI394504 tf79h02.x
c	129	8	5.4	637	10	CL579206 CL579206 OB__Ba003
c	130	8	5.4	642	6	CB844714 CB844714 M2PN-0266
	131	8	5.4	646	3	BJ109333 BJ109333 BJ109333
c	132	8	5.4	649	9	AQ949380 AQ949380 Sheared D
c	133	8	5.4	650	6	CB175129 CB175129 pk80c06.y
c	134	8	5.4	650	9	BZ876403 BZ876403 CH240_276
	135	8	5.4	651	10	CZ709038 CZ709038 OC__Ba002
	136	8	5.4	654	10	CW374967 CW374967 fsbb001f0
c	137	8	5.4	655	3	BJ709096 BJ709096 BJ709096
	138	8	5.4	655	9	AQ486839 AQ486839 RPCI-11-2
c	139	8	5.4	660	6	CA109183 CA109183 SCSGHR106
c	140	8	5.4	661	6	CF178983 CF178983 813064 MA
	141	8	5.4	663	5	BW897615 BW897615 BW897615
	142	8	5.4	667	5	BQ601356 BQ601356 MI-P-H3-a
	143	8	5.4	673	9	AQ162291 AQ162291 mgxb0012E
	144	8	5.4	675	5	BQ871017 BQ871017 QGI10K17.
	145	8	5.4	675	8	CX550948 CX550948 ydb11b05.
	146	8	5.4	676	6	CD469335 CD469335 LeukoS2_3
c	147	8	5.4	677	9	BZ828795 BZ828795 PUFJI02TB
c	148	8	5.4	679	5	BX315327 BX315327 BX315327
c	149	8	5.4	682	5	BW693385 BW693385 BW693385
	150	8	5.4	686	9	AQ162008 AQ162008 mgxb0010N
	151	8	5.4	687	9	BZ020270 BZ020270 oeh04c01.
c	152	8	5.4	690	7	CN773154 CN773154 tae61d03.
c	153	8	5.4	690	10	CL718269 CL718269 OR_BBa004
c	154	8	5.4	694	6	CB469308 CB469308 sn05_H01.
c	155	8	5.4	695	7	CV640950 CV640950 EST919703
c	156	8	5.4	695	10	CL723289 CL723289 OR_BBa005
	157	8	5.4	699	9	AQ325209 AQ325209 mgxb0021E
	158	8	5.4	700	2	BI186153 BI186153 UNL-P-FN-
c	159	8	5.4	703	10	CW317755 CW317755 104_809_1
	160	8	5.4	704	5	BY764463 BY764463 BY764463
	161	8	5.4	704	10	BX165160 BX165160 Danio rer
	162	8	5.4	706	9	BZ457449 BZ457449 BONLG01TR
	163	8	5.4	707	10	CG860257 CG860257 ZMMBBc026
c	164	8	5.4	708	10	CL709205 CL709205 OR_BBa003
c	165	8	5.4	714	10	CL532812 CL532812 trib007xn
c	166	8	5.4	716	9	CC745957 CC745957 ZMMBBb012
c	167	8	5.4	716	10	CW084955 CW084955 104_428_1
	168	8	5.4	720	5	BQ967514 BQ967514 QHB30A16.
	169	8	5.4	725	6	CF451510 CF451510 EST687855
c	170	8	5.4	727	10	BX997809 BX997809 Forward s
c	171	8	5.4	735	2	BE265970 BE265970 601193067
	172	8	5.4	735	7	CN992675 CN992675 70736_125
	173	8	5.4	736	3	BP677084 BP677084 BP677084
c	174	8	5.4	736	8	DR722025 DR722025 AGENCOURT
c	175	8	5.4	738	10	CW037725 CW037725 104_269_1
	176	8	5.4	740	1	AJ820130 AJ820130 AJ820130
	177	8	5.4	741	8	CX453714 CX453714 JGI_XZG54
	178	8	5.4	743	9	BH506672 BH506672 BOGYO10TR
	179	8	5.4	746	10	CW373064 CW373064 fsbb001f0
c	180	8	5.4	747	7	CK369353 CK369353 zmrws485_
	181	8	5.4	749	10	CG353606 CG353606 OGYBH40TH
	182	8	5.4	758	2	BI089654 BI089654 602854348
	183	8	5.4	764	6	CA464875 CA464875 AGENCOURT
	184	8	5.4	767	7	CO119554 CO119554 GR__Eb022
	185	8	5.4	768	8	CX826354 CX826354 JGI_CAAK5
	186	8	5.4	771	8	DR103654 DR103654 JHU040H05
c	187	8	5.4	773	7	CO430592 CO430592 UI-M-HX0-
	188	8	5.4	773	10	CG214786 CG214786 OGWJJ60TH
c	189	8	5.4	774	5	BX315328 BX315328 BX315328
c	190	8	5.4	778	10	CL736616 CL736616 OR_BBa007
c	191	8	5.4	780	6	CD610627 CD610627 56085460H
c	192	8	5.4	780	9	BZ733456 BZ733456 OGFBC05TC
c	193	8	5.4	781	3	BP169552 BP169552 BP169552
	194	8	5.4	782	6	CA464247 CA464247 AGENCOURT
c	195	8	5.4	784	9	CC331257 CC331257 OGIAV03TH
c	196	8	5.4	785	10	CG455625 CG455625 PUIKE96TB
	197	8	5.4	786	9	CC667997 CC667997 OGUJG28TV
c	198	8	5.4	787	8	CX453713 CX453713 JGI_XZG54
c	199	8	5.4	787	8	DN887911 DN887911 nag09d09.
	200	8	5.4	787	9	AQ361965 AQ361965 mgxb0005O
	201	8	5.4	789	7	CO386739 CO386739 AGENCOURT
c	202	8	5.4	792	9	CC421388 CC421388 PUHTR28TD
	203	8	5.4	797	3	BP682823 BP682823 BP682823
	204	8	5.4	799	6	CA464558 CA464558 AGENCOURT
	205	8	5.4	799	10	CG180786 CG180786 PUFOT92TD
	206	8	5.4	800	8	CX775407 CX775407 UI-EH-HG2
c	207	8	5.4	800	9	CC789371 CC789371 ZMMBBb015
	208	8	5.4	801	2	BI183017 BI183017 UNL-P-FN-
	209	8	5.4	802	10	CW375126 CW375126 fsbb001f0
c	210	8	5.4	804	10	CW375127 CW375127 fsbb001f0
	211	8	5.4	805	5	BU461485 BU461485 603367342
	212	8	5.4	805	7	CJ012468 CJ012468
	213	8	5.4	806	9	CC353395 CC353395 PUHJH88TB
	214	8	5.4	813	9	BZ753068 BZ753068 PUDCO76TB
	215	8	5.4	815	5	BU939004 BU939004 AGENCOURT
c	216	8	5.4	819	10	CL769197 CL769197 OR_BBa014
c	217	8	5.4	824	7	CO451511 CO451511 MZCCL1016
c	218	8	5.4	827	10	CG958899 CG958899 MBEIW28TF
c	219	8	5.4	830	8	DN888824 DN888824 nag18d11.
	220	8	5.4	832	2	BF142361 BF142361 601786610
c	221	8	5.4	833	8	DR878831 DR878831 JGI_CABJ3
	222	8	5.4	834	5	BQ881742 BQ881742 AGENCOURT
	223	8	5.4	835	8	DN111917 DN111917 1111068 M
	224	8	5.4	839	9	CC985214 CC985214 ZUAAK62TH
	225	8	5.4	841	10	CG455664 CG455664 PUIKE96TD
	226	8	5.4	843	8	DN569719 DN569719 93846465

227	8	5.4	845	6	CD328246	CD328246 AGENCOURT
c 228	8	5.4	850	8	DN111551	DN111551 1110684 M
229	8	5.4	853	10	CZ396435	CZ396435 ZMMBF0176
c 230	8	5.4	859	10	CZ324174	CZ324174 ZMMBF0028
231	8	5.4	860	10	CZ545514	CZ545514 SRAA-aad6
c 232	8	5.4	862	10	CNS01X56	AL171267 Tetraodon
c 233	8	5.4	868	9	CC856290	CC856290 NDL.17G6.
234	8	5.4	870	10	CZ275121	CZ275121 ZMMBF0057
c 235	8	5.4	873	3	BI736716	BI736716 603360410
c 236	8	5.4	877	10	CG416560	CG416560 ZMMBBc002
c 237	8	5.4	882	9	CC425002	CC425002 PUHPN28TD
238	8	5.4	883	9	AQ739590	AQ739590 HS_5381_B
c 239	8	5.4	891	10	CG396452	CG396452 ZMMBBc001
c 240	8	5.4	895	6	CD329929	CD329929 AGENCOURT
c 241	8	5.4	897	10	CG304718	CG304718 OG1AU17TH
c 242	8	5.4	906	10	CG180785	CG180785 PUFOT92TB
c 243	8	5.4	908	6	CD381747	CD381747 PTMM06917
244	8	5.4	908	10	CZ395458	CZ395458 ZMMBF0175
c 245	8	5.4	913	2	BF671210	BF671210 602151051
246	8	5.4	914	11	CR211685	CR211685 Forward s
c 247	8	5.4	917	6	CD327959	CD327959 AGENCOURT
248	8	5.4	917	8	CX894219	CX894219 JGI_CAAM5
249	8	5.4	920	5	BX845875	BX845875 BX845875
c 250	8	5.4	925	5	BU910719	BU910719 AGENCOURT
251	8	5.4	926	10	CZ930980	CZ930980 248803 To
252	8	5.4	927	6	CB590358	CB590358 AGENCOURT
c 253	8	5.4	928	6	CD099541	CD099541 AGENCOURT
254	8	5.4	951	11	CNS0793X	AL434803 T7 end of
255	8	5.4	954	9	CC298491	CC298491 CH261-178
c 256	8	5.4	957	9	CC238535	CC238535 CH261-75D
257	8	5.4	958	9	CC331268	CC331268 OGIAV03TV
258	8	5.4	958	10	CG304729	CG304729 OG1AU17TV
c 259	8	5.4	962	10	CG873564	CG873564 ZMMBBc028
260	8	5.4	966	5	BX850329	BX850329 BX850329
c 261	8	5.4	969	10	CG353616	CG353616 OGYBH40TV
c 262	8	5.4	975	10	CG395175	CG395175 ZMMBBc001
c 263	8	5.4	977	10	CG399802	CG399802 ZMMBBc002
c 264	8	5.4	1000	10	CL199325	CL199325 ZMMBBc007
265	8	5.4	1007	10	CZ393728	CZ393728 ZMMBF0172
266	8	5.4	1021	10	AY404459	AY404459 Mus muscu
267	8	5.4	1025	10	CZ365859	CZ365859 ZMMBF0145
268	8	5.4	1040	4	HSM802933	AL583911 Homo sapi
c 269	8	5.4	1057	10	CL283363	CL283363 ZMMBBb062
c 270	8	5.4	1072	10	CZ378367	CZ378367 ZMMBF0137
c 271	8	5.4	1096	7	CK212287	CK212287 FGAS02415
272	8	5.4	1127	9	CC195384	CC195384 CH261-111
c 273	8	5.4	1147	8	DN699129	DN699129 CLJ21-F08
274	8	5.4	1155	6	CD507825	CD507825 CDA87-C10
c 275	8	5.4	1160	9	CC262023	CC262023 CH261-55C
276	8	5.4	1254	8	DN665505	DN665505 CFW26-F06
277	8	5.4	1321	6	CD255355	CD255355 AGENCOURT
c 278	8	5.4	1407	10	CL982654	CL982654 OsIFSC048
c 279	8	5.4	1415	5	BU298066	BU298066 603610869
280	8	5.4	1488	9	CC190824	CC190824 CH261-38K
c 281	8	5.4	1561	2	BG284160	BG284160 602408204
c 282	8	5.4	2292	4	AK033904	AK033904 Mus muscu
283	8	5.4	3765	4	CR627456	CR627456 Homo sapi
284	7	4.7	57	5	BX686788	BX686788 BX686788
c 285	7	4.7	64	7	CV304460	CV304460 th06d06.g
286	7	4.7	69	10	CG643086	CG643086 OST380909
287	7	4.7	82	1	AA933653	AA933653 om56d01.s
288	7	4.7	84	3	BJ057969	BJ057969 BJ057969
c 289	7	4.7	93	10	AG265324	AG265324 Lotus cor
290	7	4.7	94	8	W17845	W17845 mb72a08.r1
291	7	4.7	103	6	CD846883	CD846883 DH0AB51ZG
c 292	7	4.7	104	10	BX896073	BX896073 Arabidops
293	7	4.7	117	8	U78752	U78752 PFU78752 Pl
c 294	7	4.7	123	10	CW542999	CW542999 OA_ABa005
295	7	4.7	126	5	BU016174	BU016174 QHE12F10.
296	7	4.7	131	4	AK182718	AK182718 Mus muscu
297	7	4.7	133	5	BQ799305	BQ799305 EST 1474
c 298	7	4.7	133	10	AG264459	AG264459 Lotus cor
299	7	4.7	135	1	AA265896	AA265896 mz71h04.r
300	7	4.7	135	2	BF829596	BF829596 MR3-HN006
301	7	4.7	135	6	CF326941	CF326941 NACL--01-
c 302	7	4.7	136	6	CF326942	CF326942 NACL--01-
303	7	4.7	141	6	CD016403	CD016403 NXCI_043_
304	7	4.7	145	9	BH275762	BH275762 CH230-70J
c 305	7	4.7	149	1	AW284624	AW284624 LG1_271_E
306	7	4.7	152	1	AA260768	AA260768 va12c10.r
c 307	7	4.7	153	9	BH810216	BH810216 SALK_0444
c 308	7	4.7	153	11	DR31I10T	AL984781 Danio rer
309	7	4.7	156	5	BQ972783	BQ972783 QHI10I02.
c 310	7	4.7	156	6	CB602988	CB602988 M1036 Mid
c 311	7	4.7	157	10	CW521543	CW521543 OP__Ba002
c 312	7	4.7	161	1	AA327033	AA327033 EST30299
c 313	7	4.7	171	11	DR41H16S	AL974850 Danio rer
314	7	4.7	174	9	AZ750404	AZ750404 RPCI-24-7
315	7	4.7	175	1	AV352845	AV352845 AV352845
c 316	7	4.7	175	10	CG625388	CG625388 OST330902
317	7	4.7	177	6	CF719915	CF719915 CCADR10TR
318	7	4.7	179	1	AA943906	AA943906 EST199405
319	7	4.7	179	7	CK913373	CK913373 e3fmg_004
320	7	4.7	179	7	CN411272	CN411272 170006004
321	7	4.7	180	7	CK912282	CK912282 e3fmgy_00
322	7	4.7	182	2	BI277769	BI277769 UI-R-CZ0-
323	7	4.7	182	7	CK912476	CK912476 e3fmg_000
c 324	7	4.7	182	10	AL940395	AL940395 Arabidops
c 325	7	4.7	184	7	CO029617	CO029617 EST808001
326	7	4.7	184	7	CO730461	CO730461 SnESTbaa2
c 327	7	4.7	185	2	BG361676	BG361676 gb48a07.y
c 328	7	4.7	186	8	DR085613	DR085613 CAST054D0
329	7	4.7	187	5	BW696907	BW696907 BW696907
330	7	4.7	188	8	R19322	R19322 yg23e09.r1
c 331	7	4.7	189	9	AZ030517	AZ030517 RPCI-23-2
332	7	4.7	190	2	BF032093	BF032093 601559677
333	7	4.7	190	5	BY077833	BY077833 BY077833
334	7	4.7	195	8	N58991	N58991 yz19d02.r1
335	7	4.7	195	9	BH906856	BH906856 SALK_0362
336	7	4.7	197	6	CF570308	CF570308 YCS40_014
337	7	4.7	197	6	CF570334	CF570334 YCS40_086
338	7	4.7	197	7	CK913097	CK913097 e3fmg_002
c 339	7	4.7	197	9	AZ640296	AZ640296 1M0502C18
c 340	7	4.7	198	1	BB170806	BB170806 BB170806
341	7	4.7	199	7	CK912829	CK912829 e3fmg_001
c 342	7	4.7	200	5	BY001940	BY001940 BY001940
343	7	4.7	200	7	CK912710	CK912710 e3fmg_001
344	7	4.7	200	8	CV879998	CV879998 Mdst6017e
c 345	7	4.7	200	10	CL272337	CL272337 Ggal_79b_
346	7	4.7	201	7	CK912381	CK912381 e3fmgy_00
347	7	4.7	202	7	CK912063	CK912063 e3fmgy_00
348	7	4.7	202	7	CK912204	CK912204 e3fmgy_00
349	7	4.7	202	7	CK912662	CK912662 e3fmg_001
350	7	4.7	202	7	CK913126	CK913126 e3fmg_003
351	7	4.7	203	1	AI228544	AI228544 EST225239
352	7	4.7	204	7	CK910227	CK910227 e3fmgb_00
353	7	4.7	204	7	CK911765	CK911765 e3fmgj_00
354	7	4.7	204	7	CK912112	CK912112 e3fmgy_00
355	7	4.7	205	8	D79092	D79092 HUM531C03B
c 356	7	4.7	206	2	BE125725	BE125725 DG1_54_F0
357	7	4.7	207	3	BP039827	BP039827 BP039827
358	7	4.7	207	7	CK913281	CK913281 e3fmg_003
c 359	7	4.7	209	2	BB589006	BB589006 BB589006
360	7	4.7	211	1	AA963710	AA963710 UI-R-E1-g
361	7	4.7	212	7	CK910738	CK910738 e3fmgfa_0
c 362	7	4.7	213	1	AW890343	AW890343 MR0-NT003
363	7	4.7	213	7	CN929569	CN929569 000321AFB
364	7	4.7	213	10	CW774054	CW774054 OG_BBa009
365	7	4.7	214	2	BB331157	BB331157 BB331157
c 366	7	4.7	215	1	AW748420	AW748420 RC2-BT025
c 367	7	4.7	215	3	BI315256	BI315256 dah96e06.
368	7	4.7	215	6	CD130978	CD130978 MG1-0009P
369	7	4.7	216	9	AQ352194	AQ352194 CITBI-E1-
c 370	7	4.7	221	2	BG093385	BG093385 ut70g12.y
371	7	4.7	221	5	BW545127	BW545127 BW545127
c 372	7	4.7	221	6	CB412469	CB412469 ScaE_0638

c 373	7	4.7	222	1	AA215944	AA215944 hp0081.se
374	7	4.7	222	9	BZ745932	BZ745932 OGFBQ13TM
375	7	4.7	223	2	BB450399	BB450399 BB450399
376	7	4.7	224	1	AA364379	AA364379 EST74959
377	7	4.7	225	3	BM387565	BM387565 UI-R-CN1-
378	7	4.7	225	11	CPA561540	AJ561540 Cryptospo
c 379	7	4.7	226	6	CD612227	CD612227 56026033H
380	7	4.7	226	6	CD612228	CD612228 56026033J
381	7	4.7	226	10	CL257648	CL257648 ZMMBBb061
c 382	7	4.7	227	7	CV413646	CV413646 RC2-HT082
383	7	4.7	227	8	T31555	T31555 EST34704 Hu
384	7	4.7	228	2	BB662032	BB662032 BB662032
385	7	4.7	229	9	CC565568	CC565568 CH240_478
386	7	4.7	230	1	AW389421	AW389421 CM4-ST016
c 387	7	4.7	230	1	AA363875	AA363875 EST74349
c 388	7	4.7	231	2	BE159944	BE159944 RC4-HT041
c 389	7	4.7	232	8	T19636	T19636 710R Heart
390	7	4.7	233	1	AV280172	AV280172 AV280172
c 391	7	4.7	233	9	AZ048127	AZ048127 LMAJFV1_1
392	7	4.7	234	2	BF950262	BF950262 CM3-NN118
393	7	4.7	235	8	T19635	T19635 710F Heart
394	7	4.7	235	10	CZ655888	CZ655888 OM__Ba020
395	7	4.7	236	8	T08793	T08793 EST06685 In
396	7	4.7	237	1	AA996988	AA996988 UI-R-C0-h
c 397	7	4.7	237	5	BQ821135	BQ821135 1030089F0
398	7	4.7	240	2	BF950260	BF950260 CM3-NN118
399	7	4.7	240	6	CD612226	CD612226 56025941J
400	7	4.7	241	2	BF950326	BF950326 CM3-NN118
401	7	4.7	241	7	CN411278	CN411278 170005999
402	7	4.7	241	8	CX001369	CX001369 iv40f07.b
c 403	7	4.7	242	1	AI002311	AI002311 or73c03.s
404	7	4.7	242	7	CN411273	CN411273 170004241
405	7	4.7	243	3	BI816349	BI816349 PfESToaa3
c 406	7	4.7	243	6	CD612225	CD612225 56025941H
c 407	7	4.7	243	6	CF646791	CF646791 3530_1_32
408	7	4.7	245	2	BG144215	BG144215 ut70g12.x
409	7	4.7	245	2	BE357350	BE357350 DG1_148_C
410	7	4.7	247	8	DR112357	DR112357 RTS1_27_D
c 411	7	4.7	248	1	AW528512	AW528512 UI-R-BT1-
c 412	7	4.7	248	2	BE529804	BE529804 M75L16STM
413	7	4.7	249	9	BZ127243	BZ127243 CH230-298
414	7	4.7	251	3	BQ358524	BQ358524 IL3-HT061
415	7	4.7	252	2	BB498197	BB498197 BB498197
c 416	7	4.7	253	7	CV475356	CV475356 23889.1 D
417	7	4.7	254	2	BF950317	BF950317 CM3-NN118
c 418	7	4.7	254	2	BB415727	BB415727 BB415727
c 419	7	4.7	257	1	AA958216	AA958216 TENS1655
c 420	7	4.7	257	1	AW672585	AW672585 56B Expla
421	7	4.7	257	5	BQ568352	BQ568352 gi106f10.
c 422	7	4.7	258	2	BB249971	BB249971 BB249971
423	7	4.7	259	1	AI119346	AI119346 ue98e04.y
c 424	7	4.7	259	8	D52539	D52539 HUM081A11B
c 425	7	4.7	261	2	BF918627	BF918627 CM0-NT013
426	7	4.7	261	2	BI142985	BI142985 rk69b07.y
c 427	7	4.7	261	5	BX429249	BX429249 BX429249
428	7	4.7	262	7	CK565524	CK565524 dor6sp6a1
429	7	4.7	263	8	T30923	T30923 EST24807 Hu
c 430	7	4.7	263	10	CW617412	CW617412 OA_ABa016
431	7	4.7	264	2	BF950254	BF950254 CM3-NN118
c 432	7	4.7	264	3	BM688583	BM688583 UI-E-CR0-
433	7	4.7	264	3	BM895731	BM895731 952062G07
c 434	7	4.7	265	4	AY431455	AY431455 Aedes aeg
435	7	4.7	265	10	CW139339	CW139339 104_529_1
436	7	4.7	266	2	BG932756	BG932756 h91-9 h91
437	7	4.7	266	9	AZ512629	AZ512629 1M0358B24
c 438	7	4.7	268	1	AA364980	AA364980 EST75647
439	7	4.7	268	7	CK576956	CK576956 IST_WI5_1
c 440	7	4.7	268	7	CK931809	CK931809 p5rmgc_00
c 441	7	4.7	268	7	CO329651	CO329651 EK293329.
442	7	4.7	268	7	CR458734	CR458734 CR458734
c 443	7	4.7	270	1	AA867937	AA867937 TENS0045
c 444	7	4.7	270	1	AJ499602	AJ499602 AJ499602
445	7	4.7	270	10	AJ597697	AJ597697 Arabidops
446	7	4.7	271	6	CB945229	CB945229 AGENCOURT
447	7	4.7	272	7	CN140921	CN140921 OX1_48_C0
c 448	7	4.7	272	9	BZ641832	BZ641832 OGAMU53TC
449	7	4.7	272	10	AB157849	AB157849 Oryza sat
c 450	7	4.7	273	1	AV014687	AV014687 AV014687
451	7	4.7	273	2	BB718626	BB718626 BB718626
452	7	4.7	273	6	CD441862	CD441862 EL01N0401
c 453	7	4.7	273	7	CJ398281	CJ398281 CJ398281
c 454	7	4.7	274	1	AL830715	AL830715 AL830715
c 455	7	4.7	274	1	BB150563	BB150563 BB150563
456	7	4.7	275	1	AA882527	AA882527 TENS0097
c 457	7	4.7	275	6	CB549086	CB549086 MMPL0021_
458	7	4.7	276	1	AW359025	AW359025 44708 MAR
c 459	7	4.7	276	1	AW594154	AW594154 hg60d01.x
460	7	4.7	276	7	CO055136	CO055136 TgESTzyo2
c 461	7	4.7	277	1	AA952398	AA952398 TENS1340
462	7	4.7	277	2	BB348902	BB348902 BB348902
c 463	7	4.7	277	6	CD141149	CD141149 MG1-0069T
464	7	4.7	278	1	AV227004	AV227004 AV227004
465	7	4.7	278	2	BB291999	BB291999 BB291999
466	7	4.7	278	10	BX178518	BX178518 Danio rer
c 467	7	4.7	279	1	AA365761	AA365761 EST76875
c 468	7	4.7	279	10	CG837308	CG837308 ZMMBBc021
469	7	4.7	280	1	AL838938	AL838938 AL838938
c 470	7	4.7	280	1	AW457001	AW457001 UI-M-BH3-
c 471	7	4.7	280	6	CD138207	CD138207 MG1-0051T
c 472	7	4.7	280	7	CO186699	CO186699 EK022302.
c 473	7	4.7	280	7	CO267664	CO267664 EK151452.
c 474	7	4.7	280	7	CO268613	CO268613 EK092131.
c 475	7	4.7	280	7	CO287591	CO287591 EK066240.
c 476	7	4.7	280	9	CE219576	CE219576 tigr-gss-
c 477	7	4.7	280	10	CZ605288	CZ605288 OM__Ba012
478	7	4.7	281	7	CF949263	CF949263 UI-M-HK0-
c 479	7	4.7	282	6	CF810589	CF810589 CA288F cD
480	7	4.7	282	9	AQ909115	AQ909115 GSSTc0754
c 481	7	4.7	282	9	AZ589303	AZ589303 1M0398M07
482	7	4.7	282	9	CC839222	CC839222 ZMMBBc049
c 483	7	4.7	283	1	AA685139	AA685139 EST106352
c 484	7	4.7	283	6	CD612217	CD612217 55100358H
485	7	4.7	283	6	CD612218	CD612218 55100358J
c 486	7	4.7	284	1	AA496775	AA496775 ae30g09.r
487	7	4.7	284	3	BQ208748	BQ208748 UI-R-DY1-
c 488	7	4.7	284	7	CO261928	CO261928 EK082031.
c 489	7	4.7	284	10	CG835650	CG835650 ZMMBBc021
c 490	7	4.7	285	1	AA364927	AA364927 EST75606
c 491	7	4.7	285	10	CG415127	CG415127 ZMMBBc002
c 492	7	4.7	286	10	CE595561	CE595561 tigr-gss-
493	7	4.7	287	6	CD410466	CD410466 Gm_ck3831
494	7	4.7	288	1	AV165746	AV165746 AV165746
c 495	7	4.7	289	2	BB266804	BB266804 BB266804
496	7	4.7	289	10	CNS01S7D	AL164866 Tetraodon
497	7	4.7	290	2	BB371363	BB371363 BB371363
498	7	4.7	291	1	AI710925	AI710925 UI-R-AE1-
499	7	4.7	291	2	BB720628	BB720628 BB720628
500	7	4.7	291	6	CB393632	CB393632 OSTR122G1
501	7	4.7	291	7	CO375579	CO375579 tah38d10.
502	7	4.7	291	8	W05239	W05239 za78f01.r1
503	7	4.7	292	5	BW855836	BW855836 BW855836
504	7	4.7	292	9	AQ378545	AQ378545 RPCI11-15
c 505	7	4.7	293	10	CW051314	CW051314 104_291_1
506	7	4.7	294	3	BP718407	BP718407 BP718407
507	7	4.7	294	5	BY361782	BY361782 BY361782
508	7	4.7	294	10	AL950974	AL950974 Arabidops
509	7	4.7	295	10	CG822575	CG822575 SOYEK81TH
510	7	4.7	296	1	AA309753	AA309753 EST180702
511	7	4.7	296	2	BG060431	BG060431 L0902H06-
512	7	4.7	296	7	CK534887	CK534887 rswgb0_00
c 513	7	4.7	296	10	CW654947	CW654947 OG_BBa000
514	7	4.7	297	1	AJ346364	AJ346364 sHr-00001
515	7	4.7	298	8	DN909439	DN909439 Cucl_3_F1
516	7	4.7	299	1	AA849832	AA849832 EST192599
517	7	4.7	299	2	BE343174	BE343174 EST396018
518	7	4.7	299	9	AZ025393	AZ025393 RPCI-23-3

	519	7	4.7	299	9	BH874920 BH874920 hq82d12.b
	520	7	4.7	300	1	AU099276 AU099276 AU099276
c	521	7	4.7	300	1	AV184036 AV184036 AV184036
c	522	7	4.7	300	5	C54240 C54240 Yuji
c	523	7	4.7	300	5	C55282 C55282 Yuji
c	524	7	4.7	300	5	C55303 C55303 Yuji
c	525	7	4.7	300	8	CX838551 JGI_CAAK8
c	526	7	4.7	300	9	BZ384643 SALK_1358
c	527	7	4.7	301	1	AI430990 mh76f05.x
c	528	7	4.7	302	1	AI083158 TENU3835
	529	7	4.7	302	1	AJ540020 AJ540020
	530	7	4.7	302	1	AJ540035 AJ540035
	531	7	4.7	303	9	BH275328 CH230-1D6
	532	7	4.7	304	2	BE075744 MR2-BT059
c	533	7	4.7	304	7	CF974201 PSU_nep1\
	534	7	4.7	304	7	CV352408 MR3-HN006
	535	7	4.7	306	1	AA925636 UI-R-A1-e
	536	7	4.7	306	1	AI712342 UI-R-AF1-
	537	7	4.7	307	5	BU025190 QHF8B09.y
c	538	7	4.7	308	1	AA338631 EST43673
	539	7	4.7	310	6	CF571010 MCS008E11
	540	7	4.7	311	1	AV170012 AV170012
	541	7	4.7	311	2	BE075514 MR2-BT059
c	542	7	4.7	312	8	DR022042 STRS1_48_
	543	7	4.7	313	1	AW346045 AW346045 27060_MAR
c	544	7	4.7	314	5	BW641865 BW641865
	545	7	4.7	314	9	AQ094982 HS_3017_B
	546	7	4.7	315	1	AW928285 AW928285 EST00005
	547	7	4.7	315	2	BE484280 170829 BA
	548	7	4.7	315	7	CN411270 CN411270 170004245
c	549	7	4.7	316	6	CF564388 CF564388 1115091E0
	550	7	4.7	316	8	D42942 D42942 Rice
	551	7	4.7	317	6	CB751517 CB751517 Ac021 rat
c	552	7	4.7	317	7	CO903301 CO903301 Mddb5022a
c	553	7	4.7	317	8	CX647684 COLD1_19_
c	554	7	4.7	318	1	BB011531 BB011531 BB011531
c	555	7	4.7	318	8	DR166811 DR166811 RTPHOS1_1
	556	7	4.7	318	9	BZ768419 SALK_1401
	557	7	4.7	319	2	BG345544 dd88e02.y
	558	7	4.7	319	2	BB446495 BB446495 BB446495
c	559	7	4.7	319	6	CF022718 QBQ18f12.
c	560	7	4.7	320	6	CD380836 CD380836 PTMM06005
c	561	7	4.7	320	10	CL891477 CL891477 abg08e08.
	562	7	4.7	321	1	AI713512 AI713512 UI-R-AA1-
	563	7	4.7	323	1	AI044391 AI044391 UI-R-C0-i
	564	7	4.7	323	2	BF958289 BF958289 CM2-NN024
	565	7	4.7	323	9	BH201220 BH201220 Sm1-43B8.
c	566	7	4.7	324	2	BF817328 BF817328 PM2-CI015
c	567	7	4.7	324	9	AZ389004 AZ389004 1M0149L16
c	568	7	4.7	325	2	BG159905 BG159905 dab69f01.
c	569	7	4.7	325	10	CW639008 CW639008 OA_ABa017
c	570	7	4.7	326	5	BQ454950 BQ454950 ke16f02.y
c	571	7	4.7	327	2	BE582251 BE582251 NXCI_026_
	572	7	4.7	327	6	CA288818 CA288818 SCEQSD207
	573	7	4.7	327	9	AQ279871 AQ279871 CITBI-E1-
	574	7	4.7	327	10	AB155445 AB155445 Oryza sat
c	575	7	4.7	329	7	CO171108 CO171108 NDL1_19_E
	576	7	4.7	330	1	AA205194 AA205194 zq70g07.r
	577	7	4.7	330	8	F08093 F08093 HSC2QA111 n
	578	7	4.7	330	10	CL289154 CL289154 ZMMBBb064
	579	7	4.7	331	1	AW463450 AW463450 BP230012B
	580	7	4.7	331	6	CA564419 CA564419 K0326A01-
	581	7	4.7	331	8	R10262 R10262 yf32h06.r1
c	582	7	4.7	332	2	BE497393 BE497393 WHE0751_B
c	583	7	4.7	333	1	AA364332 AA364332 EST74886
	584	7	4.7	333	6	CD181452 CD181452 MS1-0030T
	585	7	4.7	334	2	BF611344 BF611344 dd79b03.y
	586	7	4.7	334	2	BF743439 BF743439 QV0-BT084
	587	7	4.7	335	1	AV627863 AV627863 AV627863
	588	7	4.7	335	5	BQ556593 BQ556593 H4041A08-
	589	7	4.7	335	5	BX362323 BX362323 BX362323
	590	7	4.7	335	10	CG855595 CG855595 ZMMBBc025
c	591	7	4.7	335	10	CL264404 CL264404 ZMMBBb062
	592	7	4.7	336	1	AV639621 AV639621 AV639621
	593	7	4.7	336	5	BU653438 BU653438 1112106F0
	594	7	4.7	336	8	F01149 F01149 HSBA5H122 S
	595	7	4.7	337	1	AA963473 AA963473 UI-R-E1-g
	596	7	4.7	337	1	AA964784 AA964784 UI-R-E1-g
	597	7	4.7	337	1	AV021139 AV021139 AV021139
	598	7	4.7	337	6	CF048077 CF048077 QCL17d04.
	599	7	4.7	338	1	AA955410 AA955410 UI-R-A1-e
	600	7	4.7	338	1	AA998863 AA998863 UI-R-C0-h
	601	7	4.7	338	1	AW240420 AW240420 uq34c02.x
c	602	7	4.7	338	7	CO344353 CO344353 EP19117.3
	603	7	4.7	339	8	T31100 T31100 EST27370 Hu
	604	7	4.7	339	9	CC839233 CC839233 ZMMBBc049
	605	7	4.7	339	10	CZ209940 CZ209940 AIAA-aah0
	606	7	4.7	339	10	CE527688 CE527688 tigr-gss-
	607	7	4.7	339	10	CL953969 CL953969 OsIRUA005
	608	7	4.7	340	9	AQ851327 AQ851327 LMAJFV1_1
c	609	7	4.7	341	2	BF774893 BF774893 284900 MA
	610	7	4.7	341	2	BB274985 BB274985 BB274985
c	611	7	4.7	341	2	BE707382 QV2-HT049
c	612	7	4.7	341	2	BE948540 BE948540 UI-M-BH3-
	613	7	4.7	341	6	CB819550 CB819550 EST 542 G
c	614	7	4.7	341	9	BZ856968 BZ856968 CH240_285
c	615	7	4.7	342	1	AA325293 AA325293 EST28508
	616	7	4.7	342	4	AK220091 AK220091 Mus muscu
c	617	7	4.7	342	7	CN934219 CN934219 000202AVB
	618	7	4.7	343	9	AZ511048 AZ511048 1M0355I22
c	619	7	4.7	344	2	BE098392 BE098392 UI-R-BJ1-
	620	7	4.7	344	9	AZ924135 AZ924135 4906.ic27
c	621	7	4.7	344	9	CC172780 CC172780 ZMMBBc029
c	622	7	4.7	345	6	CD186668 CD186668 MS1-0055G
c	623	7	4.7	345	6	CD308720 CD308720 StrPu691.
c	624	7	4.7	345	8	R74670 R74670 MDB0819 Mou
	625	7	4.7	346	2	BF087808 BF087808 IL3-HT061
c	626	7	4.7	346	3	BM797613 BM797613 K-EST0080
	627	7	4.7	346	8	W31965 W31965 zb95e03.r1
	628	7	4.7	346	9	B33768 B33768 HS-1023-A2-
	629	7	4.7	346	10	CG701771 CG701771 ZMMBBc017
c	630	7	4.7	346	11	DR36D21S AL982737 Danio rer
c	631	7	4.7	347	1	AA338423 AA338423 EST43346
	632	7	4.7	347	2	BF472113 BF472113 UI-M-BH3-
	633	7	4.7	347	7	CN700836 CN700836 E0441D10-
	634	7	4.7	347	8	W45903 W45903 mc78f11.r1
	635	7	4.7	348	2	BF935235 BF935235 CM1-NT024
	636	7	4.7	348	7	CO722667 CO722667 Mdfr3018k
c	637	7	4.7	348	10	BX197091 BX197091 Danio rer
c	638	7	4.7	349	6	CB539156 CB539156 PVEPLE100
c	639	7	4.7	350	1	AA144129 AA144129 mq53d09.r
	640	7	4.7	350	2	BF943879 BF943879 CM2-NN020
c	641	7	4.7	350	2	BE150287 BE150287 QV4-HT026
c	642	7	4.7	350	5	BW635649 BW635649 BW635649
	643	7	4.7	351	3	BQ361465 BQ361465 PM4-OT022
	644	7	4.7	351	8	T47657 T47657 yb16b11.r1
	645	7	4.7	352	1	AA859762 AA859762 UI-R-E0-b
	646	7	4.7	352	2	BF659108 BF659108 maa11b12.
c	647	7	4.7	352	7	CO293904 CO293904 EK205060.
c	648	7	4.7	352	10	CL936103 CL936103 OA_ABa004
	649	7	4.7	353	1	AI059197 AI059197 UI-R-C1-1
c	650	7	4.7	353	6	CD121604 CD121604 ME1-0068P
	651	7	4.7	353	6	CF334488 CF334488 JMT--03-M
	652	7	4.7	353	7	CR541615 CR541615 DKFZp459O
	653	7	4.7	353	9	CE205392 CE205392 tigr-gss-
c	654	7	4.7	353	10	AG266017 AG266017 Homo sapi
c	655	7	4.7	354	1	AJ689383 AJ689383 AJ689383
c	656	7	4.7	354	10	CL907374 CL907374 OA_ABa000
	657	7	4.7	355	1	AA633601 AA633601 ae66a11.s
c	658	7	4.7	355	1	AW860296 AW860296 RC0-CT038
c	659	7	4.7	355	3	BM278120 BM278120 As_tgz_53
	660	7	4.7	355	8	W86362 W86362 zh54f08.r1
c	661	7	4.7	355	10	CW599467 CW599467 OA_ABa013
	662	7	4.7	356	1	AA351624 AA351624 EST59419
c	663	7	4.7	356	6	CA370660 CA370660 650898 NC
	664	7	4.7	356	8	DR029125 DR029125 bda010071

	665	7	4.7	357	6	CD612231 CD612231 56052694H
c	666	7	4.7	357	10	CW603142 CW603142 OA_ABa014
	667	7	4.7	358	1	AA448373 AA448373 zw96d02.r
	668	7	4.7	360	1	AA449580 AA449580 zx06e08.r
c	669	7	4.7	360	2	BI173262 BI173262 RE16048.5
c	670	7	4.7	360	5	C48673 C48673 C48673 Yuji
c	671	7	4.7	360	5	C49996 C49996 C49996 Yuji
	672	7	4.7	360	5	C61689 C61689 C61689 Yuji
	673	7	4.7	360	8	D35698 D35698 CELK024D2F
c	674	7	4.7	361	8	D33101 D33101 CELK026CXR
	675	7	4.7	361	8	R91083 R91083 yp93a11.s1
	676	7	4.7	361	8	W10814 W10814 ma54g04.r1
	677	7	4.7	361	9	AQ099010 AQ099010 HS_3046_A
	678	7	4.7	362	1	AV191049 AV191049 AV191049
c	679	7	4.7	362	2	BF844913 BF844913 RC4-HT097
	680	7	4.7	362	3	BP098634 BP098634 BP098634
c	681	7	4.7	363	1	AA110632 AA110632 mp52b02.r
	682	7	4.7	363	8	R14300 R14300 yf80c04.r1
	683	7	4.7	364	7	CO290906 CO290906 EK075529.
c	684	7	4.7	364	7	CO721627 CO721627 TgESTzyq1
	685	7	4.7	365	1	AA726896 AA726896 vu36f06.r
	686	7	4.7	365	2	BF850703 BF850703 CM0-EN004
c	687	7	4.7	365	10	AG260484 AG260484 Lotus cor
c	688	7	4.7	366	9	BH361473 BH361473 CH230-164
c	689	7	4.7	366	10	CL324452 CL324452 RPCI44_47
	690	7	4.7	367	1	AA544465 AA544465 vk33g09.r
	691	7	4.7	367	3	BP429194 BP429194 BP429194
	692	7	4.7	367	9	AZ808965 AZ808965 2M0072E14
c	693	7	4.7	368	3	BP062893 BP062893 BP062893
c	694	7	4.7	368	8	DN317915 DN317915 LIB3171-0
	695	7	4.7	368	8	DN910520 DN910520 Cuc5_4_H0
	696	7	4.7	368	8	DR178440 DR178440 RTMNUT1_1
c	697	7	4.7	369	6	CD165451 CD165451 ML1-0096P
	698	7	4.7	369	8	D78934 D78934 HUM527D08B
c	699	7	4.7	370	1	AL813184 AL813184 AL813184
c	700	7	4.7	370	2	BF738024 BF738024 CM2-KT003
c	701	7	4.7	370	2	BF869438 BF869438 QV0-ET014
c	702	7	4.7	370	3	BM378883 BM378883 MEST570-B
	703	7	4.7	370	3	BM845190 BM845190 K-EST0123
	704	7	4.7	370	6	CA389130 CA389130 cs05h03.y
c	705	7	4.7	370	6	CA855281 CA855281 PfESToac3
	706	7	4.7	370	9	BH391371 BH391371 AG-ND-135
	707	7	4.7	371	5	BY608619 BY608619 BY608619
	708	7	4.7	371	9	AZ559339 AZ559339 RPCI-23-2
c	709	7	4.7	372	6	CB931026 CB931026 ri67d08.y
c	710	7	4.7	373	2	BG132154 BG132154 EST465046
c	711	7	4.7	373	7	CO344622 CO344622 EP19623.3
	712	7	4.7	374	3	BJ088089 BJ088089 BJ088089
	713	7	4.7	375	2	BI011354 BI011354 QV2-EN009
	714	7	4.7	375	3	BQ329286 BQ329286 CM0-EN004
c	715	7	4.7	375	5	C64288 C64288 C64288 Yuji
c	716	7	4.7	375	8	DR011984 DR011984 HEAT1_9_F
c	717	7	4.7	376	1	AA956404 AA956404 UI-R-E1-f
c	718	7	4.7	376	1	AW860305 AW860305 RC0-CT038
	719	7	4.7	376	3	BP656882 BP656882 BP656882
c	720	7	4.7	376	5	BY299565 BY299565 BY299565
c	721	7	4.7	376	5	C11999 C11999 C11999 Yuji
	722	7	4.7	376	5	C49304 C49304 C49304 Yuji
	723	7	4.7	376	10	CL453284 CL453284 ZMMBBb048
c	724	7	4.7	377	1	AV186271 AV186271 AV186271
	725	7	4.7	377	5	BW575617 BW575617 BW575617
	726	7	4.7	377	9	AQ239951 AQ239951 CIT-HSP-2
	727	7	4.7	377	9	BH297482 BH297482 CH230-45E
	728	7	4.7	378	1	AI045602 AI045602 UI-R-C1-k
c	729	7	4.7	378	2	BF823058 BF823058 MR1-RT003
c	730	7	4.7	378	5	BU022093 BU022093 QHE5O01.y
c	731	7	4.7	378	5	C70551 C70551 C70551 Yuji
	732	7	4.7	379	1	AI858542 AI858542 wl64b01.x
c	733	7	4.7	379	1	AW374691 AW374691 MR1-CT005
c	734	7	4.7	379	3	BM936574 BM936574 UI-M-CG0p
	735	7	4.7	379	3	BP098262 BP098262 BP098262
c	736	7	4.7	379	11	CR219944 CR219944 Forward s
c	737	7	4.7	380	1	AA339748 AA339748 EST44863
	738	7	4.7	380	2	BF386949 BF386949 UI-R-CA1-
c	739	7	4.7	380	3	BI483853 BI483853 RE66808.5
c	740	7	4.7	380	10	CL402069 CL402069 ZMMBBb041
	741	7	4.7	381	3	BP094959 BP094959 BP094959
	742	7	4.7	381	3	BP825644 BP825644 BP825644
	743	7	4.7	381	6	CF561376 CF561376 1115064H0
	744	7	4.7	381	6	CF567381 CF567381 1115116A0
c	745	7	4.7	381	6	CF567817 CF567817 1115120A0
c	746	7	4.7	381	8	DN378750 DN378750 LIB38533_
	747	7	4.7	382	2	BB739720 BB739720 BB739720
c	748	7	4.7	382	2	BE089396 BE089396 QV0-BT070
	749	7	4.7	383	1	AA244076 AA244076 nc04f09.r
c	750	7	4.7	383	1	AW374724 AW374724 MR1-CT005
	751	7	4.7	383	3	BJ078235 BJ078235 BJ078235
	752	7	4.7	383	3	BP825265 BP825265 BP825265
	753	7	4.7	383	7	CK626259 CK626259 mj19h06.y
	754	7	4.7	383	7	CN254924 CN254924 BIP1203 B
c	755	7	4.7	383	10	CW603188 CW603188 OA_ABa014
	756	7	4.7	384	2	BF573951 BF573951 602131969
	757	7	4.7	384	6	CB703079 CB703079 AMGNNUC:N
	758	7	4.7	385	1	AA683276 AA683276 ae92c01.s
	759	7	4.7	385	3	BM510722 BM510722 ij49h09.x
c	760	7	4.7	385	9	AQ125148 AQ125148 HS_2163_B
c	761	7	4.7	386	5	BQ637572 BQ637572 hel1h02.y
c	762	7	4.7	386	5	BU005838 BU005838 QGG9D17.y
	763	7	4.7	387	1	AA073209 AA073209 mm93a04.r
	764	7	4.7	387	1	AV627256 AV627256 AV627256
	765	7	4.7	387	3	BQ328939 BQ328939 CM0-EN004
	766	7	4.7	388	1	AI411833 AI411833 EST240127
c	767	7	4.7	388	2	BI005686 BI005686 RC4-HN017
	768	7	4.7	389	1	AA007867 AA007867 mg64a03.r
	769	7	4.7	389	1	AI045832 AI045832 UI-R-C0-j
c	770	7	4.7	389	10	CW612063 CW612063 OA_ABa015
c	771	7	4.7	390	2	BG005810 BG005810 PM4-GN023
c	772	7	4.7	391	1	AA120928 AA120928 zn85g11.r
c	773	7	4.7	391	3	BP822118 BP822118 BP822118
	774	7	4.7	391	6	CB095471 CB095471 ie89h05.b
	775	7	4.7	391	7	CR751997 CR751997 DKFZp469L
c	776	7	4.7	392	1	AA174286 AA174286 ms68b01.r
	777	7	4.7	392	1	AV631727 AV631727 AV631727
c	778	7	4.7	392	3	BP063669 BP063669 BP063669
	779	7	4.7	392	7	CR459674 CR459674 CR459674
c	780	7	4.7	392	9	CC844159 CC844159 NDL.82K21
c	781	7	4.7	393	1	AW158340 AW158340 za40a11.x
	782	7	4.7	393	6	CB777372 CB777372 AMGNNUC:N
c	783	7	4.7	393	10	CW601392 CW601392 OA_ABa013
c	784	7	4.7	394	3	BP821980 BP821980 BP821980
c	785	7	4.7	394	5	BY369069 BY369069 BY369069
	786	7	4.7	394	5	C17118 C17118 C17118 Clon
	787	7	4.7	395	1	AA683017 AA683017 ae81c02.s
c	788	7	4.7	395	3	BJ066156 BJ066156 BJ066156
	789	7	4.7	395	5	BY658214 BY658214 BY658214
c	790	7	4.7	395	6	CD527092 CD527092 08D2 Pig
	791	7	4.7	395	10	CG405266 CG405266 ZMMBBb025
c	792	7	4.7	395	10	CL426132 CL426132 ZMMBBb044
c	793	7	4.7	396	6	CD527093 CD527093 08D3 Pig
	794	7	4.7	396	6	CD527094 CD527094 08D4 Pig
	795	7	4.7	397	2	BF500404 BF500404 AT15280.5
	796	7	4.7	397	6	CB304348 CB304348 wsc0012_I
	797	7	4.7	397	7	CO839917 CO839917 LM_GL5_00
	798	7	4.7	397	8	R51724 R51724 yg77h07.r1
c	799	7	4.7	397	10	CE676362 CE676362 tigr-gss-
	800	7	4.7	398	7	CN411280 CN411280 170004252
c	801	7	4.7	398	8	R80070 R80070 yi91h08.r1
	802	7	4.7	399	1	AV724731 AV724731 AV724731
c	803	7	4.7	399	5	BY189447 BY189447 BY189447
	804	7	4.7	399	5	BY378525 BY378525 BY378525
	805	7	4.7	399	5	BY378770 BY378770 BY378770
c	806	7	4.7	400	6	CB699613 CB699613 AMGNNUC:S
c	807	7	4.7	401	5	BY575085 BY575085 BY575085
c	808	7	4.7	401	6	CA232918 CA232918 SCRUFL306
c	809	7	4.7	401	8	D54696 D54696 HUM149E09B
	810	7	4.7	402	1	AI750429 AI750429 cn02h06.x

	811	7	4.7	402	1	AV630681	AV630681 AV630681
	812	7	4.7	402	9	AZ071576	AZ071576 RPCI-23-4
c	813	7	4.7	402	9	AQ638290	AQ638290 927P1-14F
c	814	7	4.7	403	2	BF822526	BF822526 CM2-RT000
	815	7	4.7	403	2	BB837733	BB837733 BB837733
	816	7	4.7	404	1	AV393577	AV393577 AV393577
c	817	7	4.7	405	1	AW056773	AW056773 ST55F08 P
c	818	7	4.7	405	3	BP855849	BP855849 BP855849
	819	7	4.7	405	7	CN552805	CN552805 tae43h05.
	820	7	4.7	406	1	AI249938	AI249938 qx47a02.x
c	821	7	4.7	406	1	AU101415	AU101415 AU101415
	822	7	4.7	406	2	BF126647	BF126647 601650923
	823	7	4.7	406	9	BH468205	BOHHM70TF
c	824	7	4.7	407	1	AW604991	AW604991 RC0-CT038
	825	7	4.7	407	2	BE720499	BE720499 QV4-HT089
	826	7	4.7	407	3	BM743678	BM743678 K-EST0016
c	827	7	4.7	407	5	BY392572	BY392572 BY392572
c	828	7	4.7	407	6	CD849544	CD849544 DH0AC021Z
c	829	7	4.7	407	10	CZ611312	CZ611312 OM_Ba013
c	830	7	4.7	408	6	CF561375	CF561375 1115064H0
	831	7	4.7	408	10	AL944868	AL944868 Arabidops
	832	7	4.7	409	2	BG515577	BG515577 dae01e06.
	833	7	4.7	409	3	BP809132	BP809132 BP809132
	834	7	4.7	409	3	BQ359573	BQ359573 MR3-HN006
c	835	7	4.7	409	6	CB804325	CB804325 AMGNNUC:N
c	836	7	4.7	409	6	CB805097	CB805097 AMGNNUC:S
	837	7	4.7	410	1	AI709889	AI709889 UI-R-AD1-
c	838	7	4.7	410	2	BF395411	BF395411 UI-R-CM0-
c	839	7	4.7	410	2	BG999953	BG999953 MR3-HN006
	840	7	4.7	410	6	CB803453	CB803453 AMGNNUC:S
	841	7	4.7	410	7	CJ329477	CJ329477 CJ329477
c	842	7	4.7	410	7	CV232098	CV232098 WS0196.B2
	843	7	4.7	410	8	W82217	W82217 me99h02.r1
	844	7	4.7	411	1	AV629918	AV629918 AV629918
c	845	7	4.7	411	3	BP067275	BP067275 BP067275
	846	7	4.7	411	5	BY523249	BY523249 BY523249
	847	7	4.7	411	9	CC411931	CC411931 PUHCX75TD
c	848	7	4.7	412	3	BP052366	BP052366 BP052366
	849	7	4.7	412	6	CA118506	CA118506 SCBGLR109
c	850	7	4.7	412	6	CD132052	CD132052 MG1-0016G
c	851	7	4.7	412	10	BX999985	BX999985 Forward s
	852	7	4.7	413	2	BI000408	BI000408 MR3-HN006
	853	7	4.7	413	3	BP093011	BP093011 BP093011
c	854	7	4.7	413	8	CX598203	CX598203 CT020020A
c	855	7	4.7	413	9	BH791677	BH791677 SALK_0608
	856	7	4.7	414	1	AA715113	AA715113 nx94h06.s
c	857	7	4.7	414	1	AW136178	AW136178 UI-H-BI1-
c	858	7	4.7	414	1	AW848886	AW848886 IL3-CT021
c	859	7	4.7	414	2	BF422277	BF422277 FM1_13_E0
c	860	7	4.7	414	2	BF825270	BF825270 CM1-HN001
	861	7	4.7	414	2	BG999961	BG999961 MR3-HN006
	862	7	4.7	414	2	BI000662	BI000662 MR3-HN006
c	863	7	4.7	414	2	BB759257	BB759257 BB759257
	864	7	4.7	414	5	BY022828	BY022828 BY022828
c	865	7	4.7	415	1	AA961194	AA961194 oo52e05.s
	866	7	4.7	415	3	BM763595	BM763595 K-EST0044
	867	7	4.7	415	6	CD122462	CD122462 ME1-0074G
	868	7	4.7	415	6	CD612884	CD612884 55114296J
	869	7	4.7	415	6	CD612885	CD612885 55114388H
c	870	7	4.7	415	9	AQ824302	AQ824302 HS_3249_B
	871	7	4.7	416	6	CA951857	CA951857 in80g08.y
c	872	7	4.7	416	6	CD612883	CD612883 55114296H
c	873	7	4.7	416	6	CD612886	CD612886 55114388J
c	874	7	4.7	416	7	CN819334	CN819334 HRO4452_G
c	875	7	4.7	416	8	D55009	D55009 HUM161H04B
	876	7	4.7	416	8	H35135	H35135 EST106351 R
	877	7	4.7	416	9	AQ110446	AQ110446 CIT-HSP-2
c	878	7	4.7	416	10	CW546120	CW546120 OA_ABa006
	879	7	4.7	417	1	AA106115	AA106115 mm18f01.r
c	880	7	4.7	417	1	AV124667	AV124667 AV124667
	881	7	4.7	417	1	AV629722	AV629722 AV629722
	882	7	4.7	417	2	BF945422	BF945422 MR0-NN019
	883	7	4.7	417	3	BI903140	BI903140 id22d08.y
	884	7	4.7	417	6	CB767110	CB767110 AMGNNUC:N
	885	7	4.7	417	7	CR766244	CR766244 DKFZp459H
c	886	7	4.7	418	3	BI447708	BI447708 dah91a05.
	887	7	4.7	418	5	BW891410	BW891410 BW891410
c	888	7	4.7	418	6	CB374276	CB374276 rq01c06.y
c	889	7	4.7	419	2	BF547014	BF547014 UI-R-C1-k
c	890	7	4.7	419	2	BG037589	BG037589 dc53c01.y
c	891	7	4.7	419	8	D54574	D54574 HUM144F01B
	892	7	4.7	419	10	CZ641887	CZ641887 OM_Ba018
	893	7	4.7	420	1	AI029483	AI029483 UI-R-C0-i
c	894	7	4.7	420	1	AI442302	AI442302 sa66c07.y
	895	7	4.7	420	3	BM327264	BM327264 PIC1_11_C
c	896	7	4.7	420	5	BY679343	BY679343 BY679343
	897	7	4.7	420	6	CD121530	CD121530 ME1-0068P
c	898	7	4.7	420	6	CD121590	CD121590 ME1-0068P
c	899	7	4.7	420	6	CF186048	CF186048 j4b07j2.r
	900	7	4.7	420	7	CO286135	CO286135 EK061853.
c	901	7	4.7	420	11	DR11P10S	AL746171 Danio rer
	902	7	4.7	421	5	BQ417501	BQ417501 ik38g08.y
	903	7	4.7	421	6	CD068446	CD068446 MA2-0001U
c	904	7	4.7	421	7	CO170073	CO170073 NDL1_11_B
c	905	7	4.7	422	1	AI267167	AI267167 aq49g10.x
	906	7	4.7	422	2	BE257834	BE257834 601109418
	907	7	4.7	422	3	BM327273	BM327273 PIC1_11_D
	908	7	4.7	422	8	CX012511	CX012511 io59h03.g
c	909	7	4.7	422	9	BH362040	BH362040 CH230-203
	910	7	4.7	423	2	BG505174	BG505174 602551639
c	911	7	4.7	423	7	CV422585	CV422585 RC4-NN026
	912	7	4.7	423	10	CW657390	CW657390 OG_BBa000
	913	7	4.7	423	11	CR022856	CR022856 Forward s
c	914	7	4.7	424	1	AA364259	AA364259 EST74830
	915	7	4.7	424	2	BF829609	BF829609 MR3-HN006
	916	7	4.7	424	3	BI815831	BI815831 PfESToaa3
	917	7	4.7	424	5	BY429713	BY429713 BY429713
c	918	7	4.7	424	7	CO424830	CO424830 UI-M-HU0-
	919	7	4.7	424	8	W08338	W08338 mb41b07.r1
c	920	7	4.7	424	10	CL340405	CL340405 RPCI44_25
c	921	7	4.7	425	2	BF325439	BF325439 su21g06.y
	922	7	4.7	425	2	BI000463	BI000463 MR3-HN006
	923	7	4.7	425	6	CD121440	CD121440 ME1-0068G
	924	7	4.7	425	6	CF186588	CF186588 j4o18j2.f
c	925	7	4.7	425	9	AQ908506	AQ908506 GSSTc0546
	926	7	4.7	426	2	BF829646	BF829646 MR3-HN006
	927	7	4.7	426	2	BI069150	BI069150 C033P01U
	928	7	4.7	426	3	BQ329087	BQ329087 CM0-EN004
	929	7	4.7	426	5	CA033466	CA033466 pw24a01.y
c	930	7	4.7	426	10	AG975616	AG975616 Drosophil
	931	7	4.7	426	10	AL944884	AL944884 Arabidops
	932	7	4.7	427	2	BF634089	BF634089 NF086C07D
	933	7	4.7	427	2	BF829605	BF829605 MR3-HN006
	934	7	4.7	427	3	BM830778	BM830778 K-EST0104
c	935	7	4.7	427	6	CB795265	CB795265 AMGNNUC:N
	936	7	4.7	427	7	CO231441	CO231441 WS0051.B2
	937	7	4.7	427	7	CO609805	CO609805 DG8-88m6
	938	7	4.7	427	9	BH240791	BH240791 ATXQD56TR
c	939	7	4.7	427	10	CW586560	CW586560 OA_ABa011
	940	7	4.7	428	2	BF829634	BF829634 MR3-HN006
	941	7	4.7	428	2	BI000658	BI000658 MR3-HN006
c	942	7	4.7	428	3	BM821667	BM821667 K-EST0090
c	943	7	4.7	428	5	BY479361	BY479361 BY479361
	944	7	4.7	428	6	CB078491	CB078491 hj68d05.g
	945	7	4.7	428	7	CV322979	CV322979 CM3-RT000
	946	7	4.7	429	1	AI104407	AI104407 EST213696
	947	7	4.7	429	1	AT007326	AT007326 AT007326
c	948	7	4.7	429	2	BG633297	BG633297 GH23816.3
	949	7	4.7	429	2	BI000576	BI000576 MR3-HN006
c	950	7	4.7	429	2	BF021576	BF021576 uy49c02.y
	951	7	4.7	429	3	BQ083541	BQ083541 K-EST0146
	952	7	4.7	429	3	BQ329287	BQ329287 CM0-EN004
	953	7	4.7	429	10	CL902226	CL902226 CSHC1601
	954	7	4.7	430	1	AV591194	AV591194 AV591194
c	955	7	4.7	430	1	AW894959	AW894959 CM1-NN003
c	956	7	4.7	430	1	AA553110	AA553110 vj50h09.r

957	7	4.7	430	6	CD347634	CD347634 AP172 And
c 958	7	4.7	430	6	CD348245	CD348245 UI-M-FY0-
c 959	7	4.7	430	7	CN352676	CN352676 170004245
960	7	4.7	431	3	BM386446	BM386446 UI-R-CN1-
c 961	7	4.7	431	5	BQ521025	BQ521025 NISC_n108
c 962	7	4.7	431	9	CE009431	CE009431 tigr-gss-
c 963	7	4.7	431	10	CW602536	CW602536 OA_ABa014
964	7	4.7	431	10	CE405627	CE405627 tigr-gss-
965	7	4.7	432	1	AV630317	AV630317 AV630317
966	7	4.7	432	5	BX926222	BX926222 BX926222
967	7	4.7	432	10	CW619077	CW619077 OA_ABa016
c 968	7	4.7	432	11	TA250G10Q	AL482872 T. brucei
969	7	4.7	433	1	AV627370	AV627370 AV627370
970	7	4.7	433	2	BF829606	BF829606 MR3-HN006
971	7	4.7	433	2	BF830239	BF830239 MR3-HN006
972	7	4.7	433	2	BE295592	BE295592 601176552
c 973	7	4.7	433	5	BY694201	BY694201
c 974	7	4.7	433	6	CD132098	CD132098 MG1-0016P
c 975	7	4.7	433	7	CO169999	CO169999 NDL1_11_B
976	7	4.7	433	7	CV399798	CV399798 QV4-GN014
977	7	4.7	433	7	CV399802	CV399802 QV4-GN014
c 978	7	4.7	433	9	AQ998369	AQ998369 RPCI-23-3
979	7	4.7	434	1	AI579101	AI579101 UI-R-AG0-
980	7	4.7	434	3	BQ023514	BQ023514 UI-1-BB0-
c 981	7	4.7	434	6	CB793737	CB793737 AMGNNUC:N
c 982	7	4.7	434	6	CD610616	CD610616 56044779J
983	7	4.7	434	9	AZ896888	AZ896888 RPCI-24-1
984	7	4.7	434	10	CL312700	CL312700 mth2-126J
c 985	7	4.7	435	5	BQ639784	BQ639784 he20d02.y
986	7	4.7	435	7	CK241965	CK241965 rx03g05.y
987	7	4.7	435	10	CW174211	CW174211 104_586_1
c 988	7	4.7	435	10	AG259358	AG259358 Lotus cor
989	7	4.7	436	6	CD610615	CD610615 56044779H
c 990	7	4.7	436	9	BH335461	BH335461 CH230-5E2
991	7	4.7	436	9	AQ673569	AQ673569 HS_5491_A
992	7	4.7	437	1	AV630216	AV630216 AV630216
993	7	4.7	437	2	BI277938	BI277938 UI-R-CY0-
994	7	4.7	437	2	BB826554	BB826554 BB826554
995	7	4.7	437	8	N61518	N61518 TgESTzy08h0
996	7	4.7	438	2	BE954283	BE954283 UI-M-CE1-
997	7	4.7	438	5	BX552028	BX552028 BX552028
998	7	4.7	438	7	CN548967	CN548967 EST 16606
c 999	7	4.7	438	7	CO176626	CO176626 NDL1_63_E
1000	7	4.7	438	8	DR843348	DR843348 JGI_CABE9

ALIGNMENTS

RESULT 1
CA838401
LOCUS CA838401 644 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT016B04_166733 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT016B04 5, mRNA sequence.
ACCESSION CA838401
VERSION CA838401.1 GI:26566166
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 644)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 016 row: B column: 04
Seq primer: T3 20mer
High quality sequence stop: 644.
FEATURES Location/Qualifiers
source 1. .644
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT016B04"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:

Pred. No.:	1.88	Length:	644
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	6.7%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-9 (1-149) x CA838401 (1-644)

```
Qy         63 AlaIleAspValThrAspValTyrValVal 72
              ||||||||||||||||||||||||||||||
Db        394 GCAATCGACGTGACAGACGTCTACGTCGTC 423
```

RESULT 2
CA838446
LOCUS CA838446 667 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT016F04_166823 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT016F04 5, mRNA sequence.
ACCESSION CA838446
VERSION CA838446.1 GI:26566211
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 667)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 016 row: F column: 04
Seq primer: T3 20mer
High quality sequence stop: 667.
FEATURES Location/Qualifiers

```
     source          1. .667
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCT016F04"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase IV (5:30 PM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.:              1.94          Length:        667
Score:                  10.00         Matches:       10
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            6.7%          Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-9 (1-149) x CA838446 (1-667)

Qy         63 AlaIleAspValThrAspValTyrValVal 72
              ||||||||||||||||||||||||||||||
Db        392 GCAATCGACGTGACAGACGTCTACGTCGTC 421

RESULT 3
AW053585
LOCUS       AW053585                672 bp    mRNA    linear   EST 20-FEB-2001
DEFINITION  L30-2143T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours
            NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-2143
            5', mRNA sequence.
ACCESSION   AW053585
VERSION     AW053585.1  GI:5916778
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T7
            BACKWARD: T3
            Plate: L30-22  row: D  column: 11
            Seq primer: T3
            High quality sequence stop: 450.
FEATURES             Location/Qualifiers
     source          1. .672
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="L30-2143"
                     /tissue_type="Leaf, 30 h 0.4M NaCl"
                     /dev_stage="Six week old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 30 hours NaCl treatment"
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.:              1.95          Length:        672
Score:                  10.00         Matches:       10
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            6.7%          Indels:        0
DB:                     1             Gaps:          0

US-10-758-902-9 (1-149) x AW053585 (1-672)

Qy         63 AlaIleAspValThrAspValTyrValVal 72
              ||||||||||||||||||||||||||||||
Db        388 GCAATCGACGTGACAGACGTCTACGTCGTC 417

RESULT 4
CA840373
LOCUS       CA840373                678 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  MCT036G03_173841 Ice plant Lambda Uni-Zap XR expression library, 5
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
            (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT036G03 5,
            mRNA sequence.
ACCESSION   CA840373
VERSION     CA840373.1  GI:26568138
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 036  row: G  column: 03
            Seq primer: T3 20mer
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
     source          1. .678
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCT036G03"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase IV (5:30 PM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.:              1.96          Length:        678
Score:                  10.00         Matches:       10
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            6.7%          Indels:        0
```

```
DB:                 6             Gaps:          0

US-10-758-902-9 (1-149) x CA840373 (1-678)

Qy         63 AlaIleAspValThrAspValTyrValVal 72
              ||||||||||||||||||||||||||||||
Db        394 GCAATCGACGTGACAGACGTCTACGTCGTC 423

RESULT 5
CA838926
LOCUS       CA838926                 698 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  MCT021H09_170947 Ice plant Lambda Uni-Zap XR expression library, 5
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
            (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT021H09 5,
            mRNA sequence.
ACCESSION   CA838926
VERSION     CA838926.1  GI:26566691
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 021  row: H  column: 09
            Seq primer: T3 20mer
            High quality sequence stop: 698.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCT021H09"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase IV (5:30 PM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

Alignment Scores:
Pred. No.:              2.01          Length:        698
Score:                  10.00         Matches:       10
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            6.7%          Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-9 (1-149) x CA838926 (1-698)

Qy         63 AlaIleAspValThrAspValTyrValVal 72
              ||||||||||||||||||||||||||||||
Db        389 GCAATCGACGTGACAGACGTCTACGTCGTC 418

RESULT 6
BY768107
LOCUS       BY768107                 362 bp    mRNA    linear   EST 22-MAR-2004
DEFINITION  BY768107 RIKEN full-length enriched, 17.5 days embryo whole body
            Mus musculus cDNA clone L930018L23 5', mRNA sequence.
ACCESSION   BY768107
VERSION     BY768107.1  GI:39693098
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 362)
  AUTHORS   Carninci,P., Waki,K., Shiraki,T., Konno,H., Shibata,K., Itoh,M.,
            Aizawa,K., Arakawa,T., Ishii,Y., Sasaki,D., Bono,H., Kondo,S.,
            Sugahara,Y., Saito,R., Osato,N., Fukuda,S., Sato,K., Watahiki,A.,
            Hirozane-Kishikawa,T., Nakamura,M., Shibata,Y., Yasunishi,A.,
            Kikuchi,N., Yoshiki,A., Kusakabe,M., Gustincich,S., Beisel,K.,
            Pavan,W., Aidinis,V., Nakagawara,A., Held,W.A., Iwata,H., Kono,T.,
            Nakauchi,H., Lyons,P., Wells,C., Hume,D.A., Fagiolini,M.,
            Hensch,T.K., Brinkmeier,M., Camper,S., Hirota,J., Mombaerts,P.,
            Muramatsu,M., Okazaki,Y., Kawai,J. and Hayashizaki,Y.
  TITLE     Targeting a complex transcriptome: the construction of the mouse
            full-length cDNA encyclopedia
  JOURNAL   Genome Res. 13 (6B), 1273-1289 (2003)
  PUBMED    12819125
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.jp/) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .362
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="L930018L23"
                     /tissue_type="whole body"
                     /dev_stage="17.5 days embryo"
                     /clone_lib="RIKEN full-length enriched, 17.5 days embryo
                     whole body"
ORIGIN

Alignment Scores:
Pred. No.:              15.3          Length:        362
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            6.0%          Indels:        0
DB:                     5             Gaps:          0

US-10-758-902-9 (1-149) x BY768107 (1-362)

Qy         49 LeuValAspIleThrThrThrSerLys 57
              |||||||||||||||||||||||||||
Db        305 CTTGTGGACATCACCACCACCTCGAAA 331

RESULT 7
AY067954/c
LOCUS       AY067954                 371 bp    mRNA    linear   HTC 07-NOV-2002
DEFINITION  Schmidtea mediterranea clone H.39.7f(T3) unknown mRNA sequence.
ACCESSION   AY067954
```

```
VERSION     AY067954.1  GI:21308587
KEYWORDS    HTC.
SOURCE      Schmidtea mediterranea
  ORGANISM  Schmidtea mediterranea
            Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata;
            Tricladida; Paludicola; Dugesiidae; Schmidtea.
REFERENCE   1  (bases 1 to 371)
  AUTHORS   Alvarado,A.S., Newmark,P.A., Robb,S.M.C. and Juste,R.B.
  TITLE     The Schmidtea mediterranea database as a molecular resource for
            studying platyhelminthes, stem cells and regeneration
  JOURNAL   Development 129 (24), 5659-5665 (2002)
   PUBMED   12421706
REFERENCE   2  (bases 1 to 371)
  AUTHORS   Alvarado,A.S., Newmark,P.A., Juste,R.B. and Robb,S.M.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-DEC-2001) Neurobiology & Anatomy, University of Utah
            School of Medicine, 50 North Medical Drive, Salt Lake City, UT
            84132, USA
COMMENT     Clone names suffixed with 'T3' were sequenced from their 5' ends.
            All other clones were obtained by sequencing from their 3' ends.
            More details and other relevant information can be found at
            http://planaria.neuro.utah.edu.
FEATURES             Location/Qualifiers
     source          1. .371
                     /organism="Schmidtea mediterranea"
                     /mol_type="mRNA"
                     /strain="CIW4"
                     /db_xref="taxon:79327"
                     /clone="H.39.7f(T3)"
     misc_feature    1. .371
                     /note="similar to (AE003628) CG4995 gene product
                     Drosophila melanogaster"
ORIGIN

Alignment Scores:
Pred. No.:              15.6          Length:         371
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            6.0%          Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-9 (1-149) x AY067954 (1-371)

Qy         55 ThrSerLysLysThrValLysValAla 63
              |||||||||||||||||||||||||||
Db        141 ACATCTAAAAAGACCGTAAAAGTGGCG 115

RESULT 8
CZ581766/c
LOCUS       CZ581766                 499 bp    DNA     linear   GSS 20-JUN-2005
DEFINITION  OA_BBa0180K02.f OA_BBa Oryza alta genomic clone OA_BBa0180K02 5',
            genomic survey sequence.
ACCESSION   CZ581766
VERSION     CZ581766.1  GI:68030594
KEYWORDS    GSS.
SOURCE      Oryza alta
  ORGANISM  Oryza alta
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wissotski,M., Yost,D.,
            Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
            Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
  TITLE     OMAP (Oryza Map Alignment Project)- Purdue University
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Scott A. Jackson
            Jackson Laboratory
            Purdue University
            915 W. State St., West Lafayette, IN 47907, USA
            Tel: 7654963621
            Fax: 7654967255
            Email: sjackson@purdue.edu
            Basecalling by phred version 0.020425.c. This sequence was derived
            from the raw sequence read by clipping with lucy version 1.19s.
            Bases 23-521 of the raw sequence (length 1068) were retained after
            clipping.
            Plate: 0180  row: K  column: 02
            Seq primer: TAA TAC GAC TCA CTA TAG GG
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="Oryza alta"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:52545"
                     /clone="OA_BBa0180K02"
                     /tissue_type="young leaves"
                     /lab_host="DH10B-T1 phage resistant"
                     /clone_lib="OA_BBa"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Alignment Scores:
Pred. No.:              20.3          Length:         499
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            6.0%          Indels:         0
DB:                     10            Gaps:           0

US-10-758-902-9 (1-149) x CZ581766 (1-499)

Qy         34 LeuProValThrLeuGlnThrIleAla 42
              ||||||||||||||||||||||||||||
Db        440 TTACCTGTCACCCTCCAAACAATTGCC 414

RESULT 9
BZ494782/c
LOCUS       BZ494782                 602 bp    DNA     linear   GSS 16-DEC-2002
DEFINITION  BONOG63TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONOG63,
            genomic survey sequence.
ACCESSION   BZ494782
VERSION     BZ494782.1  GI:27005844
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
            Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea and its
            application to gene discovery and annotation in Arabidopsis
  JOURNAL   Genome Res. 15 (4), 487-495 (2005)
   PUBMED   15805490
COMMENT     Other_GSSs: BONOG63TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BONOG63"
                     /clone_lib="BO_1.6_2_KB_tot"
                     /note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
```

```
                    total DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

Alignment Scores:
Pred. No.:              23.9            Length:         602
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.0%            Indels:         0
DB:                     9               Gaps:           0

US-10-758-902-9 (1-149) x BZ494782 (1-602)

Qy         89 LysValProThrValAlaThrSerLys 97
              |||||||||||||||||||||||||||
Db         31 AAAGTTCCGACCGTGGCGACTTCGAAA 5

RESULT 10
BX849231/c
LOCUS       BX849231                720 bp    mRNA    linear   EST 11-DEC-2003
DEFINITION  BX849231 NICHD_XGC_OO1 Xenopus laevis cDNA clone IMAGp998M0614215 ;
            IMAGE:6637806 5', mRNA sequence.
ACCESSION   BX849231
VERSION     BX849231.1  GI:39738015
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Heil,O., Neubert,P., Peters,M., Radelof,U., Schneider,D.,
            Schroth,A., Korn,B. and Landgrebe,J.
  TITLE     Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998M0614215.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB
            No.998) http://www.rzpd.de/cgi-
            bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus
            laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
            bin/products/showLib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            SP6, 5' ATTTAGGTGACACTATAG 3'.
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGp998M0614215 ; IMAGE:6637806"
                     /tissue_type="oocytes"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_OO1"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.2 kb. Constructed by Life Technologies."
ORIGIN

Alignment Scores:
Pred. No.:              28              Length:         720
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.0%            Indels:         0
DB:                     5               Gaps:           0

US-10-758-902-9 (1-149) x BX849231 (1-720)

Qy         18 IleGlnAspLeuArgAsnGluLeuAla 26
              |||||||||||||||||||||||||||
Db        199 ATTCAGGATTTGAGAAATGAGTTGGCA 173

RESULT 11
CL170043
LOCUS       CL170043                740 bp    DNA     linear   GSS 06-JAN-2004
DEFINITION  104_370_10813488_116_31789_192 Sorghum methylation-filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10813488, genomic survey
            sequence.
ACCESSION   CL170043
VERSION     CL170043.1  GI:40682455
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 740)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 370  row: h  column: 24
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 740.
FEATURES             Location/Qualifiers
     source          1. .740
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10813488"
                     /clone_lib="Sorghum methylation-filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation-filtered library."
ORIGIN

Alignment Scores:
Pred. No.:              28.7            Length:         740
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.0%            Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-9 (1-149) x CL170043 (1-740)

Qy         35 ProValThrLeuGlnThrIleAlaAsp 43
              |||||||||||||||||||||||||||
Db        568 CCCGTCACCCTGCAGACGATCGCAGAT 594

RESULT 12
CW444509/c
```

```
LOCUS       CW444509                746 bp    DNA     linear   GSS 02-NOV-2004
DEFINITION  fsbb001f166c15f0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fsbb001f166c15, genomic survey
            sequence.
ACCESSION   CW444509
VERSION     CW444509.1  GI:55192470
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: fsbb001f166  row: c  column: 15
            Seq primer: f Forward
            Class: methylation filtered
            High quality sequence stop: 746.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="fsbb001f166c15"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:              28.9          Length:         746
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            6.0%          Indels:         0
DB:                     10            Gaps:           0

US-10-758-902-9 (1-149) x CW444509 (1-746)

Qy         35 ProValThrLeuGlnThrIleAlaAsp 43
              |||||||||||||||||||||||||||
Db        116 CCCGTCACCCTGCAGACGATCGCAGAT 90

RESULT 13
CW431584
LOCUS       CW431584                756 bp    DNA     linear   GSS 02-NOV-2004
DEFINITION  fsbb001f145n18f0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fsbb001f145n18, genomic survey
            sequence.
ACCESSION   CW431584
VERSION     CW431584.1  GI:55179545
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: fsbb001f145  row: n  column: 18
            Seq primer: f Forward
            Class: methylation filtered
            High quality sequence stop: 756.
FEATURES             Location/Qualifiers
     source          1. .756
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="fsbb001f145n18"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:              29.2          Length:         756
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            6.0%          Indels:         0
DB:                     10            Gaps:           0

US-10-758-902-9 (1-149) x CW431584 (1-756)

Qy         46 ArgPheValLeuValAspIleThrThr 54
              |||||||||||||||||||||||||||
Db         33 CGTTTTGTCCTAGTTGATATTACCACT 59

RESULT 14
BU911748/c
LOCUS       BU911748                909 bp    mRNA    linear   EST 17-OCT-2002
DEFINITION  AGENCOURT_10463950 NICHD_XGC_001 Xenopus laevis cDNA clone
            IMAGE:6637806 5', mRNA sequence.
ACCESSION   BU911748
VERSION     BU911748.1  GI:24093662
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 909)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
```

```
           Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM14215  row: m  column: 06
           High quality sequence start: 35
           High quality sequence stop: 669.
FEATURES             Location/Qualifiers
     source          1. .909
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:6637806"
                     /tissue_type="oocytes"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_OO1"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.2 kb. Constructed by Life Technologies."
ORIGIN

Alignment Scores:
Pred. No.:              34.3          Length:         909
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            6.0%          Indels:         0
DB:                     5             Gaps:           0

US-10-758-902-9 (1-149) x BU911748 (1-909)

Qy         18 IleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||||||||||||||
Db        213 ATTCAGGATTTGAGAAATGAGTTGGCA 187

RESULT 15
BU368460
LOCUS       BU368460                935 bp    mRNA    linear   EST 28-NOV-2002
DEFINITION  603789346F1 CSEQCHN72 Gallus gallus cDNA clone ChEST750k12 5', mRNA
           sequence.
ACCESSION   BU368460
VERSION     BU368460.1  GI:25876461
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
           Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
           Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
           Department of Biomolecular Sciences
           University of Manchester Institute of Science and Technology
           (UMIST)
           PO Box 88, Manchester, M60 1QD, UK
           Tel: 01612008930
           Fax: 01612360409
           Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Compton Line 15I"
                     /db_xref="taxon:9031"
                     /clone="ChEST750k12"
                     /sex="Female"
                     /tissue_type="cerebrum"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN72"
                     /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
                     EcoRI; Site_2: NotI; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN

Alignment Scores:
Pred. No.:              35.2          Length:         935
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            6.0%          Indels:         0
DB:                     5             Gaps:           0

US-10-758-902-9 (1-149) x BU368460 (1-935)

Qy         112 GlySerTyrGlnLysLeuValAsnAla 120
               |||||||||||||||||||||||||||
Db         745 GGCTCATATCAGAAGTTGGTTAATGCC 771

RESULT 16
CD965140/c
LOCUS       CD965140                70 bp    mRNA    linear   EST 16-JUL-2003
DEFINITION  SEH_234 GeneTag2 Zea mays cDNA, mRNA sequence.
ACCESSION   CD965140
VERSION     CD965140.1  GI:32825418
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
           Genoplante
           93, rue Henri Rochefort 91025 EVRY CEDEX France
           Tel: 33 1 69 47 54 00
           Fax: 33 1 69 47 54 10
           This sequence has been generated in the framework of the french
           plant genomics programme 'Genoplante' (http://www.genoplante.com
           and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="mixture"
                     /db_xref="taxon:4577"
                     /clone_lib="GeneTag2"
ORIGIN

Alignment Scores:
Pred. No.:              49            Length:         70
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
```

```
DB:                 6           Gaps:          0

US-10-758-902-9 (1-149) x CD965140 (1-70)

Qy         52 IleThrThrThrSerLysLysThr 59
              ||||||||||||||||||||||||
Db         63 ATTACTACAACAAGCAAGAAGACC 40

RESULT 17
BJ063727
LOCUS       BJ063727                 84 bp    mRNA    linear   EST 29-SEP-2003
DEFINITION  BJ063727 NIBB Mochii normalized Xenopus tailbud library Xenopus
            laevis cDNA clone XL077c15 5', mRNA sequence.
ACCESSION   BJ063727
VERSION     BJ063727.1  GI:17470887
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 84)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .84
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL077c15"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 25"
                     /clone_lib="NIBB Mochii normalized Xenopus tailbud
                     library"
ORIGIN

Alignment Scores:
Pred. No.:              57.5          Length:         84
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-9 (1-149) x BJ063727 (1-84)

Qy         60 ValLysValAlaIleAspValThr 67
              |||||||||||||||||||||||
Db         56 GTTAAGGTTGCCATAGACGTAACA 79

RESULT 18
BM417113/c
LOCUS       BM417113                103 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  952003H01.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
            mays cDNA, mRNA sequence.
ACCESSION   BM417113
VERSION     BM417113.1  GI:18383913
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 103)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 952003  row: H  column: 01.
FEATURES             Location/Qualifiers
     source          1. .103
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="BMS (Black Mexican Sweet)"
                     /db_xref="taxon:4577"
                     /tissue_type="suspension culture"
                     /dev_stage="mixed logarithmic and stationary growth
                     phases"
                     /lab_host="DH10B"
                     /clone_lib="952 - BMS tissue from Walbot Lab (reduced
                     rRNA)"
                     /note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The
                     library was prepared by George Rudenko using poly (A)
                     selected RNA and Universal Riboclone cDNA Synthesis System
                     (Promega). cDNA was synthesized using both random and
                     oligo(dT) primers in separate reactions and equipped with
                     EcoRI adaptors. Library was size-fractionated on agarose
                     gels (for insert size >400bp) and non-directionally cloned
                     into EcoRI-digested pUC19 vector. Blue/white selection on
                     carbenicillin-containing plates was used to recover
                     positive clones."
ORIGIN

Alignment Scores:
Pred. No.:              68.8          Length:         103
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-9 (1-149) x BM417113 (1-103)

Qy         83 ArgAlaValPheLeuAspLysVal 90
              |||||||||||||||||||||||
Db         41 CGCGCGGTATTCCTTGATAAGGTT 18

RESULT 19
BF748333/c
LOCUS       BF748333                161 bp    mRNA    linear   EST 10-JAN-2001
DEFINITION  CM3-BN0383-021000-389-g09 BN0383 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF748333
VERSION     BF748333.1  GI:12075009
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 161)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
```

```
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-BN0383-
            021000-389-g09&t3=2000-10-02&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 37
            High quality sequence stop: 161.
FEATURES             Location/Qualifiers
     source          1. .161
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="BN0383"
                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              102             Length:         161
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-9 (1-149) x BF748333 (1-161)

Qy         94 AlaThrSerLysLeuPheProGly 101
              ||||||||||||||||||||||||
Db        109 GCGACATCAAAACTGTTTCCTGGG 86

RESULT 20
BB141468/c
LOCUS       BB141468                 166 bp    mRNA    linear   EST 28-JUN-2000
DEFINITION  BB141468 RIKEN full-length enriched, adult female vagina Mus
            musculus cDNA clone 9930009M02 3', mRNA sequence.
ACCESSION   BB141468
VERSION     BB141468.1  GI:8796405
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 166)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .166
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="9930009M02"
                     /sex="female"
                     /tissue_type="vagina"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult female
                     vagina"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 185.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
ORIGIN

Alignment Scores:
Pred. No.:              105             Length:         166
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     1               Gaps:           0

US-10-758-902-9 (1-149) x BB141468 (1-166)

Qy         25 LeuAlaLysGlyThrProValCys 32
              ||||||||||||||||||||||||
Db         32 CTGGCCAAGGGCACACCCGTATGT 9

RESULT 21
```

```
AI784781/c
LOCUS       AI784781                210 bp    mRNA    linear   EST 02-JUL-1999
DEFINITION  SWAMCAC40E09SK Brugia malayi adult male cDNA (SAW94NL-BmAM) Brugia
            malayi cDNA clone SWAMCAC40E09 5', mRNA sequence.
ACCESSION   AI784781
VERSION     AI784781.1  GI:5332575
KEYWORDS    EST.
SOURCE      Brugia malayi
  ORGANISM  Brugia malayi
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Brugia.
REFERENCE   1  (bases 1 to 210)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in adult males of Brugia malayi
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .210
                     /organism="Brugia malayi"
                     /mol_type="mRNA"
                     /strain="TRS Labs"
                     /db_xref="taxon:6279"
                     /clone="SWAMCAC40E09"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Brugia malayi adult male cDNA (SAW94NL-BmAM)"
                     /note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2:
                     Xho I; Lymphatic filarial nematode parasite of humans.
                     mRNA was prepared from adult males of Brugia malayi
                     isolated from jirds and converted to double stranded cDNA
                     using reverse transcriptase and oligo(dT) followed by
                     RNase H and DNApol I. The library had 4.6 x 10E6
                     independent recombinants and average insert size was 800
                     base pairs.  The library was constructed by Noelle Ling.
                     The library is available from Dr. S.A. Williams, email
                     genome@smith.edu."
ORIGIN

Alignment Scores:
Pred. No.:              128             Length:         210
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     1               Gaps:           0

US-10-758-902-9 (1-149) x AI784781 (1-210)

Qy         52 IleThrThrThrSerLysLysThr 59
              |||||||||||||||||||||||
Db         66 ATAACAACAACATCAAAAAAGACN 43

RESULT 22
AA328059
LOCUS       AA328059                225 bp    mRNA    linear   EST 20-APR-1997
DEFINITION  EST31482 Embryo, 12 week I Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION   AA328059
VERSION     AA328059.1  GI:1980303
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 225)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
   PUBMED   7566098
COMMENT     Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .225
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):129689"
                     /db_xref="taxon:9606"
                     /dev_stage="embryo, 12 wks"
                     /clone_lib="Embryo, 12 week I"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

Alignment Scores:
Pred. No.:              136             Length:         225
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     1               Gaps:           0

US-10-758-902-9 (1-149) x AA328059 (1-225)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              |||||||||||||||||||||||
Db        170 ACAGTGTCATTTAATTTGGGAGAG 193

RESULT 23
AU241088/c
LOCUS       AU241088                226 bp    mRNA    linear   EST 15-JAN-2002
DEFINITION  AU241088 UV irradiated OLHNI cell line cDNA library (OLc) Oryzias
            latipes cDNA clone OLc34.04f similar to gb|U19860|MMU19860 Mus
            musculus growth arrest specific mRNA, clone 3544, mRNA sequence.
ACCESSION   AU241088
VERSION     AU241088.1  GI:18153667
KEYWORDS    EST.
SOURCE      Oryzias latipes (Japanese medaka)
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 226)
```

```
  AUTHORS   Naruse,K., Mitani,H. and Tanaka,M.
  TITLE     Medaka EST Project in University of Tokyo (2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Kiyoshi Naruse
            Department of Biological Sciences
            Graduate School of Science, University of Tokyo
            Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
            Tel: 81-3-5841-4443
            Fax: 81-3-5841-4410
            Email: naruse@biol.s.u-tokyo.ac.jp
            This clone was isolated from UV irradiated OLHNI cell line cDNA
            library (OLc) 5' end sequences.
FEATURES             Location/Qualifiers
     source          1. .226
                     /organism="Oryzias latipes"
                     /mol_type="mRNA"
                     /strain="HNI"
                     /db_xref="taxon:8090"
                     /clone="OLc34.04f"
                     /clone_lib="UV irradiated OLHNI cell line cDNA library
                     (OLc)"
ORIGIN

Alignment Scores:
Pred. No.:              137           Length:        226
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     1             Gaps:          0

US-10-758-902-9 (1-149) x AU241088 (1-226)

Qy         93 ValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||
Db        223 GTAGCGACCAGCAAGCTGTTTCCG 200

RESULT 24
CG689981/c
LOCUS       CG689981                233 bp    DNA     linear   GSS 08-OCT-2003
DEFINITION  ZMMBBc0133L23f ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0133L23
            5', genomic survey sequence.
ACCESSION   CG689981
VERSION     CG689981.1  GI:37587371
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 233)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003c)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: T7
            Class: BAC ends
            High quality sequence start: 84.
FEATURES             Location/Qualifiers
     source          1. .233
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0133L23"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc (EcoRI)"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              141           Length:        233
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     10            Gaps:          0

US-10-758-902-9 (1-149) x CG689981 (1-233)

Qy         94 AlaThrSerLysLeuPheProGly 101
              |||||||||||||||||||||||
Db        133 GCTACCTCTAAACTCTTCCCAGGT 110

RESULT 25
CL232182/c
LOCUS       CL232182                241 bp    DNA     linear   GSS 08-JAN-2004
DEFINITION  ZMMBBc0188H08r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0188H08
            3', genomic survey sequence.
ACCESSION   CL232182
VERSION     CL232182.1  GI:40774280
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 241)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003c)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .241
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0188H08"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc (EcoRI)"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              145           Length:        241
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.4%          Indels:        0
DB:                     10            Gaps:          0

US-10-758-902-9 (1-149) x CL232182 (1-241)

Qy         94 AlaThrSerLysLeuPheProGly 101
              |||||||||||||||||||||||
Db         43 GCTACCTCTAAACTCTTCCCAGGT 20
```

```
RESULT 26
BF352328/c
LOCUS       BF352328                246 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  RC6-HT0594-180500-011-G06 HT0594 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF352328
VERSION     BF352328.1  GI:11311402
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 246)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC6&t2=RC6-HT0594-
            180500-011-G06&t3=2000-05-18&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 12
            High quality sequence stop: 246.
FEATURES             Location/Qualifiers
     source          1. .246
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0594"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                148             Length:         246
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       2               Gaps:           0

US-10-758-902-9 (1-149) x BF352328 (1-246)

Qy          3 ThrValSerPheAsnLeuGlyGlu 10
              ||||||||||||||||||||||||
Db         69 ACAGTGTCATTTAATTTGGGAGAG 46

RESULT 27
CV372077/c
LOCUS       CV372077                258 bp    mRNA    linear   EST 27-SEP-2004
DEFINITION  PM3-CT0800-010601-008-d04 CT0800 Homo sapiens cDNA, mRNA sequence.
ACCESSION   CV372077
VERSION     CV372077.1  GI:52722132
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 258)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. http://www.ludwig.org.br.
FEATURES             Location/Qualifiers
     source          1. .258
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="CT0800"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No.
                     196,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                154             Length:         258
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       7               Gaps:           0

US-10-758-902-9 (1-149) x CV372077 (1-258)

Qy          34 LeuProValThrLeuGlnThrIle 41
               |||||||||||||||||||||||
Db          45 CTCCCCGTGACCCTCCAAACCATC 22

RESULT 28
BF929992/c
LOCUS       BF929992                259 bp    mRNA    linear   EST 19-JAN-2001
DEFINITION  CM4-NT0215-091200-497-b05 NT0215 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF929992
VERSION     BF929992.1  GI:12328029
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 259)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
```

```
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-NT0215-
            091200-497-b05&t3=2000-12-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 26
            High quality sequence stop: 258.
FEATURES             Location/Qualifiers
     source          1. .259
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NT0215"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                154             Length:         259
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       2               Gaps:           0

US-10-758-902-9 (1-149) x BF929992 (1-259)

Qy          89 LysValProThrValAlaThrSer 96
               ||||||||||||||||||||||||||
Db          79 AAAGTTCCCACAGTAGCCACGAGC 56

RESULT 29
AW887063
LOCUS       AW887063                264 bp    mRNA    linear   EST 23-MAY-2000
DEFINITION  RC1-OT0086-130400-022-h06 OT0086 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW887063
VERSION     AW887063.1  GI:8049076
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 264)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-OT0086-130
            400-022-h06&t3=2000-04-13&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 264.
FEATURES             Location/Qualifiers
     source          1. .264
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="OT0086"
                     /note="Organ: ovary; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No.
                     196,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                157             Length:         264
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       1               Gaps:           0

US-10-758-902-9 (1-149) x AW887063 (1-264)

Qy           3 ThrValSerPheAsnLeuGlyGlu 10
               ||||||||||||||||||||||||||
Db         178 ACAGTGTCATTTAATTTGGGAGAG 201

RESULT 30
CL232378/c
LOCUS       CL232378                295 bp    DNA     linear   GSS 08-JAN-2004
DEFINITION  ZMMBBc0190H13f ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0190H13
            5', genomic survey sequence.
ACCESSION   CL232378
VERSION     CL232378.1  GI:40774665
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 295)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003c)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
```

```
           Seq primer: T7
           Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .295
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0190H13"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc (EcoRI)"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:                173           Length:         295
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              5.4%          Indels:         0
DB:                       10            Gaps:           0

US-10-758-902-9 (1-149) x CL232378 (1-295)

Qy          94 AlaThrSerLysLeuPheProGly 101
               ||||||||||||||||||||||||
Db          34 GCTACTTCTAAACTCTTCCCAGGT 11

RESULT 31
CG834124/c
LOCUS       CG834124                  299 bp    DNA     linear   GSS 12-NOV-2003
DEFINITION  ZMMBBc0141K08r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0141K08
            3', genomic survey sequence.
ACCESSION   CG834124
VERSION     CG834124.1  GI:38298523
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 299)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003c)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
            Class: BAC ends
            High quality sequence start: 162.
FEATURES             Location/Qualifiers
     source          1. .299
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0141K08"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc (EcoRI)"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:                175           Length:         299
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              5.4%          Indels:         0
DB:                       10            Gaps:           0

US-10-758-902-9 (1-149) x CG834124 (1-299)

Qy          94 AlaThrSerLysLeuPheProGly 101
               ||||||||||||||||||||||||
Db         209 GCTACCTCTAAACTCTTCCCAGGT 186

RESULT 32
CC492594/c
LOCUS       CC492594                  346 bp    DNA     linear   GSS 17-JUN-2003
DEFINITION  CH240_326P11.TARBAC13P2 CHORI-240 Bos taurus genomic clone
            CH240_326P11, genomic survey sequence.
ACCESSION   CC492594
VERSION     CC492594.1  GI:31803508
KEYWORDS    GSS.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
            Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
            Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
            Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
            Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
            Dalrymple,B.P. and Tellam,R.
  TITLE     Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: CH240_326P11.T7
            Contact: Rob Holt
            Sequencing
            The British Columbia Cancer Agency Genome Science Centre
            600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
            Tel: 604-877-6085
            Fax: 604-877-6276
            Email: rholt@bcgsc.ca
            Clones are derived from the bovine BAC library CHORI-240
            (http://www.chori.org/bacpac/bovine240.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/ordering_information.htm). This work
            was undertaken as part of the International Bovine BAC Mapping
            Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
            British Columbia Genome Sciences Centre, Canada.
            Plate: 326  row: P  column: 11
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Hereford"
                     /db_xref="taxon:9913"
                     /clone="CH240_326P11"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-240"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
                     library (Male) produced by Pieter de Jong"
ORIGIN

Alignment Scores:
Pred. No.:                199           Length:         346
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              5.4%          Indels:         0
DB:                       9             Gaps:           0
```

```
US-10-758-902-9 (1-149) x CC492594 (1-346)

Qy         49 LeuValAspIleThrThrThrSer 56
              |||||||||||||||||||||||
Db        245 TTGGTTGACATCACCACCACCTCC 222

RESULT 33
BY370947/c
LOCUS       BY370947                357 bp    mRNA    linear   EST 09-JUL-2003
DEFINITION  BY370947 RIKEN full-length enriched, embryo RCB-0549 Cle-H3 cDNA
            Mus musculus cDNA clone G430047G07 3', mRNA sequence.
ACCESSION   BY370947
VERSION     BY370947.1  GI:26600435
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 357)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .357
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /db_xref="taxon:10090"
                      /clone="G430047G07"
                      /cell_line="RCB-0549 Cle-H3"
                      /dev_stage="embryo"
                      /clone_lib="RIKEN full-length enriched, embryo RCB-0549
                      Cle-H3 cDNA"
ORIGIN

Alignment Scores:
Pred. No.:                205             Length:         357
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       5               Gaps:           0

US-10-758-902-9 (1-149) x BY370947 (1-357)

Qy         29 ThrProValCysGlnLeuProVal 36
              |||||||||||||||||||||||||
Db         95 ACACCTGTCTGTCAGCTGCCCGTG 72

RESULT 34
BY085125
LOCUS       BY085125                360 bp    mRNA    linear   EST 07-DEC-2002
DEFINITION  BY085125 RIKEN full-length enriched, pooled tissues, adult spleen,
            etc. Mus musculus cDNA clone K630051G06 5', mRNA sequence.
ACCESSION   BY085125
VERSION     BY085125.1  GI:26195088
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 360)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
```

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .360
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="K630051G06"
/clone_lib="RIKEN full-length enriched, pooled tissues, adult spleen, etc."
/note="(dev_stage=adult,tissue_type=spleen,sex=male), (dev_stage=adult,tissue_type=kidney,sex=male), (dev_stage=adult,tissue_type=testis,sex=male), (dev_stage=adult,tissue_type=thymus,sex=male), (dev_stage=adult,tissue_type=heart,sex=male), (dev_stage=adult,tissue_type=colon,sex=male), (dev_stage=adult,tissue_type=stomach,sex=male), (dev_stage=adult,tissue_type=liver,sex=male), (dev_stage=13 days embryo,tissue_type=whole body,sex=mix),(dev_stage=14 days embryo,tissue_type=whole body,sex=mix),(dev_stage=16 days embryo,tissue_type=whole body,sex=mix),(dev_stage=17 days embryo,tissue_type=whole body,sex=mix),(dev_stage=15 days pregnant, adult,tissue_type=amnion,sex=female),(dev_stage=10 days neonate,tissue_type=brain,sex=mix),(dev_stage=10 days neonate,tissue_type=thymus,sex=mix),(dev_stage=10 days neonate,tissue_type=heart,sex=mix)"
ORIGIN

Alignment Scores:

Pred. No.:	206	Length:	360
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-9 (1-149) x BY085125 (1-360)

```
Qy         55 ThrSerLysLysThrValLysVal 62
              ||||||||||||||||||||||||
Db         97 ACATCGAAGAAGACAGTAAAAGTG 120
```

RESULT 35
CC836296
LOCUS CC836296 360 bp DNA linear GSS 23-JUL-2003
DEFINITION ZMMBBc0483O08r ZMMBBc Zea mays genomic clone ZMMBBc0483O08 3', genomic survey sequence.
ACCESSION CC836296
VERSION CC836296.1 GI:33174698
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 360)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE Sequencing of the maize genome at PGIR (2003b)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 126.
FEATURES Location/Qualifiers
source 1. .360
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBc0483O08"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBc"
/note="Vector: pTARBAC1.3; Site_1: BamHI; Site_2: BamHI"
ORIGIN

Alignment Scores:

Pred. No.:	206	Length:	360
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.4%	Indels:	0
DB:	9	Gaps:	0

US-10-758-902-9 (1-149) x CC836296 (1-360)

```
Qy         94 AlaThrSerLysLeuProGly 101
              ||||||||||||||||||||
Db        279 GCTACCTCTAAACTCTTCCCAGGT 302
```

RESULT 36
BM953604/c
LOCUS BM953604 362 bp mRNA linear EST 14-MAR-2002
DEFINITION 952064C01.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea mays cDNA, mRNA sequence.
ACCESSION BM953604
VERSION BM953604.1 GI:19437194
KEYWORDS EST.
SOURCE Zea mays

```
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 362)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 952064  row: C  column: 01.
FEATURES             Location/Qualifiers
     source          1. .362
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="BMS (Black Mexican Sweet)"
                     /db_xref="taxon:4577"
                     /tissue_type="suspension culture"
                     /dev_stage="mixed logarithmic and stationary growth
                     phases"
                     /lab_host="DH10B"
                     /clone_lib="952 - BMS tissue from Walbot Lab (reduced
                     rRNA)"
                     /note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The
                     library was prepared by George Rudenko using poly (A)
                     selected RNA and Universal Riboclone cDNA Synthesis System
                     (Promega). cDNA was synthesized using both random and
                     oligo(dT) primers in separate reactions and equipped with
                     EcoRI adaptors. Library was size-fractionated on agarose
                     gels (for insert size >400bp) and non-directionally cloned
                     into EcoRI-digested pUC19 vector. Blue/white selection on
                     carbenicillin-containing plates was used to recover
                     positive clones."
ORIGIN

Alignment Scores:
Pred. No.:              207           Length:         362
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-9 (1-149) x BM953604 (1-362)

Qy         83 ArgAlaValPheLeuAspLysVal 90
              ||||||||||||||||||||||
Db         89 CGCGCGGTATTCCTTGATAAGGTT 66

RESULT 37
CG682026/c
LOCUS       CG682026                373 bp    DNA     linear   GSS 08-OCT-2003
DEFINITION  ZMMBBc0143A11r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0143A11
            3', genomic survey sequence.
ACCESSION   CG682026
VERSION     CG682026.1  GI:37578863
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003c)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
            Class: BAC ends
            High quality sequence start: 187.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0143A11"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc (EcoRI)"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              213           Length:         373
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     10            Gaps:           0

US-10-758-902-9 (1-149) x CG682026 (1-373)

Qy         94 AlaThrSerLysLeuPheProGly 101
              |||||||||||||||||||||||
Db        214 GCTACCTCTAAACTCTTCCCAGGT 191

RESULT 38
AA561049/c
LOCUS       AA561049                378 bp    mRNA    linear   EST 18-AUG-1997
DEFINITION  vl40g06.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
            IMAGE:974746 5', mRNA sequence.
ACCESSION   AA561049
VERSION     AA561049.1  GI:2332514
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 378)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:555474
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 373.
FEATURES             Location/Qualifiers
     source          1. .378
                     /organism="Mus musculus"
```

```
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:974746"
                     /sex="females"
                     /tissue_type="whole skin"
                     /dev_stage="11 weeks old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="Stratagene mouse skin (#937313)"
                     /note="Organ: skin; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. Whole skin from 11 week old C57BL/6 female mice.
                     Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
                     adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
                     sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
ORIGIN

Alignment Scores:
Pred. No.:              215             Length:         378
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     1               Gaps:           0

US-10-758-902-9 (1-149) x AA561049 (1-378)

Qy         36 ValThrLeuGlnThrIleAlaAsp 43
              |||||||||||||||||||||||||
Db        185 GTAACCCTTCAGACTATAGCCGAC 162

RESULT 39
CG700571/c
LOCUS       CG700571                380 bp    DNA     linear   GSS 15-OCT-2003
DEFINITION  ZMMBBc0120A08f ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0120A08
            5', genomic survey sequence.
ACCESSION   CG700571
VERSION     CG700571.1  GI:37688372
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 380)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003c)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: T7
            Class: BAC ends
            High quality sequence start: 173.
FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0120A08"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc (EcoRI)"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              216             Length:         380
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     10              Gaps:           0

US-10-758-902-9 (1-149) x CG700571 (1-380)

Qy         94 AlaThrSerLysLeuPheProGly 101
              |||||||||||||||||||||||||
Db        224 GCTACCTCTAAACTCTTCCCAGGT 201

RESULT 40
BI976410
LOCUS       BI976410                391 bp    mRNA    linear   EST 23-OCT-2001
DEFINITION  485295 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BI976410
VERSION     BI976410.1  GI:16350815
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
   PUBMED   11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 113  row: A  column: 10
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .391
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 2BOV"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, thymus,
                     semitendonosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."
ORIGIN

Alignment Scores:
Pred. No.:              222             Length:         391
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.4%            Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x BI976410 (1-391)
```

```
Qy          80 GlyLysAspArgAlaValPheLeu 87
               |||||||||||||||||||||||||
Db          14 GGGAAAGATAGAGCAGTCTTTCTC 37
```

Search completed: February 20, 2006, 02:53:42
Job time : 5186.08 secs

STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 201939

TO: Sheridan Swope
Location: REM-2D19&3C70
Art Unit: 1656
Tuesday, September 19, 2006
Case Serial Number: 10/758902

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 17:38:01 ; Search time 47.4302 Seconds
(without alignments)
1775.239 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_18092006_162712_11663/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss05h -USER=US10758902_@CGN_1_1_252_@runat_18092006_162712_11663
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	111	69.4	65	3	US-09-445-160B-5	Sequence 5, Appli
2	72	45.0	363	3	US-09-445-160B-8	Sequence 8, Appli
3	61	38.1	1195	2	US-08-373-858-1	Sequence 1, Appli
4	61	38.1	1195	2	US-08-342-786B-1	Sequence 1, Appli
5	61	38.1	1379	2	US-08-500-611-1	Sequence 1, Appli
6	61	38.1	1379	2	US-08-500-694-1	Sequence 1, Appli
7	61	38.1	1379	3	US-07-865-169-1	Sequence 1, Appli
8	61	38.1	1379	3	US-09-005-273-1	Sequence 1, Appli
9	61	38.1	1379	3	US-08-501-253A-1	Sequence 1, Appli
10	61	38.1	1379	5	US-09-721-047A-1	Sequence 1, Appli
11	61	38.1	1379	7	PCT-US96-11546-1	Sequence 1, Appli
12	57.5	35.9	678	3	US-09-107-532A-3648	Sequence 3648, Ap
13	56	35.0	945	5	US-10-128-713A-15	Sequence 15, Appl
14	56	35.0	1379	3	US-07-865-169-2	Sequence 2, Appli
15	56	35.0	1379	3	US-09-005-273-3	Sequence 3, Appli
16	55.5	34.7	38844	3	US-09-734-675-3	Sequence 3, Appli
17	55.5	34.7	38844	3	US-10-060-333-3	Sequence 3, Appli
c 18	53.5	33.4	601	3	US-09-949-016-62787	Sequence 62787, A
c 19	53.5	33.4	601	3	US-09-949-016-62788	Sequence 62788, A
20	53.5	33.4	103792	3	US-09-949-016-13553	Sequence 13553, A
21	53.5	33.4	103993	3	US-09-949-016-12317	Sequence 12317, A
22	53	33.1	962	2	US-08-324-301-14	Sequence 14, Appl
23	52	32.5	999	3	US-09-428-034-3	Sequence 3, Appli
24	52	32.5	1364	3	US-09-428-034-1	Sequence 1, Appli
25	52	32.5	1380	3	US-09-902-540-3259	Sequence 3259, Ap
26	52	32.5	19954	3	US-09-902-540-1150	Sequence 1150, Ap
27	52	32.5	51822	3	US-09-949-016-15233	Sequence 15233, A
28	51.5	32.2	717	3	US-09-902-540-8868	Sequence 8868, Ap
29	51.5	32.2	12028	3	US-09-902-540-1071	Sequence 1071, Ap
30	51.5	32.2	109974	4	US-09-531-120-204	Sequence 204, App
31	51	31.9	3702	3	US-09-134-000C-1566	Sequence 1566, Ap
32	51	31.9	4249	3	US-09-071-035-403	Sequence 403, App
33	51	31.9	4249	3	US-10-206-576-403	Sequence 403, App
34	51	31.9	4359	3	US-09-071-035-401	Sequence 401, App
35	51	31.9	4359	3	US-10-206-576-401	Sequence 401, App
36	51	31.9	13222	3	US-09-736-116-60	Sequence 60, Appl
37	50	31.2	670	3	US-09-306-446C-15	Sequence 15, Appl
38	50	31.2	5108	3	US-09-306-446C-8	Sequence 8, Appli
39	50	31.2	133559	3	US-09-949-016-15845	Sequence 15845, A
40	49.5	30.9	4953	3	US-09-602-787A-13	Sequence 13, Appl
41	49.5	30.9	4953	3	US-09-602-787A-55	Sequence 55, Appl
c 42	49.5	30.9	6053	3	US-09-573-080A-22	Sequence 22, Appl
c 43	49.5	30.9	6053	5	US-09-854-867-22	Sequence 22, Appl
44	49.5	30.9	6567	3	US-09-328-352-3637	Sequence 3637, Ap
45	49	30.6	949	3	US-09-221-017B-615	Sequence 615, App
46	49	30.6	6960	2	US-08-841-349-3	Sequence 3, Appli
47	49	30.6	6960	3	US-09-431-184A-3	Sequence 3, Appli
48	49	30.6	8176	2	US-08-841-349-5	Sequence 5, Appli
49	49	30.6	8176	3	US-09-431-184A-5	Sequence 5, Appli
50	49	30.6	134890	3	US-09-949-016-15602	Sequence 15602, A
c 51	49	30.6	174493	3	US-09-804-471A-3	Sequence 3, Appli
c 52	49	30.6	174493	3	US-10-238-709-3	Sequence 3, Appli
c 53	49	30.6	174493	3	US-10-724-594-3	Sequence 3, Appli
c 54	48.5	30.3	80706	3	US-09-949-016-15347	Sequence 15347, A
55	48	30.0	162	3	US-09-513-999C-30353	Sequence 30353, A
56	48	30.0	405	3	US-09-401-064-194	Sequence 194, App
57	48	30.0	887	3	US-09-949-016-5729	Sequence 5729, Ap
58	48	30.0	887	3	US-09-949-016-5730	Sequence 5730, Ap
59	48	30.0	887	3	US-09-949-016-5731	Sequence 5731, Ap
60	48	30.0	1083	3	US-09-549-831-12	Sequence 12, Appl
61	48	30.0	1119	3	US-08-911-321-2	Sequence 2, Appli
62	48	30.0	1125	2	US-08-105-483-290	Sequence 290, App
63	48	30.0	1125	2	US-08-709-209-290	Sequence 290, App
64	48	30.0	1125	2	US-08-458-101-290	Sequence 290, App
65	48	30.0	1195	3	US-09-549-831-9	Sequence 9, Appli
66	48	30.0	1491	3	US-09-902-540-3335	Sequence 3335, Ap
c 67	48	30.0	1659	3	US-09-252-991A-9018	Sequence 9018, Ap
68	48	30.0	2139	3	US-09-614-221A-341	Sequence 341, App
69	48	30.0	2330	7	PCT-US95-13975-71	Sequence 71, Appl
c 70	48	30.0	3365	3	US-09-221-017B-318	Sequence 318, App
71	48	30.0	3687	3	US-09-891-641-1	Sequence 1, Appli
72	48	30.0	6176	3	US-08-911-321-6	Sequence 6, Appli
c 73	48	30.0	7347	4	US-10-324-967-17	Sequence 17, Appl
c 74	48	30.0	7374	3	US-09-252-991A-9100	Sequence 9100, Ap
75	48	30.0	16387	3	US-09-902-540-1156	Sequence 1156, Ap
76	48	30.0	92387	3	US-09-949-016-14563	Sequence 14563, A
77	48	30.0	151295	3	US-09-949-016-14568	Sequence 14568, A
78	48	30.0	151295	3	US-09-949-016-14569	Sequence 14569, A
79	48	30.0	151295	3	US-09-949-016-14570	Sequence 14570, A
80	48	30.0	151295	3	US-09-949-016-14571	Sequence 14571, A
81	48	30.0	151295	3	US-09-949-016-14572	Sequence 14572, A

82	48	30.0	269223	3	US-09-596-002-41	Sequence 41, Appl
83	48	30.0	319608	3	US-09-539-333D-1	Sequence 1, Appli
84	48	30.0	319608	3	US-09-679-409-1	Sequence 1, Appli
85	48	30.0	393753	3	US-09-949-016-14573	Sequence 14573, A
86	48	30.0	393753	3	US-09-949-016-14574	Sequence 14574, A
c 87	48	30.0	670689	3	US-09-949-016-12505	Sequence 12505, A
c 88	48	30.0	670690	3	US-09-949-016-14207	Sequence 14207, A
89	48	30.0	678533	3	US-09-949-016-14577	Sequence 14577, A
90	48	30.0	678533	3	US-09-949-016-14578	Sequence 14578, A
91	48	30.0	818128	3	US-09-949-016-14546	Sequence 14546, A
92	48	30.0	818128	3	US-09-949-016-14547	Sequence 14547, A
93	48	30.0	818128	3	US-09-949-016-14548	Sequence 14548, A
94	48	30.0	818128	3	US-09-949-016-14549	Sequence 14549, A
95	48	30.0	818128	3	US-09-949-016-14550	Sequence 14550, A
96	48	30.0	818128	3	US-09-949-016-14551	Sequence 14551, A
97	48	30.0	818128	3	US-09-949-016-14552	Sequence 14552, A
98	48	30.0	818128	3	US-09-949-016-14553	Sequence 14553, A
99	48	30.0	818128	3	US-09-949-016-14554	Sequence 14554, A
100	48	30.0	818128	3	US-09-949-016-14555	Sequence 14555, A

ALIGNMENTS

RESULT 1
US-09-445-160B-5
; Sequence 5, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenza
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
; FILE REFERENCE: Stirpe
; CURRENT APPLICATION NUMBER: US/09/445,160B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/NL98/00336
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 5
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Bougainvillea spectrabilis
; PUBLICATION INFORMATION:
US-09-445-160B-5

Alignment Scores:

Pred. No.:	1.85e-11	Length:	65
Score:	111.00	Matches:	21
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	69.4%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-445-160B-5 (1-65)

```
Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63
```

RESULT 2
US-09-445-160B-8
; Sequence 8, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenza
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
; FILE REFERENCE: Stirpe
; CURRENT APPLICATION NUMBER: US/09/445,160B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/NL98/00336
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 8
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Bougainvillea spectrabilis
; PUBLICATION INFORMATION:
US-09-445-160B-8

Alignment Scores:

Pred. No.:	0.0012	Length:	363
Score:	72.00	Matches:	14
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	45.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-445-160B-8 (1-363)

```
Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43
```

RESULT 3
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byeong-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytolacca
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; TITLE OF INVENTION: Plant Transformed Thereof.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Peter
; REGISTRATION NUMBER: 25,351

```
;      REFERENCE/DOCKET NUMBER:  0136/17986-US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7770
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Phytolacca americana
;      TISSUE TYPE:  Leaf
US-08-373-858-1

Alignment Scores:
Pred. No.:                0.475          Length:          1195
Score:                    61.00          Matches:         12
Percent Similarity:       68.0%          Conservative:    5
Best Local Similarity:    48.0%          Mismatches:      6
Query Match:              38.1%          Indels:          2
DB:                       2              Gaps:            1

US-10-758-902-1 (1-30) x US-08-373-858-1 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   |||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 4
US-08-342-786B-1
; Sequence 1, Application US/08342786B
; Patent No. 5648234
;  GENERAL INFORMATION:
;    APPLICANT:  Moon, Young-Ho
;    APPLICANT:  Jeon, Hong-Seob
;    APPLICANT:  Choi, Kyu-Whan
;    APPLICANT:  Lee, Kwan-Ho
;    APPLICANT:  Kim, Man-Keun
;    TITLE OF INVENTION:  A No. 5648234el Expression Vector for Phytolacca
;    TITLE OF INVENTION:  Antiviral Protein
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby
;      STREET:  805 Third Ave.
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/342,786B
;      FILING DATE:  21-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/147,024
;      FILING DATE:  01-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, S. Peter
;      REGISTRATION NUMBER:  25,351
;      REFERENCE/DOCKET NUMBER:  0136/08862-US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)527-7700
;      TELEFAX:  (212)753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Phytolacca americana L.
;    IMMEDIATE SOURCE:
;      CLONE:  PAP
US-08-342-786B-1

Alignment Scores:
Pred. No.:                0.475          Length:          1195
Score:                    61.00          Matches:         12
Percent Similarity:       68.0%          Conservative:    5
Best Local Similarity:    48.0%          Mismatches:      6
Query Match:              38.1%          Indels:          2
DB:                       2              Gaps:            1

US-10-758-902-1 (1-30) x US-08-342-786B-1 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   |||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||||
Db        162 GATCTTCGTAATGAA 176

RESULT 5
US-08-500-611-1
; Sequence 1, Application US/08500611
; Patent No. 5756322
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  Pokeweed Antiviral Protein Mutants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/500,611
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.0-034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;      TELEX:  139-125
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
```

```
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(233, "a")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(349, "g")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(435, "c")
US-08-500-611-1

Alignment Scores:
Pred. No.:              0.57          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     2             Gaps:           1

US-10-758-902-1 (1-30) x US-08-500-611-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 6
US-08-500-694-1
; Sequence 1, Application US/08500694
; Patent No. 5880329
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  DNAs Encoding Pokeweed Antiviral Protein
;    TITLE OF INVENTION:  Mutants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/500,694
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.0-039
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;      TELEX:  139-125
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(233, "a")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(349, "g")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(435, "c")
US-08-500-694-1

Alignment Scores:
Pred. No.:              0.57          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     2             Gaps:           1

US-10-758-902-1 (1-30) x US-08-500-694-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 7
US-07-865-169-1
; Sequence 1, Application US/07865169
; Patent No. 6015940
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    APPLICANT:  Lodge, Jennifer K.
;    APPLICANT:  Kaniewski, Wojciech K.
;    TITLE OF INVENTION:  Virus Resistant Potato Plants
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis R. Hoerner, Jr., Monsanto Co.  BB4F
;      STREET:  700 Chesterfield Parkway No. 6015940th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/865,169
;      FILING DATE:  19920407
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoerner Jr., Dennis R.
;      REGISTRATION NUMBER:  30,914
;      REFERENCE/DOCKET NUMBER:  38-21(10547)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6099
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-865-169-1

Alignment Scores:
```

```
Pred. No.:              0.57          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-07-865-169-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||          :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 8
US-09-005-273-1
; Sequence 1, Application US/09005273
; Patent No. 6137030
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
;    TITLE OF INVENTION:  AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ &
;      ADDRESSEE:  MENTILIK
;      STREET:  600 South, Avenue West
;      CITY:  Westfield
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07090
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/005,273
;      FILING DATE:  09-JAN-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,611
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,694
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11546
;      FILING DATE:  11-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REGISTRATION NUMBER:  33,071
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.3-034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  225..290
US-09-005-273-1

Alignment Scores:
Pred. No.:              0.57          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-09-005-273-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||          :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 9
US-08-501-253A-1
; Sequence 1, Application US/08501253A
; Patent No. 6146628
;  GENERAL INFORMATION:
;    APPLICANT:  Uckun, Fatih
;    APPLICANT:  Tumer, Nilgun
;    TITLE OF INVENTION:  Biotherapeutic Agents Comprising
;    TITLE OF INVENTION:  Recombinant PAp and PAP Mutants
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  90 South 7th Street, 3100 No. 6146628west Center
;      CITY:  Minneapolis
;      STATE:  MM
;      COUNTRY:  US
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/501,253A
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M.
;      REGISTRATION NUMBER:  33,924
;      REFERENCE/DOCKET NUMBER:  600.323US01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
US-08-501-253A-1

Alignment Scores:
Pred. No.:              0.57          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-08-501-253A-1 (1-1379)
```

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 10
US-09-721-047A-1
; Sequence 1, Application US/09721047A
; Patent No. 7019126
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  WANG, PINGER
;  TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
;  FILE REFERENCE: OCIRS 3.9-060 CONT
;  CURRENT APPLICATION NUMBER: US/09/721,047A
;  CURRENT FILING DATE:  2000-11-22
;  PRIOR APPLICATION NUMBER: PCT/US99/11301
;  PRIOR FILING DATE: 1999-05-21
;  PRIOR APPLICATION NUMBER: 60/086,374
;  PRIOR FILING DATE: 1998-05-22
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
;   LENGTH: 1379
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (225)..(1163)
US-09-721-047A-1

Alignment Scores:
Pred. No.:              0.57          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     5             Gaps:           1

US-10-758-902-1 (1-30) x US-09-721-047A-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 11
PCT-US96-11546-1
; Sequence 1, Application PC/TUS9611546
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  DNAs Encoding Pokeweed Antiviral Protein
;    TITLE OF INVENTION:  Mutants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11546
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,694
;      FILING DATE:  11-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.0-039
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;      TELEX:  139-125
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(233, "a")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(349, "g")
;    FEATURE:
;      NAME/KEY:  mutation
;      LOCATION:  replace(435, "c")
PCT-US96-11546-1

Alignment Scores:
Pred. No.:              0.57          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     7             Gaps:           1

US-10-758-902-1 (1-30) x PCT-US96-11546-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 12
US-09-107-532A-3648
; Sequence 3648, Application US/09107532A
; Patent No. 6583275
;  GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
```

```
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3648:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 678 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: circular
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...678
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3648:
US-09-107-532A-3648

Alignment Scores:
Pred. No.:              0.947          Length:         678
Score:                  57.50          Matches:        11
Percent Similarity:     62.9%          Conservative:   11
Best Local Similarity:  31.4%          Mismatches:     8
Query Match:            35.9%          Indels:         5
DB:                     3              Gaps:           1

US-10-758-902-1 (1-30) x US-09-107-532A-3648 (1-678)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::      |||   :::|||||||||   |||:::::      |||:::::|||
Db        112 TTCTCAAAAACTTCTATGGATTTGGGAGAAAGATATGATTTTAAGGGGTTTATGGAAGAT 171

Qy         21 LeuArgAsnGluLeuAla--------------LysGlyThrPro 30
                 :::|||::::::                :::|||||||||
Db        172 AAAATGGACGAGGTATCAAGTAGGGAAATTCCAGAAGGCACACCT 216

RESULT 13
US-10-128-713A-15
; Sequence 15, Application US/10128713A
; Patent No. 7034140
; GENERAL INFORMATION:
;  APPLICANT: Bramucci, Michael G
;  TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production
;  FILE REFERENCE: CL-1788
;  CURRENT APPLICATION NUMBER: US/10/128,713A
;  CURRENT FILING DATE:  2002-04-22
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Rhodococcus erythropolis
US-10-128-713A-15

Alignment Scores:
Pred. No.:              2.66           Length:         945
Score:                  56.00          Matches:        10
Percent Similarity:     72.7%          Conservative:   6
Best Local Similarity:  45.5%          Mismatches:     6
Query Match:            35.0%          Indels:         0
DB:                     5              Gaps:           0

US-10-758-902-1 (1-30) x US-10-128-713A-15 (1-945)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||::::::          ||||||:::|||:::      :::|||
Db        520 AATCTCGGTGAGGCGTTTCAGCTGACCAACTTCATCCGCGACGTCGGTGAAGACCTCGAC 579

Qy         27 LysGly 28
              :::|||
Db        580 CGGGGA 585

RESULT 14
US-07-865-169-2
; Sequence 2, Application US/07865169
; Patent No. 6015940
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    APPLICANT:  Lodge, Jennifer K.
;    APPLICANT:  Kaniewski, Wojciech K.
;    TITLE OF INVENTION:  Virus Resistant Potato Plants
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis R. Hoerner, Jr., Monsanto Co.  BB4F
;      STREET:  700 Chesterfield Parkway No. 6015940th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/865,169
;      FILING DATE:  19920407
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoerner Jr., Dennis R.
;      REGISTRATION NUMBER:  30,914
;      REFERENCE/DOCKET NUMBER:  38-21(10547)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6099
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-865-169-2

Alignment Scores:
Pred. No.:              4.32           Length:         1379
Score:                  56.00          Matches:        12
Percent Similarity:     64.0%          Conservative:   4
Best Local Similarity:  48.0%          Mismatches:     7
Query Match:            35.0%          Indels:         2
DB:                     3              Gaps:           1

US-10-758-902-1 (1-30) x US-07-865-169-2 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCGGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368
```

```
RESULT 15
US-09-005-273-3
; Sequence 3, Application US/09005273
; Patent No. 6137030
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
;    TITLE OF INVENTION:  AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ &
;      ADDRESSEE:  MENTILIK
;      STREET:  600 South, Avenue West
;      CITY:  Westfield
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07090
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/005,273
;      FILING DATE:  09-JAN-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,611
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,694
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11546
;      FILING DATE:  11-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REGISTRATION NUMBER:  33,071
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.3-034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  225..290
US-09-005-273-3

Alignment Scores:
Pred. No.:               4.32          Length:          1379
Score:                   56.00         Matches:         12
Percent Similarity:      64.0%         Conservative:    4
Best Local Similarity:   48.0%         Mismatches:      7
Query Match:             35.0%         Indels:          2
DB:                      3             Gaps:            1

US-10-758-902-1 (1-30) x US-09-005-273-3 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||             :::|||   ||||||
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCGGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 16
US-09-734-675-3
; Sequence 3, Application US/09734675
; Patent No. 6365391
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL000862
;  CURRENT APPLICATION NUMBER: US/09/734,675
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 38844
;   TYPE: DNA
;   ORGANISM: Human
US-09-734-675-3

Alignment Scores:
Pred. No.:               380           Length:          38844
Score:                   55.50         Matches:         10
Percent Similarity:      48.7%         Conservative:    9
Best Local Similarity:   25.6%         Mismatches:      11
Query Match:             34.7%         Indels:          9
DB:                      3             Gaps:            1

US-10-758-902-1 (1-30) x US-09-734-675-3 (1-38844)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr------------------------ 12
              ||||||::::::   |||:::          |||
Db      38592 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 38651

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 :::::|||   ::::::      :::|||||||||   :::      ||||||
Db      38652 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 38708

RESULT 17
US-10-060-333-3
; Sequence 3, Application US/10060333
; Patent No. 6927054
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL000862DIV
;  CURRENT APPLICATION NUMBER: US/10/060,333
;  CURRENT FILING DATE:  2002-08-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 38844
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-060-333-3

Alignment Scores:
Pred. No.:               380           Length:          38844
Score:                   55.50         Matches:         10
Percent Similarity:      48.7%         Conservative:    9
Best Local Similarity:   25.6%         Mismatches:      11
Query Match:             34.7%         Indels:          9
DB:                      3             Gaps:            1

US-10-758-902-1 (1-30) x US-10-060-333-3 (1-38844)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr------------------------ 12
              ||||||::::::   |||:::          |||
Db      38592 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 38651
```

```
Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                  ::::::|||   :::::.      :::||||||||||   :::       ||||||
Db      38652 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 38708

RESULT 18
US-09-949-016-62787/c
; Sequence 62787, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62787
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-62787

Alignment Scores:
Pred. No.:              4.1          Length:        601
Score:                  53.50        Matches:       14
Percent Similarity:     46.2%        Conservative:  4
Best Local Similarity:  35.9%        Mismatches:    8
Query Match:            33.4%        Indels:        13
DB:                     3            Gaps:          1

US-10-758-902-1 (1-30) x US-09-949-016-62787 (1-601)

Qy          1 TyrAsnThrValSerPheAsnLeuGly------------------------------- 9
                |||       ::::::|||||||||||
Db        425 TATTTCTTTATTACATTTAATCTTGGCAGACCATCTCTGATCTTTGAACTATGAATGAAT 366

Qy          10 ------GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
                    :::       ||||||   ||||||      ||||||||||:::||||||
Db        365 CAGACCAAGTTTCTTCATTATCCTTTTTTCATCTCTTTTCTGCGTAATCAACTAGCT 309

RESULT 19
US-09-949-016-62788/c
; Sequence 62788, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62788
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-62788

Alignment Scores:
Pred. No.:              4.1          Length:        601
Score:                  53.50        Matches:       14
Percent Similarity:     46.2%        Conservative:  4
Best Local Similarity:  35.9%        Mismatches:    8
Query Match:            33.4%        Indels:        13
DB:                     3            Gaps:          1

US-10-758-902-1 (1-30) x US-09-949-016-62788 (1-601)

Qy          1 TyrAsnThrValSerPheAsnLeuGly------------------------------- 9
                |||       ::::::|||||||||||
Db        454 TATTTCTTTATTACATTTAATCTTGGCAGACCATCTCTGATCTTTGAACTATGAATGAAT 395

Qy          10 ------GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
                    :::       ||||||   ||||||      ||||||||||:::||||||
Db        394 CAGACCAAGTTTCTTCATTATCCTTTTTTCATCTCTTTTCTGCGTAATCAACTAGCT 338

RESULT 20
US-09-949-016-13553
; Sequence 13553, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13553
;   LENGTH: 103792
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(103792)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13553

Alignment Scores:
Pred. No.:              3e+03        Length:        103792
Score:                  53.50        Matches:       14
Percent Similarity:     46.2%        Conservative:  4
Best Local Similarity:  35.9%        Mismatches:    8
Query Match:            33.4%        Indels:        13
DB:                     3            Gaps:          1

US-10-758-902-1 (1-30) x US-09-949-016-13553 (1-103792)

Qy          1 TyrAsnThrValSerPheAsnLeuGly------------------------------- 9
                |||       ::::::|||||||||||
Db      12558 TATTTCTTTATTACATTTAATCTTGGCAGACCATCTCTGATCTTTGAACTATGAATGAAT 12617

Qy          10 ------GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
                    :::       ||||||   ||||||      ||||||||||:::||||||
Db      12618 CAGACCAAGTTTCTTCATTATCCTTTTTTCATCTCTTTTCTGCGTAATCAACTAGCT 12674

RESULT 21
US-09-949-016-12317
; Sequence 12317, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

```
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12317
;   LENGTH: 103993
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(103993)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12317

Alignment Scores:
Pred. No.:              3.01e+03        Length:         103993
Score:                  53.50           Matches:        14
Percent Similarity:     46.2%           Conservative:   4
Best Local Similarity:  35.9%           Mismatches:     8
Query Match:            33.4%           Indels:         13
DB:                     3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-949-016-12317 (1-103993)

Qy          1 TyrAsnThrValSerPheAsnLeuGly---------------------------------- 9
              |||      ::::::||||||||||||
Db      12558 TATTTCTTTATTACATTTAATCTTGGCAGACCATCTCTGATCTTTGAACTATGAATGAAT 12617

Qy         10 ------GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
                  :::          ||||||   ||||||      ||||||||||:::||||||
Db      12618 CAGACCAAGTTTCTTCATTATCCTTTTTTCATCTCTTTTCTGCGTAATCAACTAGCT 12674

RESULT 22
US-08-324-301-14
; Sequence 14, Application US/08324301
; Patent No. 5597569
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    APPLICANT:  Gawlak, Susan L.
;    APPLICANT:  Marquardt, Hans
;    TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;    TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONICA DIOICA
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,301
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/141,891
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0109A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-728-4800
;      TELEFAX:  206-727-3601
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  962 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
;      TISSUE TYPE:  leaf
US-08-324-301-14

Alignment Scores:
Pred. No.:              9.17            Length:         962
Score:                  53.00           Matches:        10
Percent Similarity:     76.5%           Conservative:   3
Best Local Similarity:  58.8%           Mismatches:     4
Query Match:            33.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-758-902-1 (1-30) x US-08-324-301-14 (1-962)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||   |||||||||:::::||||||   :::|||      |||||||||
Db        133 TACAAAACTTTTATAAGGAATCTGCGCACCAAACTCACGGTTGGAACTCCA 183

RESULT 23
US-09-428-034-3
; Sequence 3, Application US/09428034
; Patent No. 6428996
; GENERAL INFORMATION:
;  APPLICANT:  Cheng, Kuo-Joan
;  APPLICANT:  Liu, Jin-Hao
;  APPLICANT:  Tsai, Cheng-Fang
;  APPLICANT:  Hsu, Yih-Chin
;  TITLE OF INVENTION:  CELLULASE ENZYMES
;  FILE REFERENCE:  08919/036001
;  CURRENT APPLICATION NUMBER: US/09/428,034
;  CURRENT FILING DATE:  1999-10-27
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 999
;   TYPE: DNA
;   ORGANISM: Piromyces rhizinflata
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(996)
US-09-428-034-3

Alignment Scores:
Pred. No.:              14.4            Length:         999
Score:                  52.00           Matches:        10
Percent Similarity:     61.5%           Conservative:   6
Best Local Similarity:  38.5%           Mismatches:     10
Query Match:            32.5%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-428-034-3 (1-999)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::|||   |||   |||   |||      |||   ||||||:::::::::   :::
Db         19 AACTTTTTCTTAAATGAAATTTATGCTAATCCAAAATTCATTGAAGAAGTTGAAGATTCC 78

Qy         25 LeuAlaLysGlyThrPro 30
              :::   |||   ||||||
Db         79 ATTGAAAAATTAACTCCT 96
```

```
RESULT 24
US-09-428-034-1
; Sequence 1, Application US/09428034
; Patent No. 6428996
; GENERAL INFORMATION:
;  APPLICANT:  Cheng, Kuo-Joan
;  APPLICANT:  Liu, Jin-Hao
;  APPLICANT:  Tsai, Cheng-Fang
;  APPLICANT:  Hsu, Yih-Chin
;  TITLE OF INVENTION:  CELLULASE ENZYMES
;  FILE REFERENCE:  08919/036001
;  CURRENT APPLICATION NUMBER: US/09/428,034
;  CURRENT FILING DATE:  1999-10-27
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1364
;   TYPE: DNA
;   ORGANISM: Piromyces rhizinflata
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1128)
US-09-428-034-1

Alignment Scores:
Pred. No.:              21.5          Length:         1364
Score:                  52.00         Matches:        10
Percent Similarity:     61.5%         Conservative:   6
Best Local Similarity:  38.5%         Mismatches:     10
Query Match:            32.5%         Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-428-034-1 (1-1364)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::|||   |||   |||   |||      |||   ||||||:::::::::   :::
Db        148 AACTTTTTCTTAAATGAAATTTATGCTAATCCAAAATTCATTGAAGAAGTTGAAGATTCC 207

Qy         25 LeuAlaLysGlyThrPro 30
              :::   |||   ||||||
Db        208 ATTGAAAAATTAACTCCT 225

RESULT 25
US-09-902-540-3259
; Sequence 3259, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3259
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-3259

Alignment Scores:
Pred. No.:              21.8          Length:         1380
Score:                  52.00         Matches:        10
Percent Similarity:     71.4%         Conservative:   5
Best Local Similarity:  47.6%         Mismatches:     6
Query Match:            32.5%         Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-902-540-3259 (1-1380)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              |||   |||   ||||||:::|||      :::::::::||||||||   |||   :::
Db       1006 CTCTTCGAGGGCTATGAGTGGCCGGGCAACGTGCGCGAGCTGCGCAACGTGCTGGAGCGC 1065

Qy         28 Gly 28
              |||
Db       1066 GGC 1068

RESULT 26
US-09-902-540-1150
; Sequence 1150, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1150
;   LENGTH: 19954
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-1150

Alignment Scores:
Pred. No.:              667           Length:         19954
Score:                  52.00         Matches:        10
Percent Similarity:     71.4%         Conservative:   5
Best Local Similarity:  47.6%         Mismatches:     6
Query Match:            32.5%         Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-902-540-1150 (1-19954)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              |||   |||   ||||||:::|||      :::::::::||||||||   |||   :::
Db      12372 CTCTTCGAGGGCTATGAGTGGCCGGGCAACGTGCGCGAGCTGCGCAACGTGCTGGAGCGC 12431

Qy         28 Gly 28
              |||
Db      12432 GGC 12434

RESULT 27
US-09-949-016-15233
; Sequence 15233, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15233
;   LENGTH: 51822
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
```

```
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(51822)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15233

Alignment Scores:
Pred. No.:              2.27e+03        Length:         51822
Score:                  52.00           Matches:        11
Percent Similarity:     70.4%           Conservative:   8
Best Local Similarity:  40.7%           Mismatches:     7
Query Match:            32.5%           Indels:         1
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-15233 (1-51822)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGlu-TyrProThrPheIleGlnAspLeuArgAsnGl 24
              |||   |||:::||||||:::   ||| :::|||   |||::::::      ||||||::
Db      19503 TCCAAAAACATGGGTGAAAGTTCAGAATCACCCCCTTTTTGTGAAGACTTTCCGTAATGA 19562

Qy         24 uLeuAlaLysGlyThrPro 30
              :|||   :::   :::|||
Db      19563 TCTTCCCAGAAAGTCCCCC 19581

RESULT 28
US-09-902-540-8868
; Sequence 8868, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8868
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-8868

Alignment Scores:
Pred. No.:              11.5            Length:         717
Score:                  51.50           Matches:        14
Percent Similarity:     56.2%           Conservative:   4
Best Local Similarity:  43.8%           Mismatches:     11
Query Match:            32.2%           Indels:         3
DB:                     3               Gaps:           2

US-10-758-902-1 (1-30) x US-09-902-540-8868 (1-717)

Qy          1 TyrAsnThrVal------SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              |||   |||:::      ||||||      ||||||            ||||||   :::
Db        178 TACAAGACACTCGGCGGCTCATTCACC---GGTGAGCTCGTCGTGGACCCGACTCATCTG 234

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              :::|||:::|||      ||||||   |||   |||
Db        235 CGGGACATGCGCCGTCGGCTCGCGGCTGGAGAGCCA 270

RESULT 29
US-09-902-540-1071
; Sequence 1071, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1071
;   LENGTH: 12028
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-1071

Alignment Scores:
Pred. No.:              427             Length:         12028
Score:                  51.50           Matches:        14
Percent Similarity:     56.2%           Conservative:   4
Best Local Similarity:  43.8%           Mismatches:     11
Query Match:            32.2%           Indels:         3
DB:                     3               Gaps:           2

US-10-758-902-1 (1-30) x US-09-902-540-1071 (1-12028)

Qy          1 TyrAsnThrVal------SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              |||   |||:::      ||||||      ||||||            ||||||   :::
Db        564 TACAAGACACTCGGCGGCTCATTCACC---GGTGAGCTCGTCGTGGACCCGACTCATCTG 620

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              :::|||:::|||      ||||||   |||   |||
Db        621 CGGGACATGCGCCGTCGGCTCGCGGCTGGAGAGCCA 656

RESULT 30
US-09-531-120-204
; Sequence 204, Application US/09531120
; Patent No. 6972197
; GENERAL INFORMATION:
;  APPLICANT: PREUSS, DAPHNE
;  APPLICANT:  COPENHAVER, GREGORY
;  TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
;  FILE REFERENCE: ARCD:309US
;  CURRENT APPLICATION NUMBER: US/09/531,120
;  CURRENT FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,219
;  PRIOR FILING DATE: 1999-03-18
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 204
;   LENGTH: 109974
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-531-120-204

Alignment Scores:
Pred. No.:              7.27e+03        Length:         109974
Score:                  51.50           Matches:        10
Percent Similarity:     69.6%           Conservative:   6
Best Local Similarity:  43.5%           Mismatches:     4
Query Match:            32.2%           Indels:         3
DB:                     4               Gaps:           1

US-10-758-902-1 (1-30) x US-09-531-120-204 (1-109974)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAsp---------LeuArgAsnGluLeuAlaLys 27
              |||   :::|||||||||||||   ::::::         ||||||:::   ::::::
Db      23327 GCCGAGAAGTATCCTACCTTCTTTGAAGAACTCCTCACACTGAGAAGTTCAATCAGTTCG 23386

Qy         28 GlyThrPro 30
              |||||||||
Db      23387 GGAACCCCG 23395

RESULT 31
US-09-134-000C-1566
; Sequence 1566, Application US/09134000C
; Patent No. 6617156
```

```
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1566
;   LENGTH: 3702
;   TYPE: DNA
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-1566

Alignment Scores:
Pred. No.:              116          Length:        3702
Score:                  51.00        Matches:       10
Percent Similarity:     57.7%        Conservative:  5
Best Local Similarity:  38.5%        Mismatches:    11
Query Match:            31.9%        Indels:        0
DB:                     3            Gaps:          0

US-10-758-902-1 (1-30) x US-09-134-000C-1566 (1-3702)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||   |||   |||:::   |||          |||          :::
Db       2710 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2769

Qy         21 LeuArgAsnGluLeuAla 26
                  |||:::::::::
Db       2770 ACATTGAACCAGATGTCT 2787

RESULT 32
US-09-071-035-403
; Sequence 403, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  403:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4249 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-071-035-403

Alignment Scores:
Pred. No.:              138          Length:        4249
Score:                  51.00        Matches:       10
Percent Similarity:     57.7%        Conservative:  5
Best Local Similarity:  38.5%        Mismatches:    11
Query Match:            31.9%        Indels:        0
DB:                     3            Gaps:          0

US-10-758-902-1 (1-30) x US-09-071-035-403 (1-4249)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||   |||   |||:::   |||          |||          :::
Db       2618 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2677

Qy         21 LeuArgAsnGluLeuAla 26
                  |||:::::::::
Db       2678 ACATTGAACCAGATGTCT 2695

RESULT 33
US-10-206-576-403
; Sequence 403, Application US/10206576
; Patent No. 6913907
;  GENERAL INFORMATION:
;       APPLICANT: Choi et al.
;       TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;       NUMBER OF SEQUENCES: 497
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Human Genome Sciences, Inc.
;            STREET: 9410 Key West Avenue
;            CITY: Rockville
;            STATE: Maryland
;            COUNTRY: USA
;            ZIP: 20850
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: Dell Latitude
;            OPERATING SYSTEM: Windows 98
;            SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/206,576
;            FILING DATE: 29-Jul-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 09/071,035
;            FILING DATE: 1998-05-04
;            APPLICATION NUMBER: US 60/046,655
;            FILING DATE: 1997-05-16
;            APPLICATION NUMBER: US 60/044,031
;            FILING DATE: 1997-05-06
;            APPLICATION NUMBER: US 60/066,009
;            FILING DATE: 1997-11-14
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hyman, Mark J.
;            REGISTRATION NUMBER: 46,789
;            REFERENCE/DOCKET NUMBER: PB369P1D1
;  INFORMATION FOR SEQ ID NO: 403:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 4249 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 403:
US-10-206-576-403

Alignment Scores:
Pred. No.:              138          Length:        4249
Score:                  51.00        Matches:       10
Percent Similarity:     57.7%        Conservative:  5
Best Local Similarity:  38.5%        Mismatches:    11
```

```
Query Match:            31.9%          Indels:        0
DB:                     3              Gaps:          0

US-10-758-902-1 (1-30) x US-10-206-576-403 (1-4249)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||   |||   |||:::   |||         |||         :::
Db       2618 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2677

Qy         21 LeuArgAsnGluLeuAla 26
                ||||:::::::::
Db       2678 ACATTGAACCAGATGTCT 2695

RESULT 34
US-09-071-035-401
; Sequence 401, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  401:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4359 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-071-035-401

Alignment Scores:
Pred. No.:              143            Length:        4359
Score:                  51.00          Matches:       10
Percent Similarity:     57.7%          Conservative:  5
Best Local Similarity:  38.5%          Mismatches:    11
Query Match:            31.9%          Indels:        0
DB:                     3              Gaps:          0

US-10-758-902-1 (1-30) x US-09-071-035-401 (1-4359)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||   |||   |||:::   |||         |||         :::
Db       2713 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2772

Qy         21 LeuArgAsnGluLeuAla 26
                ||||:::::::::
Db       2773 ACATTGAACCAGATGTCT 2790
```

```
RESULT 35
US-10-206-576-401
; Sequence 401, Application US/10206576
; Patent No. 6913907
;  GENERAL INFORMATION:
;       APPLICANT: Choi et al.
;       TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;       NUMBER OF SEQUENCES: 497
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Human Genome Sciences, Inc.
;            STREET: 9410 Key West Avenue
;            CITY: Rockville
;            STATE: Maryland
;            COUNTRY: USA
;            ZIP: 20850
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: Dell Latitude
;            OPERATING SYSTEM: Windows 98
;            SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/206,576
;            FILING DATE: 29-Jul-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 09/071,035
;            FILING DATE: 1998-05-04
;            APPLICATION NUMBER: US 60/046,655
;            FILING DATE: 1997-05-16
;            APPLICATION NUMBER: US 60/044,031
;            FILING DATE: 1997-05-06
;            APPLICATION NUMBER: US 60/066,009
;            FILING DATE: 1997-11-14
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hyman, Mark J.
;            REGISTRATION NUMBER: 46,789
;            REFERENCE/DOCKET NUMBER: PB369P1D1
;   INFORMATION FOR SEQ ID NO: 401:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 4359 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 401:
US-10-206-576-401

Alignment Scores:
Pred. No.:              143            Length:        4359
Score:                  51.00          Matches:       10
Percent Similarity:     57.7%          Conservative:  5
Best Local Similarity:  38.5%          Mismatches:    11
Query Match:            31.9%          Indels:        0
DB:                     3              Gaps:          0

US-10-758-902-1 (1-30) x US-10-206-576-401 (1-4359)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||   |||   |||:::   |||         |||         :::
Db       2713 TACAATACGGTCTCTGCAAACGCTGGCCAAATCTATACAGAAACAACAATCGACTCTGAA 2772

Qy         21 LeuArgAsnGluLeuAla 26
                ||||:::::::::
Db       2773 ACATTGAACCAGATGTCT 2790

RESULT 36
US-09-736-116-60
; Sequence 60, Application US/09736116
; Patent No. 6727085
; GENERAL INFORMATION:
;  APPLICANT: Sejersgard, Tina
;  APPLICANT:  Mikkelsen, Frank
;  TITLE OF INVENTION: Subtilase variants having an improved wash peformance on egg stair
;  FILE REFERENCE: 6108.410
```

```
;  CURRENT APPLICATION NUMBER: US/09/736,116
;  CURRENT FILING DATE:  2001-05-24
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 60
;   LENGTH: 13222
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-736-116-60

Alignment Scores:
Pred. No.:              591          Length:         13222
Score:                  51.00        Matches:        12
Percent Similarity:     44.4%        Conservative:   4
Best Local Similarity:  33.3%        Mismatches:     14
Query Match:            31.9%        Indels:         6
DB:                     3            Gaps:           1

US-10-758-902-1 (1-30) x US-09-736-116-60 (1-13222)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||         ||||||||||||         :::   |||   ::::::
Db       9100 CATAATAACTATAAATTCAATTTGGGTCATTTACTTCAGGTACCTTATTATCTTTCTCTT 9159

Qy         21 LeuArg-----------------AsnGluLeuAlaLysGlyThrPro 30
                 |||                 |||   |||   ||||||   |||
Db       9160 TTTCGTAAAAGTCCATATCCACAAAACCCTTTGTTAAAGGGCGAACCA 9207

RESULT 37
US-09-306-446C-15
; Sequence 15, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
;  APPLICANT: KIM, Dong Soo
;  APPLICANT:  KIM, Chul Geun
;  APPLICANT:  NAM, Yoon Kwon
;  APPLICANT:  NOH, Jae Koo
;  APPLICANT:  CHO, Kyou Nam
;  TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
;  FILE REFERENCE: P06344US0/BAS
;  CURRENT APPLICATION NUMBER: US/09/306,446C
;  CURRENT FILING DATE:  1999-05-06
;  PRIOR APPLICATION NUMBER: KR 98/20255
;  PRIOR FILING DATE: 1998-06-01
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 670
;   TYPE: DNA
;   ORGANISM: Misgurnus mizolepus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (15)..(644)
US-09-306-446C-15

Alignment Scores:
Pred. No.:              19.4         Length:         670
Score:                  50.00        Matches:        12
Percent Similarity:     55.2%        Conservative:   4
Best Local Similarity:  41.4%        Mismatches:     11
Query Match:            31.2%        Indels:         2
DB:                     3            Gaps:           1

US-10-758-902-1 (1-30) x US-09-306-446C-15 (1-670)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrPro------ThrPheIleGlnAspLeu 21
              :::||||||   |||   |||::::::|||||||||      |||           :::
Db        300 ATCTCCTTCCGCCTCATTGAGTCTTGGGAGTATCCCAGCCAGACCCTTAGTGGAACCATC 359

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
                |||   |||     |||   |||
Db        360 TCAAACAGCCTGACCATCGGCAACCCC 386

RESULT 38
US-09-306-446C-8
; Sequence 8, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
;  APPLICANT: KIM, Dong Soo
;  APPLICANT:  KIM, Chul Geun
;  APPLICANT:  NAM, Yoon Kwon
;  APPLICANT:  NOH, Jae Koo
;  APPLICANT:  CHO, Kyou Nam
;  TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
;  FILE REFERENCE: P06344US0/BAS
;  CURRENT APPLICATION NUMBER: US/09/306,446C
;  CURRENT FILING DATE:  1999-05-06
;  PRIOR APPLICATION NUMBER: KR 98/20255
;  PRIOR FILING DATE: 1998-06-01
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 5108
;   TYPE: DNA
;   ORGANISM: Misgurnus mizolepus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2910)..(2921)
;   NAME/KEY: CDS
;   LOCATION: (3185)..(3322)
;   NAME/KEY: CDS
;   LOCATION: (3485)..(3601)
;   NAME/KEY: CDS
;   LOCATION: (3762)..(3923)
;   NAME/KEY: CDS
;   LOCATION: (4203)..(4403)
US-09-306-446C-8

Alignment Scores:
Pred. No.:              262          Length:         5108
Score:                  50.00        Matches:        12
Percent Similarity:     55.2%        Conservative:   4
Best Local Similarity:  41.4%        Mismatches:     11
Query Match:            31.2%        Indels:         2
DB:                     3            Gaps:           1

US-10-758-902-1 (1-30) x US-09-306-446C-8 (1-5108)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrPro------ThrPheIleGlnAspLeu 21
              :::||||||   |||   |||::::::|||||||||      |||           :::
Db       3780 ATCTCCTTCCGCCTCATTGAGTCTTGGGAGTATCCCAGCCAGACCCTTAGTGGAACCATC 3839

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
                |||   |||     |||   |||
Db       3840 TCAAACAGCCTGACCATCGGCAACCCC 3866

RESULT 39
US-09-949-016-15845
; Sequence 15845, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15845
;   LENGTH: 133559
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(133559)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15845

Alignment Scores:
Pred. No.:              1.71e+04        Length:         133559
Score:                  50.00           Matches:        9
Percent Similarity:     75.0%           Conservative:   6
Best Local Similarity:  45.0%           Mismatches:     5
Query Match:            31.2%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-15845 (1-133559)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   :::   |||   ||||||||||||||   :::   |||::::::::|||
Db     131657 TTTAATTGTTTAGATTTCTGCCTTGGTGAGGCATATCTTCATTAGACTTATCTAAAGGAC 131716

RESULT 40
US-09-602-787A-13
; Sequence 13, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr"ger, Burkhard
;  APPLICANT:  Sch"der, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CP
;  CURRENT APPLICATION NUMBER: US/09/602,787A
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932182.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932190.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932191.4
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932209.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932212.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932227.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932228.7
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932229.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932230.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932927.3
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933005.0
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933006.9
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19940764.9
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940765.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940766.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940830.0
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940831.9
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940832.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940833.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19941378.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941379.7
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941395.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19942077.7
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942078.5
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942079.3
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942088.2
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 13
;   LENGTH: 4953
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(4930)
;   OTHER INFORMATION: RXA02582
US-09-602-787A-13

Alignment Scores:
Pred. No.:              308             Length:         4953
Score:                  49.50           Matches:        11
Percent Similarity:     65.0%           Conservative:   2
Best Local Similarity:  55.0%           Mismatches:     6
Query Match:            30.9%           Indels:         1
DB:                     3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-602-787A-13 (1-4953)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||   |||:::   |||          |||   :::|||   |||
Db        311 GCTTATGAGTACCCAACG---ATCCGTAGTTTGGCGCAGCGCCTTGTTGAGGGCGAGCCT 367

RESULT 41
US-09-602-787A-55
; Sequence 55, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr"ger, Burkhard
;  APPLICANT:  Sch"der, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
```

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 55
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(4930)
; OTHER INFORMATION: RXA02582
US-09-602-787A-55

Alignment Scores:

Pred. No.:	308	Length:	4953
Score:	49.50	Matches:	11
Percent Similarity:	65.0%	Conservative:	2
Best Local Similarity:	55.0%	Mismatches:	6
Query Match:	30.9%	Indels:	1
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-602-787A-55 (1-4953)

```
Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||  |||:::  |||        |||  :::|||  |||
Db        311 GCTTATGAGTACCCAACG---ATCCGTAGTTTGGCGCAGCGCCTTGTTGAGGGCGAGCCT 367
```

RESULT 42
US-09-573-080A-22/c
; Sequence 22, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATIN
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 6053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(6053)
; OTHER INFORMATION: herv18
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
; TITLE: Prototypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-__
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE: ____-__-__
; DATABASE ENTRY DATE: 1996-01-26
US-09-573-080A-22

Alignment Scores:

Pred. No.:	398	Length:	6053
Score:	49.50	Matches:	13
Percent Similarity:	65.5%	Conservative:	6
Best Local Similarity:	44.8%	Mismatches:	9
Query Match:	30.9%	Indels:	2
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-573-080A-22 (1-6053)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::   |||         |||   |||:::   :::|||   |||||||||||||||
Db       4357 AACAGTGCCTCCACTGGGGCTGGGCC-GCCTTTCCGTGGCCA---TTCATTCAAGATTTG 4302

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
                :::::::::     |||||||||
Db       4301 GAGCACCAGGTCCAGCCTGGAACTCCA 4275
```

RESULT 43
US-09-854-867-22/c
; Sequence 22, Application US/09854867
; Patent No. 7014997
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 6053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(6053)
; OTHER INFORMATION: herv18
US-09-854-867-22

Alignment Scores:

Pred. No.:	398	Length:	6053
Score:	49.50	Matches:	13
Percent Similarity:	65.5%	Conservative:	6
Best Local Similarity:	44.8%	Mismatches:	9
Query Match:	30.9%	Indels:	2
DB:	5	Gaps:	1

US-10-758-902-1 (1-30) x US-09-854-867-22 (1-6053)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::   |||         |||   |||:::   :::|||   |||||||||||||||
Db       4357 AACAGTGCCTCCACTGGGGCTGGGCC-GCCTTTCCGTGGCCA---TTCATTCAAGATTTG 4302

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
                :::::::::     |||||||||
Db       4301 GAGCACCAGGTCCAGCCTGGAACTCCA 4275
```

RESULT 44
US-09-328-352-3637
; Sequence 3637, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3637
; LENGTH: 6567
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3637

Alignment Scores:

Pred. No.:	442	Length:	6567
Score:	49.50	Matches:	11
Percent Similarity:	69.6%	Conservative:	5
Best Local Similarity:	47.8%	Mismatches:	6
Query Match:	30.9%	Indels:	1
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-328-352-3637 (1-6567)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   :::   ||||||  |||         ||||||::::::|||   |||:::
Db        370 AGTTTGAATAAACCGTATGAA---CCTGTTTCATACCAAGACATACAAAATGTTTTGTCT 426

Qy         27 LysGlyThr 29
              |||||||||
Db        427 AAAGGTACG 435
```

RESULT 45
US-09-221-017B-615
; Sequence 615, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 615:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORYPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...949
US-09-221-017B-615

Alignment Scores:

```
Pred. No.:              45.5          Length:        949
Score:                  49.00         Matches:       12
Percent Similarity:     54.8%         Conservative:  5
Best Local Similarity:  38.7%         Mismatches:    10
Query Match:            30.6%         Indels:        4
DB:                     3             Gaps:          1

US-10-758-902-1 (1-30) x US-09-221-017B-615 (1-949)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThr---------- 16
              |||:::   :::         |||   |||   |||       |||:::
Db        558 TATTCGGAGATCAAACGTAAGTTGGTAGAAGACTATCACATCCCATCGCATGAAGTACGC 617

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              |||||||||:::   :::||||||   ||||||
Db        618 TTTATCCAAGAGTGCAAGAACGAGAAAGCCAAG 650

RESULT 46
US-08-841-349-3
; Sequence 3, Application US/08841349B
; Patent No. 5955594
; GENERAL INFORMATION:
;  APPLICANT: MISHRA, LOPA
;  TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .
;  FILE REFERENCE: XX/PO4470US0
;  CURRENT APPLICATION NUMBER: US/08/841,349B
;  CURRENT FILING DATE: 1997-04-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 6960
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (333)..(6794)
US-08-841-349-3

Alignment Scores:
Pred. No.:              583           Length:        6960
Score:                  49.00         Matches:       10
Percent Similarity:     60.0%         Conservative:  5
Best Local Similarity:  40.0%         Mismatches:    10
Query Match:            30.6%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x US-08-841-349-3 (1-6960)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||       ||||||:::   ||||||:::   |||   :::|||:::          |||
Db       5460 TCCCATGAGTTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGGTTCCGAGAA 5519

Qy         25 LeuAlaLysGlyThr 29
              |||:::   |||
Db       5520 TTTGCTCGAGACACA 5534

RESULT 47
US-09-431-184A-3
; Sequence 3, Application US/09431184A
; Patent No. 6642362
; GENERAL INFORMATION:
;  APPLICANT: MISHRA, LOPA
;  TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
;  FILE REFERENCE: P04470US1/BAS
;  CURRENT APPLICATION NUMBER: US/09/431,184A
;  CURRENT FILING DATE:  1999-11-01
;  PRIOR APPLICATION NUMBER: PCT/US98/08656
;  PRIOR FILING DATE: 1998-04-30
;  PRIOR APPLICATION NUMBER: US 08/841,349
;  PRIOR FILING DATE: 1997-04-30
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 6960
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (333)..(6794)
US-09-431-184A-3

Alignment Scores:
Pred. No.:              583           Length:        6960
Score:                  49.00         Matches:       10
Percent Similarity:     60.0%         Conservative:  5
Best Local Similarity:  40.0%         Mismatches:    10
Query Match:            30.6%         Indels:        0
DB:                     3             Gaps:          0

US-10-758-902-1 (1-30) x US-09-431-184A-3 (1-6960)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||       ||||||:::   ||||||:::   |||   :::|||:::          |||
Db       5460 TCCCATGAGTTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGGTTCCGAGAA 5519

Qy         25 LeuAlaLysGlyThr 29
              |||:::   |||
Db       5520 TTTGCTCGAGACACA 5534

RESULT 48
US-08-841-349-5
; Sequence 5, Application US/08841349B
; Patent No. 5955594
; GENERAL INFORMATION:
;  APPLICANT: MISHRA, LOPA
;  TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .
;  FILE REFERENCE: XX/PO4470US0
;  CURRENT APPLICATION NUMBER: US/08/841,349B
;  CURRENT FILING DATE: 1997-04-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 8176
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-08-841-349-5

Alignment Scores:
Pred. No.:              717           Length:        8176
Score:                  49.00         Matches:       10
Percent Similarity:     60.0%         Conservative:  5
Best Local Similarity:  40.0%         Mismatches:    10
Query Match:            30.6%         Indels:        0
DB:                     2             Gaps:          0

US-10-758-902-1 (1-30) x US-08-841-349-5 (1-8176)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||       ||||||:::   ||||||:::   |||   :::|||:::          |||
Db       5460 TCCCATGAGTTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGGTTCCGAGAA 5519

Qy         25 LeuAlaLysGlyThr 29
              |||:::   |||
Db       5520 TTTGCTCGAGACACA 5534

RESULT 49
US-09-431-184A-5
; Sequence 5, Application US/09431184A
; Patent No. 6642362
; GENERAL INFORMATION:
;  APPLICANT: MISHRA, LOPA
;  TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
;  FILE REFERENCE: P04470US1/BAS
;  CURRENT APPLICATION NUMBER: US/09/431,184A
;  CURRENT FILING DATE:  1999-11-01
;  PRIOR APPLICATION NUMBER: PCT/US98/08656
```

```
;  PRIOR FILING DATE: 1998-04-30
;  PRIOR APPLICATION NUMBER: US 08/841,349
;  PRIOR FILING DATE: 1997-04-30
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 8176
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-431-184A-5

Alignment Scores:
Pred. No.:              717          Length:        8176
Score:                  49.00        Matches:       10
Percent Similarity:     60.0%        Conservative:  5
Best Local Similarity:  40.0%        Mismatches:    10
Query Match:            30.6%        Indels:        0
DB:                     3            Gaps:          0

US-10-758-902-1 (1-30) x US-09-431-184A-5 (1-8176)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5460 TCCCATGAGTTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGGTTCCGAGAA 5519

Qy         25 LeuAlaLysGlyThr 29
                ||||:::   |||
Db       5520 TTTGCTCGAGACACA 5534

RESULT 50
US-09-949-016-15602
; Sequence 15602, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15602
;   LENGTH: 134890
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15602

Alignment Scores:
Pred. No.:              2.6e+04      Length:        134890
Score:                  49.00        Matches:       11
Percent Similarity:     60.9%        Conservative:  3
Best Local Similarity:  47.8%        Mismatches:    7
Query Match:            30.6%        Indels:        2
DB:                     3            Gaps:          1

US-10-758-902-1 (1-30) x US-09-949-016-15602 (1-134890)

Qy          9 GlyGluAlaTyrGlu------TyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||   |||           ||||||::::::   ||||||   |||       |||
Db      30842 GGGGAGGAGTATGTGCGTTTCATACCAACATACCTGAGTGATCTGACAAATGCTTGTGCT 30901

Qy         27 LysGlyThr 29
              :::||||||
Db      30902 GAGGGGACT 30910

RESULT 51
```

```
US-09-804-471A-3/c
; Sequence 3, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001164
;  CURRENT APPLICATION NUMBER: US/09/804,471A
;  CURRENT FILING DATE:  2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 174493
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174493)
;   OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Alignment Scores:
Pred. No.:              3.59e+04     Length:        174493
Score:                  49.00        Matches:       16
Percent Similarity:     62.1%        Conservative:  2
Best Local Similarity:  55.2%        Mismatches:    9
Query Match:            30.6%        Indels:        2
DB:                     3            Gaps:          2

US-10-758-902-1 (1-30) x US-09-804-471A-3 (1-174493)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||      |||   |||   |||          |||   |||||||||:::   |||
Db      55197 AATACGTTCCTTTTCCTTTTGGTTGAAACTAAAACATAT---ACATTTATCAGAGCCTTA 55141

Qy         22 ArgAsnGluLeuAlaLys---GlyThr 29
              ||||||||||||   :::   ||||||
Db      55140 AGAAATGAGCTTCACAGGCTAGGCACA 55114

RESULT 52
US-10-238-709-3/c
; Sequence 3, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001164DIV
;  CURRENT APPLICATION NUMBER: US/10/238,709
;  CURRENT FILING DATE:  2002-09-11
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 174493
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174493)
;   OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

Alignment Scores:
Pred. No.:              3.59e+04     Length:        174493
Score:                  49.00        Matches:       16
Percent Similarity:     62.1%        Conservative:  2
Best Local Similarity:  55.2%        Mismatches:    9
Query Match:            30.6%        Indels:        2
DB:                     3            Gaps:          2
```

```
US-10-758-902-1 (1-30) x US-10-238-709-3 (1-174493)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||      |||   |||   |||         |||   |||||||||:::   |||
Db      55197 AATACGTTCCTTTTCCTTTTGGTTGAAACTAAAACATAT---ACATTTATCAGAGCCTTA 55141

Qy         22 ArgAsnGluLeuAlaLys---GlyThr 29
              ||||||||||||   :::   ||||||
Db      55140 AGAAATGAGCTTCACAGGCTAGGCACA 55114

RESULT 53
US-10-724-594-3/c
; Sequence 3, Application US/10724594
; Patent No. 6946276
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001164DIV II
;  CURRENT APPLICATION NUMBER: US/10/724,594
;  CURRENT FILING DATE:  2003-12-02
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 174493
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174493)
;   OTHER INFORMATION: n = A,T,C or G
US-10-724-594-3

Alignment Scores:
Pred. No.:              3.59e+04      Length:          174493
Score:                  49.00         Matches:         16
Percent Similarity:     62.1%         Conservative:    2
Best Local Similarity:  55.2%         Mismatches:      9
Query Match:            30.6%         Indels:          2
DB:                     3             Gaps:            2

US-10-758-902-1 (1-30) x US-10-724-594-3 (1-174493)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||      |||   |||   |||         |||   |||||||||:::   |||
Db      55197 AATACGTTCCTTTTCCTTTTGGTTGAAACTAAAACATAT---ACATTTATCAGAGCCTTA 55141

Qy         22 ArgAsnGluLeuAlaLys---GlyThr 29
              ||||||||||||   :::   ||||||
Db      55140 AGAAATGAGCTTCACAGGCTAGGCACA 55114

RESULT 54
US-09-949-016-15347/c
; Sequence 15347, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15347
;   LENGTH: 80706
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(80706)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15347

Alignment Scores:
Pred. No.:              1.65e+04      Length:          80706
Score:                  48.50         Matches:         11
Percent Similarity:     66.7%         Conservative:    1
Best Local Similarity:  61.1%         Mismatches:      5
Query Match:            30.3%         Indels:          1
DB:                     3             Gaps:            1

US-10-758-902-1 (1-30) x US-09-949-016-15347 (1-80706)

Qy          3 ThrValSerPheAsnLeu---GlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||   ||||||||||||   |||       |||   ||||||   ||||||:::
Db       1438 ACTTTCTCATTTAACCTGTGAGGTAGGTATTACCATTATCCCCATTTTATAGAG 1385

RESULT 55
US-09-513-999C-30353
; Sequence 30353, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 30353
;   LENGTH: 162
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-30353

Alignment Scores:
Pred. No.:              7.09          Length:          162
Score:                  48.00         Matches:         9
Percent Similarity:     68.4%         Conservative:    4
Best Local Similarity:  47.4%         Mismatches:      6
Query Match:            30.0%         Indels:          0
DB:                     3             Gaps:            0

US-10-758-902-1 (1-30) x US-09-513-999C-30353 (1-162)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              :::|||   :::   ||||||   :::||||||||||||   :::|||      |||
Db        104 CAAGCCCCACAAGTGCCCACATTGCTCCAAGACCTTCGCCAACAGCTCCTACCTGGC 160

RESULT 56
US-09-401-064-194
; Sequence 194, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Secrist, Heather
;  APPLICANT: Benson, Darin R.
;  APPLICANT: Meagher, Madeline Joy
;  APPLICANT: Stolk, John A.
;  APPLICANT: Wang, Tongtong
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
;  TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
```

```
;  FILE REFERENCE: 210121.471C2
;  CURRENT APPLICATION NUMBER: US/09/401,064
;  CURRENT FILING DATE: 1999-09-22
;  NUMBER OF SEQ ID NOS: 371
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 194
;   LENGTH: 405
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-401-064-194

Alignment Scores:
Pred. No.:                22.9          Length:          405
Score:                    48.00         Matches:         9
Percent Similarity:       68.4%         Conservative:    4
Best Local Similarity:    47.4%         Mismatches:      6
Query Match:              30.0%         Indels:          0
DB:                       3             Gaps:            0

US-10-758-902-1 (1-30) x US-09-401-064-194 (1-405)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              :::|||   :::   ||||||   :::|||||||||||||   :::|||       |||
Db         69 CAAGCCCCACAAGTGCCCACATTGCTCCAAGACCTTCGCCAACAGCTCCTACCTGGC 125

RESULT 57
US-09-949-016-5729
; Sequence 5729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5729
;   LENGTH: 887
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5729

Alignment Scores:
Pred. No.:                62.5          Length:          887
Score:                    48.00         Matches:         9
Percent Similarity:       61.5%         Conservative:    7
Best Local Similarity:    34.6%         Mismatches:      10
Query Match:              30.0%         Indels:          0
DB:                       3             Gaps:            0

US-10-758-902-1 (1-30) x US-09-949-016-5729 (1-887)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              |||   |||   :::|||||||||   |||::::::   :::   :::          |||
Db        573 ACATCCAGCCAGTCCCTGGGGGAGACCTATGACTTCGACAGCATCATGCATTACGCTCGG 632

Qy         23 AsnGluLeuAlaLysGly 28
              |||      ::::::|||
Db        633 AACACATTCTCCAGGGGC 650

RESULT 58
US-09-949-016-5730
; Sequence 5730, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5730
;   LENGTH: 887
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5730

Alignment Scores:
Pred. No.:                62.5          Length:          887
Score:                    48.00         Matches:         9
Percent Similarity:       61.5%         Conservative:    7
Best Local Similarity:    34.6%         Mismatches:      10
Query Match:              30.0%         Indels:          0
DB:                       3             Gaps:            0

US-10-758-902-1 (1-30) x US-09-949-016-5730 (1-887)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              |||   |||   :::|||||||||   |||::::::   :::   :::          |||
Db        573 ACATCCAGCCAGTCCCTGGGGGAGACCTATGACTTCGACAGCATCATGCATTACGCTCGG 632

Qy         23 AsnGluLeuAlaLysGly 28
              |||      ::::::|||
Db        633 AACACATTCTCCAGGGGC 650

RESULT 59
US-09-949-016-5731
; Sequence 5731, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5731
;   LENGTH: 887
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5731

Alignment Scores:
Pred. No.:                62.5          Length:          887
Score:                    48.00         Matches:         9
Percent Similarity:       61.5%         Conservative:    7
Best Local Similarity:    34.6%         Mismatches:      10
Query Match:              30.0%         Indels:          0
DB:                       3             Gaps:            0

US-10-758-902-1 (1-30) x US-09-949-016-5731 (1-887)
```

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              |||   |||   :::|||||||||   |||::::::   :::   :::         |||
Db        573 ACATCCAGCCAGTCCCTGGGGGAGACCTATGACTTCGACAGCATCATGCATTACGCTCGG 632

Qy         23 AsnGluLeuAlaLysGly 28
              |||      ::::::|||
Db        633 AACACATTCTCCAGGGGC 650

RESULT 60
US-09-549-831-12
; Sequence 12, Application US/09549831
; Patent No. 6429305
; GENERAL INFORMATION:
;  APPLICANT:  Chang, Chi-Yao
;  APPLICANT:  Chang, Chia-Ching
;  APPLICANT:  Leu, Kuen-Lin
;  APPLICANT:  Tsai, Chih-Tung
;  APPLICANT:  Ting, Jing-Wen
;  APPLICANT:  Lin, Chih-Hung
;  TITLE OF INVENTION:  FISH GROWTH HORMONES
;  FILE REFERENCE:  08191-039001
;  CURRENT APPLICATION NUMBER: US/09/549,831
;  CURRENT FILING DATE:  2000-04-14
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 1083
;   TYPE: DNA
;   ORGANISM: Danio rerio
US-09-549-831-12

Alignment Scores:
Pred. No.:              80.7          Length:          1083
Score:                  48.00         Matches:         11
Percent Similarity:     55.2%         Conservative:    5
Best Local Similarity:  37.9%         Mismatches:      11
Query Match:            30.0%         Indels:          2
DB:                     3             Gaps:            1

US-10-758-902-1 (1-30) x US-09-549-831-12 (1-1083)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrPro------ThrPheIleGlnAspLeu 21
              :::||||||   |||   |||:::::::|||:::|||      |||          :::
Db        283 ATCTCTTTCCGCCTCATTGAATCCTGGGAGTTTCCCAGCCAGACCTTGAGCTCCACTATC 342

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
              |||   |||      |||   |||
Db        343 TCAAACAGCCTGACCATCGGAAACCCC 369

RESULT 61
US-08-911-321-2
; Sequence 2, Application US/08911321
; Patent No. 6010703
;  GENERAL INFORMATION:
;    APPLICANT:  Roger K. Maes and Stephen J. Spatz
;    TITLE OF INVENTION:  Recombinant Poxvirus
;    TITLE OF INVENTION:  Vaccine Against
;    TITLE OF INVENTION:  Feline Rhinotracheitis
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ian C. McLeod
;      STREET:  2190  Commons Parkway
;      CITY:  Okemos
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  48864
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 Kb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/911,321
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/096,183
;      FILING DATE:  July 26, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ian C. McLeod
;      REGISTRATION NUMBER:  20,931
;      REFERENCE/DOCKET NUMBER:  MSU 4.1-166
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (517) 347-4100
;      TELEFAX:  (517) 347-4103
;      TELEX:  No. 6010703e
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1119
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:
;      DESCRIPTION:  DNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Feline herpesvirus
;      STRAIN:  1
;      INDIVIDUAL ISOLATE:  C-27
;      CELL TYPE:  N/A
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:  Sequencing
;      OTHER INFORMATION:  DNA and deduced
;      OTHER INFORMATION:  polypeptide
US-08-911-321-2

Alignment Scores:
Pred. No.:              84.2          Length:          1119
Score:                  48.00         Matches:         11
Percent Similarity:     66.7%         Conservative:    5
Best Local Similarity:  45.8%         Mismatches:      6
Query Match:            30.0%         Indels:          2
DB:                     3             Gaps:            2

US-10-758-902-1 (1-30) x US-08-911-321-2 (1-1119)

Qy          1 TyrAsn---ThrValSer---PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              ||||||   |||:::|||   |||   :::   :::      |||||||||   |||:::
Db        307 TATAACGCGACTATAAGTTGGTTTAAGGTAACCCAGGGTTGTGAATACCCTATGTTTCTT 366

Qy         19 GlnAspLeuArg 22
              |||:::|||
Db        367 ATGGATATGAGA 378

RESULT 62
US-08-105-483-290
; Sequence 290, Application US/08105483
; Patent No. 5494807
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/105,483
;       FILING DATE:  12-AUG-1993
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/847,951
;       FILING DATE:  06-MAR-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Frommer, William S.
;       REGISTRATION NUMBER:  25,506
;       REFERENCE/DOCKET NUMBER:  454310-2400
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 840-3333
;       TELEFAX:  (212) 840-0712
;   INFORMATION FOR SEQ ID NO:  290:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1125 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-105-483-290

Alignment Scores:
Pred. No.:                84.8          Length:         1125
Score:                    48.00         Matches:        11
Percent Similarity:       66.7%         Conservative:   5
Best Local Similarity:    45.8%         Mismatches:     6
Query Match:              30.0%         Indels:         2
DB:                       2             Gaps:           2

US-10-758-902-1 (1-30) x US-08-105-483-290 (1-1125)

Qy          1 TyrAsn---ThrValSer---PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              ||||||   |||:::|||   |||   :::   :::       |||||||||   |||:::
Db        310 TATAACGCGACTATAAGTTGGTTTAAGGTAACCCAGGGTTGTGAATACCCTATGTTTCTT 369

Qy         19 GlnAspLeuArg 22
                ||||:::|||
Db        370 ATGGATATGAGA 381

RESULT 63
US-08-709-209-290
; Sequence 290, Application US/08709209
; Patent No. 5762938
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,209
;      FILING DATE:  21-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/105,483
;      FILING DATE:  12-AUG-1993
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  290:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1125 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-709-209-290

Alignment Scores:
Pred. No.:                84.8          Length:         1125
Score:                    48.00         Matches:        11
Percent Similarity:       66.7%         Conservative:   5
Best Local Similarity:    45.8%         Mismatches:     6
Query Match:              30.0%         Indels:         2
DB:                       2             Gaps:           2

US-10-758-902-1 (1-30) x US-08-709-209-290 (1-1125)

Qy          1 TyrAsn---ThrValSer---PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              ||||||   |||:::|||   |||   :::   :::       |||||||||   |||:::
Db        310 TATAACGCGACTATAAGTTGGTTTAAGGTAACCCAGGGTTGTGAATACCCTATGTTTCTT 369

Qy         19 GlnAspLeuArg 22
                ||||:::|||
Db        370 ATGGATATGAGA 381

RESULT 64
US-08-458-101-290
; Sequence 290, Application US/08458101
; Patent No. 5766599
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Perkus, Marion E.
;    APPLICANT:  Taylor, Jill
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  No. 5766599ton, Elizabeth K.
;    APPLICANT:  Riviere, Michel
;    APPLICANT:  de Taisne, Charles
;    APPLICANT:  Limbach, Keith J.
;    APPLICANT:  Johnson, Gerard P.
;    APPLICANT:  Pincus, Steven E.
;    APPLICANT:  Cox, William I.
;    APPLICANT:  Audonnet, Jean-Christophe Francis
;    APPLICANT:  Gettig, Russell Robert
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  467
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,101
;      FILING DATE:  01-JUN-1995
;      CLASSIFICATION:  424
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2740
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  290:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1125 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-458-101-290

Alignment Scores:
Pred. No.:              84.8          Length:         1125
Score:                  48.00         Matches:        11
Percent Similarity:     66.7%         Conservative:   5
Best Local Similarity:  45.8%         Mismatches:     6
Query Match:            30.0%         Indels:         2
DB:                     2             Gaps:           2

US-10-758-902-1 (1-30) x US-08-458-101-290 (1-1125)

Qy          1 TyrAsn---ThrValSer---PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              ||||||   |||:::|||   |||   :::   :::      |||||||||   |||:::
Db        310 TATAACGCGACTATAAGTTGGTTTAAGGTAACCCAGGGTTGTGAATACCCTATGTTTCTT 369

Qy         19 GlnAspLeuArg 22
              |||:::|||
Db        370 ATGGATATGAGA 381

RESULT 65
US-09-549-831-9
; Sequence 9, Application US/09549831
; Patent No. 6429305
; GENERAL INFORMATION:
;  APPLICANT:  Chang, Chi-Yao
;  APPLICANT:  Chang, Chia-Ching
;  APPLICANT:  Leu, Kuen-Lin
;  APPLICANT:  Tsai, Chih-Tung
;  APPLICANT:  Ting, Jing-Wen
;  APPLICANT:  Lin, Chih-Hung
;  TITLE OF INVENTION:  FISH GROWTH HORMONES
;  FILE REFERENCE:  08191-039001
;  CURRENT APPLICATION NUMBER: US/09/549,831
;  CURRENT FILING DATE:  2000-04-14
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Danio rerio
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (38)...(667)
US-09-549-831-9

Alignment Scores:
Pred. No.:              91.6          Length:         1195
Score:                  48.00         Matches:        11
Percent Similarity:     55.2%         Conservative:   5
Best Local Similarity:  37.9%         Mismatches:     11
Query Match:            30.0%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-09-549-831-9 (1-1195)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrPro------ThrPheIleGlnAspLeu 21
              :::||||||   |||   |||::::::|||:::|||      |||            :::
Db        323 ATCTCTTTCCGCCTCATTGAATCCTGGGAGTTTCCCAGCCAGACCTTGAGCTCCACTATC 382

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
              |||   |||       |||   |||
Db        383 TCAAACAGCCTGACCATCGGAAACCCC 409

RESULT 66
US-09-902-540-3335
; Sequence 3335, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3335
;   LENGTH: 1491
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-3335

Alignment Scores:
Pred. No.:              122           Length:         1491
Score:                  48.00         Matches:        9
Percent Similarity:     70.0%         Conservative:   5
Best Local Similarity:  45.0%         Mismatches:     6
Query Match:            30.0%         Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-902-540-3335 (1-1491)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              ||||||||||||:::|||      :::::::::|||   |||   |||   :::   |||
Db       1126 GAGGCCTACGAGTGGCCGGGCAACCTGCGCGAGCTGGCCAATGCGCTGGAGCGGGCCACC 1185

RESULT 67
US-09-252-991A-9018/c
; Sequence 9018, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 9018
;   LENGTH: 1659
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9018

Alignment Scores:
Pred. No.:              139           Length:         1659
Score:                  48.00         Matches:        8
Percent Similarity:     66.7%         Conservative:   4
Best Local Similarity:  44.4%         Mismatches:     6
Query Match:            30.0%         Indels:         0
DB:                     3             Gaps:           0

US-10-758-902-1 (1-30) x US-09-252-991A-9018 (1-1659)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
```

```
              ||||||:::         |||||||||   ::::::|||:::|||      |||
Db        958 CTGGGTCAGCAGCAGCCGTACCCCACTGTCGTCGAGGATATGCGCCAGGCGCTC 905

RESULT 68
US-09-614-221A-341
; Sequence 341, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
;  APPLICANT: Karunanandaa,• Balasulojini
;  APPLICANT:  Yu, Jaehyuk
;  APPLICANT:  Kishore, Ganesh M.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
;  TITLE OF INVENTION:  WITH STEROL SYNTHESIS AND METABOLISM
;  FILE REFERENCE: 16516.075
;  CURRENT APPLICATION NUMBER: US/09/614,221A
;  CURRENT FILING DATE:  2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/142,981
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 341
;   LENGTH: 2139
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-341

Alignment Scores:
Pred. No.:              193           Length:         2139
Score:                  48.00         Matches:        13
Percent Similarity:     58.1%         Conservative:   5
Best Local Similarity:  41.9%         Mismatches:     7
Query Match:            30.0%         Indels:         6
DB:                     3             Gaps:           2

US-10-758-902-1 (1-30) x US-09-614-221A-341 (1-2139)

Qy          2 AsnThrValSerPhe------AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||::::::::::|||      ||||||||||||      ||||||   ||||||   :::
Db        571 AACTCTATTAATTTTTCGAAGAATCTGGGAGAACAAAAGGAATACATCACTTTCACCAAA 630

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 |||      :::|||   |||
Db        631 ------------GAACAATTGGAAGGTGTGCCG 651

RESULT 69
PCT-US95-13975-71
; Sequence 71, Application PC/TUS9513975
;  GENERAL INFORMATION:
;    APPLICANT:  Cochran, Mark D.
;    APPLICANT:  McDonell, Michael W.
;    TITLE OF INVENTION:  Recombinant Feline Herpes virus
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John P. White
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM 330 466 DX2
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13975
;      FILING DATE:  26-OCT-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/329,883
;      FILING DATE:  26-OCT-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  39118-PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)278-0400
;      TELEFAX:  (212)391-0525
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2330 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Feline Herpesvirus
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..904
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1165..2283
PCT-US95-13975-71

Alignment Scores:
Pred. No.:              215           Length:         2330
Score:                  48.00         Matches:        11
Percent Similarity:     66.7%         Conservative:   5
Best Local Similarity:  45.8%         Mismatches:     6
Query Match:            30.0%         Indels:         2
DB:                     7             Gaps:           2

US-10-758-902-1 (1-30) x PCT-US95-13975-71 (1-2330)

Qy          1 TyrAsn---ThrValSer---PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
              ||||||   |||:::|||   |||   :::   :::      |||||||||   |||:::
Db       1471 TATAACGCGACTATAAGTTGGTTTAAGGTAACCCAGGGTTGTGAATACCCTATGTTTCTT 1530

Qy         19 GlnAspLeuArg 22
                 |||:::|||
Db       1531 ATGGATATGAGA 1542

RESULT 70
US-09-221-017B-318/c
; Sequence 318, Application US/09221017B
; Patent No. 6444799
;  GENERAL INFORMATION:
;    APPLICANT:  Ross, Bruce C.
;    TITLE OF INVENTION:  P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
;    NUMBER OF SEQUENCES:  1120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/221,017B
;      FILING DATE:  23-DEC-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1182
;      FILING DATE:  31-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1546
;      FILING DATE:  30-JAN-1998
;    PRIOR APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  PP2911
;       FILING DATE:  09-APR-1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/AU98/01023
;       FILING DATE:  10-DEC-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Monroy, Gladys H
;       REGISTRATION NUMBER:  32,430
;       REFERENCE/DOCKET NUMBER:  27340-20021.00
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-813-5600
;       TELEFAX:  650-494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  318:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3365 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  circular
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  UNKNOWN
;     ORIGINAL SOURCE:
;       ORGANISM:  PORYPHYROMONAS GINGIVALIS
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  1..3365
US-09-221-017B-318

Alignment Scores:
Pred. No.:              345          Length:         3365
Score:                  48.00        Matches:        16
Percent Similarity:     52.8%        Conservative:   3
Best Local Similarity:  44.4%        Mismatches:     11
Query Match:            30.0%        Indels:         6
DB:                     3            Gaps:           3

US-10-758-902-1 (1-30) x US-09-221-017B-318 (1-3365)

Qy          1 TyrAsn---------ThrValSerPheAsnLeu------GlyGluAlaTyrGluTyrPro 15
              ||||||           :::||||||   |||        |||   :::      |||
Db       3210 TACAATCCCAATAAGAATCTCAGCTTCCGACTCTCATACAGCGAAGGATTCCGCGCTCCT 3151

Qy         16 Thr---PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 |||   :::||||||      |||||||||   |||||||||
Db       3150 CAGTATTTCGATGAAGATCTGCACGTAGAGTTGGCCGGTGGTACTCCT 3103

RESULT 71
US-09-891-641-1
; Sequence 1, Application US/09891641
; Patent No. 6617148
; GENERAL INFORMATION:
;  APPLICANT: Ye, Rick
;  APPLICANT:  Bedzyk, Laura
;  APPLICANT:  Wang, Tao
;  TITLE OF INVENTION: NATURAL PROMOTERS FOR GENE EXPRESSION IN BACILLUS SPECIES
;  FILE REFERENCE: CL1686 US NA
;  CURRENT APPLICATION NUMBER: US/09/891,641
;  CURRENT FILING DATE:  2001-06-26
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: Microsoft 97
; SEQ ID NO 1
;   LENGTH: 3687
;   TYPE: DNA
;   ORGANISM: Bacillus subtilis
US-09-891-641-1

Alignment Scores:
Pred. No.:              388          Length:         3687
Score:                  48.00        Matches:        15
Percent Similarity:     47.2%        Conservative:   2
Best Local Similarity:  41.7%        Mismatches:     13
Query Match:            30.0%        Indels:         6
DB:                     3            Gaps:           2

US-10-758-902-1 (1-30) x US-09-891-641-1 (1-3687)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln--- 19
              ||||||   ::::::      ||||||          ||||||||||||   |||
Db       1906 TACAATGTGCTGGCGGCGCGGCTAGGGTGGCTTCCGTCTTACCCGACTTTCAATCAAAAT 1965

Qy         20 ------AspLeuArgAsnGluLeuAlaLys---------GlyThrPro 30
                    ||||||      |||      |||           |||||||
Db       1966 GGCATCGATCTGTATAAAGAAGCTGAAAAAGCAGGGGCAGCAACACCT 2013

RESULT 72
US-08-911-321-6
; Sequence 6, Application US/08911321
; Patent No. 6010703
;  GENERAL INFORMATION:
;    APPLICANT:  Roger K. Maes and Stephen J. Spatz
;    TITLE OF INVENTION:  Recombinant Poxvirus
;    TITLE OF INVENTION:  Vaccine Against
;    TITLE OF INVENTION:  Feline Rhinotracheitis
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ian C. McLeod
;      STREET:  2190  Commons Parkway
;      CITY:  Okemos
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  48864
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 Kb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/911,321
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/096,183
;      FILING DATE:  July 26, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ian C. McLeod
;      REGISTRATION NUMBER:  20,931
;      REFERENCE/DOCKET NUMBER:  MSU 4.1-166
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (517) 347-4100
;      TELEFAX:  (517) 347-4103
;      TELEX:  No. 6010703e
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6176
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:
;      DESCRIPTION:  DNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Feline herpesvirus-1
;      STRAIN:  1
;      INDIVIDUAL ISOLATE:  C-27
;      CELL TYPE:  N/A
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:  Sequencing
;      OTHER INFORMATION:  DNA encoding PK, gG, gD,
;      OTHER INFORMATION:  gI, gE
US-08-911-321-6
```

Alignment Scores:
Pred. No.: 750 Length: 6176
Score: 48.00 Matches: 11
Percent Similarity: 66.7% Conservative: 5
Best Local Similarity: 45.8% Mismatches: 6
Query Match: 30.0% Indels: 2
DB: 3 Gaps: 2

US-10-758-902-1 (1-30) x US-08-911-321-6 (1-6176)

Qy 1 TyrAsn---ThrValSer---PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
Db 2336 TATAACGCGACTATAAGTTGGTTTAAGGTAACCCAGGGTTGTGAATACCCTATGTTTCTT 2395

Qy 19 GlnAspLeuArg 22
Db 2396 ATGGATATGAGA 2407

RESULT 73
US-10-324-967-17/c
; Sequence 17, Application US/10324967
; Patent No. 6974680
; GENERAL INFORMATION:
; APPLICANT: Cosson, Pierre
; APPLICANT: Kohler, Thilo
; APPLICANT: Benghezal, Mohammed
; APPLICANT: Marchetti, Anna
; APPLICANT: van Delden, Christian
; TITLE OF INVENTION: VIRULENCE GENES, PROTEINS, AND THEIR USE
; FILE REFERENCE: 25421-502
; CURRENT APPLICATION NUMBER: US/10/324,967
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 7347
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-324-967-17

Alignment Scores:
Pred. No.: 937 Length: 7347
Score: 48.00 Matches: 8
Percent Similarity: 66.7% Conservative: 4
Best Local Similarity: 44.4% Mismatches: 6
Query Match: 30.0% Indels: 0
DB: 4 Gaps: 0

US-10-758-902-1 (1-30) x US-10-324-967-17 (1-7347)

Qy 8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
Db 5001 CTGGGTCAGCAGCAGCCGTACCCCACTGTCGTCGAGGATATGCGCCAGGCGCTC 4948

RESULT 74
US-09-252-991A-9100/c
; Sequence 9100, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9100
; LENGTH: 7374
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9100

Alignment Scores:
Pred. No.: 942 Length: 7374
Score: 48.00 Matches: 8
Percent Similarity: 66.7% Conservative: 4
Best Local Similarity: 44.4% Mismatches: 6
Query Match: 30.0% Indels: 0
DB: 3 Gaps: 0

US-10-758-902-1 (1-30) x US-09-252-991A-9100 (1-7374)

Qy 8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
Db 5028 CTGGGTCAGCAGCAGCCGTACCCCACTGTCGTCGAGGATATGCGCCAGGCGCTC 4975

RESULT 75
US-09-902-540-1156
; Sequence 1156, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1156
; LENGTH: 16387
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1156

Alignment Scores:
Pred. No.: 2.62e+03 Length: 16387
Score: 48.00 Matches: 9
Percent Similarity: 70.0% Conservative: 5
Best Local Similarity: 45.0% Mismatches: 6
Query Match: 30.0% Indels: 0
DB: 3 Gaps: 0

US-10-758-902-1 (1-30) x US-09-902-540-1156 (1-16387)

Qy 10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
Db 13617 GAGGCCTACGAGTGGCCGGGCAACCTGCGCGAGCTGGCCAATGCGCTGGAGCGGGCCACC 13676

RESULT 76
US-09-949-016-14563
; Sequence 14563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14563

; LENGTH: 92387
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(92387)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14563

Alignment Scores:

Pred. No.:	2.4e+04	Length:	92387
Score:	48.00	Matches:	8
Percent Similarity:	76.9%	Conservative:	2
Best Local Similarity:	61.5%	Mismatches:	3
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-949-016-14563 (1-92387)

```
Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||||      ||||||:::
Db       6508 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 6546
```

RESULT 77
US-09-949-016-14568
; Sequence 14568, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14568
; LENGTH: 151295
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(151295)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14568

Alignment Scores:

Pred. No.:	4.47e+04	Length:	151295
Score:	48.00	Matches:	8
Percent Similarity:	76.9%	Conservative:	2
Best Local Similarity:	61.5%	Mismatches:	3
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-949-016-14568 (1-151295)

```
Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||||      ||||||:::
Db       6508 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 6546
```

RESULT 78
US-09-949-016-14569
; Sequence 14569, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14569
; LENGTH: 151295
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(151295)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14569

Alignment Scores:

Pred. No.:	4.47e+04	Length:	151295
Score:	48.00	Matches:	8
Percent Similarity:	76.9%	Conservative:	2
Best Local Similarity:	61.5%	Mismatches:	3
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-949-016-14569 (1-151295)

```
Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||||      ||||||:::
Db       6508 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 6546
```

RESULT 79
US-09-949-016-14570
; Sequence 14570, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14570
; LENGTH: 151295
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(151295)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14570

Alignment Scores:

Pred. No.:	4.47e+04	Length:	151295
Score:	48.00	Matches:	8
Percent Similarity:	76.9%	Conservative:	2
Best Local Similarity:	61.5%	Mismatches:	3
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

```
US-10-758-902-1 (1-30) x US-09-949-016-14570 (1-151295)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||      ||||||:::
Db       6508 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 6546

RESULT 80
US-09-949-016-14571
; Sequence 14571, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14571
;   LENGTH: 151295
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(151295)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14571

Alignment Scores:
Pred. No.:                4.47e+04        Length:          151295
Score:                    48.00           Matches:         8
Percent Similarity:       76.9%           Conservative:    2
Best Local Similarity:    61.5%           Mismatches:      3
Query Match:              30.0%           Indels:          0
DB:                       3               Gaps:            0

US-10-758-902-1 (1-30) x US-09-949-016-14571 (1-151295)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||      ||||||:::
Db       6508 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 6546

RESULT 81
US-09-949-016-14572
; Sequence 14572, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14572
;   LENGTH: 151295
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(151295)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14572

Alignment Scores:
Pred. No.:                4.47e+04        Length:          151295
Score:                    48.00           Matches:         8
Percent Similarity:       76.9%           Conservative:    2
Best Local Similarity:    61.5%           Mismatches:      3
Query Match:              30.0%           Indels:          0
DB:                       3               Gaps:            0

US-10-758-902-1 (1-30) x US-09-949-016-14572 (1-151295)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||      ||||||:::
Db       6508 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 6546

RESULT 82
US-09-596-002-41
; Sequence 41, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
;  APPLICANT:      Lagace, Robert, E.
;  APPLICANT:  Patterson, Chandra
;  APPLICANT:  Berg, Kim, L.
;  TITLE OF INVENTION:  NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
;  FILE REFERENCE:  PM-0008-4 US
;  CURRENT APPLICATION NUMBER: US/09/596,002
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER:  60/140,121
;  PRIOR FILING DATE:  1999-06-18
;  NUMBER OF SEQ ID NOS:      41
;  SOFTWARE:      PERL Program
; SEQ ID NO 41
;   LENGTH: 269223
;   TYPE: DNA
;   ORGANISM: Moraxella catarrhalis
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte template ID No. 6632636 41
;  PUBLICATION INFORMATION:
US-09-596-002-41

Alignment Scores:
Pred. No.:                9.28e+04        Length:          269223
Score:                    48.00           Matches:         9
Percent Similarity:       54.5%           Conservative:    3
Best Local Similarity:    40.9%           Mismatches:      10
Query Match:              30.0%           Indels:          0
DB:                       3               Gaps:            0

US-10-758-902-1 (1-30) x US-09-596-002-41 (1-269223)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              ||||||||||||   :::||||||   :::        :::              |||
Db     138773 TTGGGTGAGGCGATCAAATATCCCGTCTATACGCCAAAAATGGAAACCGCCACTGAAAAA 138832

Qy         28 GlyThr 29
              ||||||
Db     138833 GGTACG 138838

RESULT 83
US-09-539-333D-1
; Sequence 1, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
```

; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 319608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31..1107
; OTHER INFORMATION: 5'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1108..1289
; OTHER INFORMATION: exon A g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 14877..14920
; OTHER INFORMATION: exon B g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 18778..18862
; OTHER INFORMATION: exon Bbis g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 25593..25740
; OTHER INFORMATION: exon C g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29388..29502
; OTHER INFORMATION: exon D g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29967..30282
; OTHER INFORMATION: exon E g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 64666..64812
; OTHER INFORMATION: exon F g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 65505..65853
; OTHER INFORMATION: exon G g35018 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 65854..67854
; OTHER INFORMATION: 3'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 94124..94964
; OTHER INFORMATION: exon g35017
; FEATURE:
; NAME/KEY: exon
; LOCATION: 201188..201234
; OTHER INFORMATION: exon S g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 214676..214793
; OTHER INFORMATION: exon T g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215702..215746
; OTHER INFORMATION: exon U g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216836..216915
; OTHER INFORMATION: exon V g35030 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 213818..215818
; OTHER INFORMATION: 3'regulatory region g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215819..215941
; OTHER INFORMATION: exon R complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215819..215975
; OTHER INFORMATION: exon Rbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216661..216952
; OTHER INFORMATION: exon Qbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216661..217061
; OTHER INFORMATION: exon Q complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 217027..217061
; OTHER INFORMATION: exon Q1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 229647..229742
; OTHER INFORMATION: exon X complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 230408..230721
; OTHER INFORMATION: exon P complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231272..231412
; OTHER INFORMATION: exon Obis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231787..231880
; OTHER INFORMATION: exon O2 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231870..231879
; OTHER INFORMATION: exon O1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 234174..234321
; OTHER INFORMATION: exon O complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 237406..237428
; OTHER INFORMATION: exon Nbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 239719..239807
; OTHER INFORMATION: exon N2 complement g34872 gene
; FEATURE:

; NAME/KEY: exon
; LOCATION: 239719..239853
; OTHER INFORMATION: exon N complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240569
; OTHER INFORMATION: exon M1117 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240596
; OTHER INFORMATION: exon M1090 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240617
; OTHER INFORMATION: exon M1069 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240644
; OTHER INFORMATION: exon MS2 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240824
; OTHER INFORMATION: exon M862 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240994
; OTHER INFORMATION: exon M692 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..241685
; OTHER INFORMATION: exon M1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240800..240993
; OTHER INFORMATION: exon MS1 complement g34872 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 241686..243685
; OTHER INFORMATION: 5'regulatory region g34872 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 290652..292652
; OTHER INFORMATION: 3'regulatory region g34665 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 292653..292841

Alignment Scores:

Pred. No.:	1.15e+05	Length:	319608
Score:	48.00	Matches:	10
Percent Similarity:	64.7%	Conservative:	1
Best Local Similarity:	58.8%	Mismatches:	6
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-539-333D-1 (1-319608)

```
Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||         ||||||||||||||||||:::      ||||||
Db      89428 TATATCTATGACATTCTGATACAAGATCTGAGAAATAAACAGAAAAAGGGT 89478
```

RESULT 84
US-09-679-409-1
; Sequence 1, Application US/09679409
; Patent No. 6555316
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENE, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: 53.US15.CIP
; CURRENT APPLICATION NUMBER: US/09/679,409
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 09/539,333
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 09/416,384
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/168,088
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 319608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 199122..201122
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 201123..201234
; OTHER INFORMATION: exon S
; NAME/KEY: exon
; LOCATION: 201123..201560
; OTHER INFORMATION: exon S2
; NAME/KEY: exon
; LOCATION: 214676..214793
; OTHER INFORMATION: exon T
; NAME/KEY: exon
; LOCATION: 215702..215746
; OTHER INFORMATION: exon U
; NAME/KEY: exon
; LOCATION: 216836..216994
; OTHER INFORMATION: exon V
; NAME/KEY: exon
; LOCATION: 216836..217077
; OTHER INFORMATION: exon V2
; NAME/KEY: exon
; LOCATION: 217671..217764
; OTHER INFORMATION: exon V1
; NAME/KEY: exon
; LOCATION: 227655..227736
; OTHER INFORMATION: exon V4
; NAME/KEY: exon
; LOCATION: 238715..238919
; OTHER INFORMATION: exon V3
; NAME/KEY: exon
; LOCATION: 240440..240673
; OTHER INFORMATION: exon W
; NAME/KEY: exon
; LOCATION: 240440..241153
; OTHER INFORMATION: exon W2
; NAME/KEY: exon
; LOCATION: 241072..241291
; OTHER INFORMATION: exon X
; NAME/KEY: exon
; LOCATION: 244353..244561
; OTHER INFORMATION: exon Y
; NAME/KEY: exon
; LOCATION: 246273..247802
; OTHER INFORMATION: exon Z
; NAME/KEY: misc_feature
; LOCATION: 247803..249803
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 8316
; OTHER INFORMATION: 99-27943-150 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 21672
; OTHER INFORMATION: 99-27935-193 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 65485
; OTHER INFORMATION: 8-128-33 : polymorphic base C or T
; NAME/KEY: allele

; LOCATION: 95396
; OTHER INFORMATION: 99-31960-363 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 107281
; OTHER INFORMATION: 99-24656-260 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 160640
; OTHER INFORMATION: 99-24639-163 : polymorphic base A or C
; NAME/KEY: allele
; LOCATION: 160876
; OTHER INFORMATION: 99-24634-108 : polymorphic base A or T
; NAME/KEY: allele
; LOCATION: 168974
; OTHER INFORMATION: 99-7652-162 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 170810
; OTHER INFORMATION: 99-16100-147 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 173358
; OTHER INFORMATION: 99-5862-167 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 189957
; OTHER INFORMATION: 99-5919-215 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 197163
; OTHER INFORMATION: 99-24658-410 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 200778
; OTHER INFORMATION: 8-303-235 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 202651
; OTHER INFORMATION: 8-300-221 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 202679
; OTHER INFORMATION: 8-300-193 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 203378
; OTHER INFORMATION: 8-299-128 : polymorphic base A or T
; NAME/KEY: allele
; LOCATION: 204138
; OTHER INFORMATION: 8-296-213 : polymorphic base A or T
; NAME/KEY: allele
; LOCATION: 204605
; OTHER INFORMATION: 8-252-190 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 204934
; OTHER INFORMATION: 99-24644-194 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 205206
; OTHER INFORMATION: 8-295-248 : polymorphic base A or C
; NAME/KEY: allele
; LOCATION: 205329
; OTHER INFORMATION: 8-295-125 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 206064
; OTHER INFORMATION: 8-293-130 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 206545
; OTHER INFORMATION: 8-292-198 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 207313
; OTHER INFORMATION: 8-251-322 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 208285
; OTHER INFORMATION: 8-289-322 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 208960
; OTHER INFORMATION: 8-287-249 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 209123
; OTHER INFORMATION: 8-287-86 : polymorphic base A or T
; NAME/KEY: allele
; LOCATION: 209631
; OTHER INFORMATION: 8-285-319 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 210361
; OTHER INFORMATION: 8-283-278 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 210463
; OTHER INFORMATION: 8-283-176 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 210486
; OTHER INFORMATION: 8-283-153 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 210583
; OTHER INFORMATION: 8-283-56 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 210879
; OTHER INFORMATION: 8-282-345 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 210964
; OTHER INFORMATION: 8-282-260 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 210979
; OTHER INFORMATION: 8-282-245 : polymorphic base A or C
; NAME/KEY: allele
; LOCATION: 211050
; OTHER INFORMATION: 8-282-174 : variable motif AAAGG or GAAGGAAGGAAGGAAGGAAGA
; NAME/KEY: allele
; LOCATION: 211132
; OTHER INFORMATION: 8-282-92 : polymorphic base A or T
; NAME/KEY: allele
; LOCATION: 211247
; OTHER INFORMATION: 8-281-367 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 211315
; OTHER INFORMATION: 8-281-299 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 211366
; OTHER INFORMATION: 8-281-248 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 212520
; OTHER INFORMATION: 8-279-197 : polymorphic base A or C
; NAME/KEY: allele
; LOCATION: 212821
; OTHER INFORMATION: 8-278-289 : polymorphic base C or T
; NAME/KEY: allele

Alignment Scores:

Pred. No.:	1.15e+05	Length:	319608
Score:	48.00	Matches:	10
Percent Similarity:	64.7%	Conservative:	1
Best Local Similarity:	58.8%	Mismatches:	6
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-679-409-1 (1-319608)

```
Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||          ||||||||||||||||||:::      ||||||
Db      89428 TATATCTATGACATTCTGATACAAGATCTGAGAAATAAACAGAAAAAGGGT 89478
```

RESULT 85
US-09-949-016-14573
; Sequence 14573, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

```
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14573
;   LENGTH: 393753
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(393753)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14573

Alignment Scores:
Pred. No.:              1.49e+05        Length:         393753
Score:                  48.00           Matches:        8
Percent Similarity:     76.9%           Conservative:   2
Best Local Similarity:  61.5%           Mismatches:     3
Query Match:            30.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-14573 (1-393753)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||      ||||||:::
Db     248966 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 249004

RESULT 86
US-09-949-016-14574
; Sequence 14574, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14574
;   LENGTH: 393753
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(393753)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14574

Alignment Scores:
Pred. No.:              1.49e+05        Length:         393753
Score:                  48.00           Matches:        8
Percent Similarity:     76.9%           Conservative:   2
Best Local Similarity:  61.5%           Mismatches:     3
Query Match:            30.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-14574 (1-393753)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||      ||||||:::
Db     248966 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 249004

RESULT 87
```

```
US-09-949-016-12505/c
; Sequence 12505, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12505
;   LENGTH: 670689
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(670689)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12505

Alignment Scores:
Pred. No.:              2.88e+05        Length:         670689
Score:                  48.00           Matches:        8
Percent Similarity:     73.7%           Conservative:   6
Best Local Similarity:  42.1%           Mismatches:     5
Query Match:            30.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-12505 (1-670689)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              :::|||   |||:::|||:::      |||:::|||   :::|||:::|||   |||
Db     610175 TTCAACAAAGTCAATTTTCATTTTTTTGAAAGCTACATTTTTCCTTCCTTTTATCAA 610119

RESULT 88
US-09-949-016-14207/c
; Sequence 14207, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14207
;   LENGTH: 670690
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(670690)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14207

Alignment Scores:
Pred. No.:              2.88e+05        Length:         670690
```

```
Score:                 48.00          Matches:       8
Percent Similarity:    73.7%          Conservative:  6
Best Local Similarity: 42.1%          Mismatches:    5
Query Match:           30.0%          Indels:        0
DB:                    3              Gaps:          0

US-10-758-902-1 (1-30) x US-09-949-016-14207 (1-670690)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              :::|||   |||:::|||:::      |||:::|||   :::|||:::|||   |||
Db     610175 TTCAACAAAGTCAATTTTCATTTTTTTGAAAGCTACATTTTTCCTTCCTTTTATCAA 610119

RESULT 89
US-09-949-016-14577
; Sequence 14577, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14577
;   LENGTH: 678533
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(678533)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14577

Alignment Scores:
Pred. No.:             2.92e+05       Length:        678533
Score:                 48.00          Matches:       11
Percent Similarity:    53.3%          Conservative:  5
Best Local Similarity: 36.7%          Mismatches:    14
Query Match:           30.0%          Indels:        0
DB:                    3              Gaps:          0

US-10-758-902-1 (1-30) x US-09-949-016-14577 (1-678533)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||           ::::::   :::   :::   |||      |||||||||
Db     214678 TATAACCATAGGTATTTACATGTGATCCAGCAGTTCCACTACTAGGTATTTATCCAAAGA 214737

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
                ||||||:::      ||||||   |||
Db     214738 AAAAGAAATCAGCATATCAAAGGGATACCT 214767

RESULT 90
US-09-949-016-14578
; Sequence 14578, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14578
;   LENGTH: 678533
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(678533)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14578

Alignment Scores:
Pred. No.:             2.92e+05       Length:        678533
Score:                 48.00          Matches:       11
Percent Similarity:    53.3%          Conservative:  5
Best Local Similarity: 36.7%          Mismatches:    14
Query Match:           30.0%          Indels:        0
DB:                    3              Gaps:          0

US-10-758-902-1 (1-30) x US-09-949-016-14578 (1-678533)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||           ::::::   :::   :::   |||      |||||||||
Db     214678 TATAACCATAGGTATTTACATGTGATCCAGCAGTTCCACTACTAGGTATTTATCCAAAGA 214737

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
                ||||||:::      ||||||   |||
Db     214738 AAAAGAAATCAGCATATCAAAGGGATACCT 214767

RESULT 91
US-09-949-016-14546
; Sequence 14546, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14546
;   LENGTH: 818128
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(818128)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14546

Alignment Scores:
Pred. No.:             3.65e+05       Length:        818128
Score:                 48.00          Matches:       8
Percent Similarity:    76.9%          Conservative:  2
Best Local Similarity: 61.5%          Mismatches:    3
Query Match:           30.0%          Indels:        0
DB:                    3              Gaps:          0

US-10-758-902-1 (1-30) x US-09-949-016-14546 (1-818128)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
```

```
            :::|||   ||||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379
```

RESULT 92
US-09-949-016-14547
; Sequence 14547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14547
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14547

Alignment Scores:

Pred. No.:	3.65e+05	Length:	818128
Score:	48.00	Matches:	8
Percent Similarity:	76.9%	Conservative:	2
Best Local Similarity:	61.5%	Mismatches:	3
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-949-016-14547 (1-818128)

```
Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379
```

RESULT 93
US-09-949-016-14548
; Sequence 14548, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14548
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14548

Alignment Scores:

Pred. No.:	3.65e+05	Length:	818128
Score:	48.00	Matches:	8
Percent Similarity:	76.9%	Conservative:	2
Best Local Similarity:	61.5%	Mismatches:	3
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-949-016-14548 (1-818128)

```
Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379
```

RESULT 94
US-09-949-016-14549
; Sequence 14549, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14549
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14549

Alignment Scores:

Pred. No.:	3.65e+05	Length:	818128
Score:	48.00	Matches:	8
Percent Similarity:	76.9%	Conservative:	2
Best Local Similarity:	61.5%	Mismatches:	3
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

US-10-758-902-1 (1-30) x US-09-949-016-14549 (1-818128)

```
Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379
```

RESULT 95
US-09-949-016-14550
; Sequence 14550, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

```
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14550
;   LENGTH: 818128
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(818128)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14550

Alignment Scores:
Pred. No.:              3.65e+05        Length:         818128
Score:                  48.00           Matches:        8
Percent Similarity:     76.9%           Conservative:   2
Best Local Similarity:  61.5%           Mismatches:     3
Query Match:            30.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-14550 (1-818128)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379

RESULT 96
US-09-949-016-14551
; Sequence 14551, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14551
;   LENGTH: 818128
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(818128)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14551

Alignment Scores:
Pred. No.:              3.65e+05        Length:         818128
Score:                  48.00           Matches:        8
Percent Similarity:     76.9%           Conservative:   2
Best Local Similarity:  61.5%           Mismatches:     3
Query Match:            30.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-14551 (1-818128)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379

RESULT 97
US-09-949-016-14552
; Sequence 14552, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14552
;   LENGTH: 818128
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(818128)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14552

Alignment Scores:
Pred. No.:              3.65e+05        Length:         818128
Score:                  48.00           Matches:        8
Percent Similarity:     76.9%           Conservative:   2
Best Local Similarity:  61.5%           Mismatches:     3
Query Match:            30.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-14552 (1-818128)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379

RESULT 98
US-09-949-016-14553
; Sequence 14553, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14553
;   LENGTH: 818128
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(818128)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14553

Alignment Scores:
Pred. No.:              3.65e+05        Length:         818128
```

```
Score:                  48.00          Matches:        8
Percent Similarity:     76.9%          Conservative:   2
Best Local Similarity:  61.5%          Mismatches:     3
Query Match:            30.0%          Indels:         0
DB:                     3              Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-14553 (1-818128)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379

RESULT 99
US-09-949-016-14554
; Sequence 14554, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14554
;   LENGTH: 818128
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(818128)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14554

Alignment Scores:
Pred. No.:              3.65e+05       Length:         818128
Score:                  48.00          Matches:        8
Percent Similarity:     76.9%          Conservative:   2
Best Local Similarity:  61.5%          Mismatches:     3
Query Match:            30.0%          Indels:         0
DB:                     3              Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-14554 (1-818128)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379

RESULT 100
US-09-949-016-14555
; Sequence 14555, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14555
;   LENGTH: 818128
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(818128)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14555

Alignment Scores:
Pred. No.:              3.65e+05       Length:         818128
Score:                  48.00          Matches:        8
Percent Similarity:     76.9%          Conservative:   2
Best Local Similarity:  61.5%          Mismatches:     3
Query Match:            30.0%          Indels:         0
DB:                     3              Gaps:           0

US-10-758-902-1 (1-30) x US-09-949-016-14555 (1-818128)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   ||||||||||||||      ||||||:::
Db     673341 ATAGGCTCTGCATATGAGTACCCAAATATCATTCAGAAC 673379


Search completed: September 18, 2006, 17:56:53
Job time : 736.43 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 19:05:31 ; Search time 338.715 Seconds
(without alignments)
1632.474 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_18092006_162718_11769/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10758902_@CGN_1_1_2326_@runat_18092006_162718_11769 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	100.0	2404	13	US-11-084-080-15	Sequence 15, Appl
2	160	100.0	2404	13	US-11-084-080-19	Sequence 19, Appl
3	160	100.0	2404	13	US-11-084-080-21	Sequence 21, Appl
4	160	100.0	2404	13	US-11-084-080-23	Sequence 23, Appl
5	160	100.0	2431	13	US-11-084-080-27	Sequence 27, Appl
6	111	69.4	65	9	US-10-758-902-5	Sequence 5, Appli
7	72	45.0	363	9	US-10-758-902-8	Sequence 8, Appli
8	61	38.1	1360	16	US-11-010-795-19	Sequence 19, Appl
9	61	38.1	1376	9	US-10-467-009-1	Sequence 1, Appli
10	61	38.1	1379	3	US-09-978-274A-30	Sequence 30, Appl
11	61	38.1	1379	13	US-11-106-187-1	Sequence 1, Appli
c 12	60.5	37.8	569	12	US-10-301-480-72772	Sequence 72772, A
c 13	60.5	37.8	569	12	US-10-301-480-72773	Sequence 72773, A
c 14	60.5	37.8	569	12	US-10-301-480-686181	Sequence 686181,
c 15	60.5	37.8	569	12	US-10-301-480-686182	Sequence 686182,
c 16	60.5	37.8	596	6	US-10-027-632-230755	Sequence 230755,
c 17	60.5	37.8	596	6	US-10-027-632-230756	Sequence 230756,
c 18	60.5	37.8	596	6	US-10-027-632-230757	Sequence 230757,
c 19	60.5	37.8	596	7	US-10-027-632-230755	Sequence 230755,
c 20	60.5	37.8	596	7	US-10-027-632-230756	Sequence 230756,
c 21	60.5	37.8	596	7	US-10-027-632-230757	Sequence 230757,
c 22	60.5	37.8	627	12	US-10-301-480-572047	Sequence 572047,
c 23	60.5	37.8	627	12	US-10-301-480-1185456	Sequence 1185456,
24	59	36.9	526	8	US-10-424-599-70917	Sequence 70917, A
25	57	35.6	1452	8	US-10-437-963-43964	Sequence 43964, A
26	56	35.0	465	3	US-09-978-274A-5	Sequence 5, Appli
27	56	35.0	655	8	US-10-767-701-6363	Sequence 6363, Ap
28	56	35.0	791	9	US-10-425-115-166418	Sequence 166418,
29	56	35.0	792	3	US-09-978-274A-3	Sequence 3, Appli
30	56	35.0	945	3	US-09-978-274A-1	Sequence 1, Appli
31	56	35.0	945	7	US-10-128-713A-15	Sequence 15, Appl
32	56	35.0	1020	9	US-10-425-115-166417	Sequence 166417,
33	56	35.0	1092	3	US-09-978-274A-19	Sequence 19, Appl
34	56	35.0	1368	3	US-09-978-274A-31	Sequence 31, Appl
35	56	35.0	2197	8	US-10-425-114-31620	Sequence 31620, A
36	56	35.0	2380	9	US-10-425-115-166421	Sequence 166421,
37	55.5	34.7	38844	6	US-10-060-333-3	Sequence 3, Appli
38	55.5	34.7	38844	13	US-11-074-697-3	Sequence 3, Appli
c 39	55	34.4	2139	10	US-10-450-763-18022	Sequence 18022, A
c 40	55	34.4	2558	9	US-10-343-903-34	Sequence 34, Appl
c 41	55	34.4	2776	10	US-10-750-185-24916	Sequence 24916, A
c 42	55	34.4	2776	10	US-10-750-623-24916	Sequence 24916, A
43	54.5	34.1	1142	8	US-10-424-599-131861	Sequence 131861,
c 44	54	33.8	333	9	US-10-425-115-72394	Sequence 72394, A
45	54	33.8	546	4	US-09-925-065A-373047	Sequence 373047,
46	54	33.8	546	5	US-09-925-065A-373047	Sequence 373047,
47	54	33.8	560	12	US-10-301-480-442950	Sequence 442950,
48	54	33.8	560	12	US-10-301-480-1056359	Sequence 1056359,
49	54	33.8	569	4	US-09-925-065A-748607	Sequence 748607,
50	54	33.8	569	4	US-09-925-065A-748608	Sequence 748608,
51	54	33.8	569	4	US-09-925-065A-748609	Sequence 748609,
52	54	33.8	569	5	US-09-925-065A-748607	Sequence 748607,
53	54	33.8	569	5	US-09-925-065A-748608	Sequence 748608,
54	54	33.8	569	5	US-09-925-065A-748609	Sequence 748609,
55	54	33.8	570	4	US-09-925-065A-799267	Sequence 799267,
56	54	33.8	570	4	US-09-925-065A-799268	Sequence 799268,
57	54	33.8	570	4	US-09-925-065A-799269	Sequence 799269,
58	54	33.8	570	5	US-09-925-065A-799267	Sequence 799267,
59	54	33.8	570	5	US-09-925-065A-799268	Sequence 799268,
60	54	33.8	570	5	US-09-925-065A-799269	Sequence 799269,
61	54	33.8	592	4	US-09-925-065A-891048	Sequence 891048,
62	54	33.8	592	5	US-09-925-065A-891048	Sequence 891048,
63	54	33.8	593	4	US-09-925-065A-871708	Sequence 871708,
64	54	33.8	593	5	US-09-925-065A-871708	Sequence 871708,
c 65	54	33.8	651	9	US-10-425-115-74403	Sequence 74403, A
66	54	33.8	1683	8	US-10-424-599-72856	Sequence 72856, A
c 67	53	33.1	903	6	US-10-010-901-14	Sequence 14, Appl
68	53	33.1	5366	13	US-11-097-143-40124	Sequence 40124, A
69	53	33.1	31068	13	US-11-097-143-40123	Sequence 40123, A
70	52.5	32.8	710	8	US-10-424-599-26095	Sequence 26095, A
c 71	52	32.5	590	12	US-10-301-480-451151	Sequence 451151,
c 72	52	32.5	590	12	US-10-301-480-1064560	Sequence 1064560,
c 73	52	32.5	593	4	US-09-925-065A-382110	Sequence 382110,
c 74	52	32.5	593	5	US-09-925-065A-382110	Sequence 382110,

	75	52	32.5	1040	6	US-10-198-846-11177	Sequence 11177, A
	76	52	32.5	1689	8	US-10-425-114-25526	Sequence 25526, A
	77	52	32.5	1692	8	US-10-425-114-17777	Sequence 17777, A
	78	52	32.5	2622	9	US-10-425-115-68440	Sequence 68440, A
	79	51.5	32.2	258	7	US-10-029-386-16475	Sequence 16475, A
	80	51.5	32.2	543	7	US-10-029-386-2775	Sequence 2775, Ap
c	81	51.5	32.2	549	7	US-10-149-930-2	Sequence 2, Appli
c	82	51.5	32.2	1398	3	US-09-893-321-1	Sequence 1, Appli
c	83	51.5	32.2	1446	8	US-10-380-727-48	Sequence 48, Appl
c	84	51.5	32.2	1455	8	US-10-092-900A-7	Sequence 7, Appli
c	85	51.5	32.2	1457	8	US-10-092-900A-3	Sequence 3, Appli
c	86	51.5	32.2	1562	16	US-11-096-568A-15041	Sequence 15041, A
c	87	51.5	32.2	1568	3	US-09-893-321-5	Sequence 5, Appli
c	88	51.5	32.2	1672	10	US-10-482-834A-99	Sequence 99, Appl
c	89	51.5	32.2	1672	10	US-10-482-834A-100	Sequence 100, App
	90	51.5	32.2	2355	8	US-10-437-963-34100	Sequence 34100, A
c	91	51.5	32.2	2819	3	US-09-818-657-1	Sequence 1, Appli
c	92	51.5	32.2	2819	13	US-11-136-623-1	Sequence 1, Appli
c	93	51.5	32.2	82938	3	US-09-818-657-3	Sequence 3, Appli
c	94	51.5	32.2	82938	13	US-11-136-623-3	Sequence 3, Appli
	95	51.5	32.2	109974	15	US-11-117-187-204	Sequence 204, App
	96	51	31.9	460	8	US-10-767-701-18898	Sequence 18898, A
	97	51	31.9	505	4	US-09-925-065A-826328	Sequence 826328,
	98	51	31.9	505	4	US-09-925-065A-826329	Sequence 826329,
	99	51	31.9	505	5	US-09-925-065A-826328	Sequence 826328,
	100	51	31.9	505	5	US-09-925-065A-826329	Sequence 826329,

ALIGNMENTS

```
RESULT 1
US-11-084-080-15
; Sequence 15, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-15

Alignment Scores:
Pred. No.:              1.29e-17        Length:         2404
Score:                  160.00          Matches:        30
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     13              Gaps:           0

US-10-758-902-1 (1-30) x US-11-084-080-15 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 884

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        885 TTGCGCAATGAATTGGCTAAGGGCACACCA 914

RESULT 2
US-11-084-080-19
; Sequence 19, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Alignment Scores:
Pred. No.:              1.29e-17        Length:         2404
Score:                  160.00          Matches:        30
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     13              Gaps:           0

US-10-758-902-1 (1-30) x US-11-084-080-19 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1643 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1702

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db       1703 TTGCGCAATGAATTGGCTAAGGGCACACCA 1732

RESULT 3
US-11-084-080-21
; Sequence 21, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
```

; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-21

Alignment Scores:

Pred. No.:	1.29e-17	Length:	2404
Score:	160.00	Matches:	30
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-1 (1-30) x US-11-084-080-21 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 191

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        192 TTGCGCAATGAATTGGCTAAGGGCACACCA 221
```

RESULT 4
US-11-084-080-23
; Sequence 23, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Alignment Scores:

Pred. No.:	1.29e-17	Length:	2404
Score:	160.00	Matches:	30
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-1 (1-30) x US-11-084-080-23 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        950 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1009

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db       1010 TTGCGCAATGAATTGGCTAAGGGCACACCA 1039
```

RESULT 5
US-11-084-080-27
; Sequence 27, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 2431
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-011
US-11-084-080-27

Alignment Scores:

Pred. No.:	1.31e-17	Length:	2431
Score:	160.00	Matches:	30
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-1 (1-30) x US-11-084-080-27 (1-2431)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 911

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        912 TTGCGCAATGAATTGGCTAAGGGCACACCA 941
```

RESULT 6
US-10-758-902-5
; Sequence 5, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenzo
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
; FILE REFERENCE: PNJ-005CN
; CURRENT APPLICATION NUMBER: US/10/758,902
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 09/445160

```
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-5

Alignment Scores:
Pred. No.:              8.18e-11        Length:         65
Score:                  111.00          Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            69.4%           Indels:         0
DB:                     9               Gaps:           0

US-10-758-902-1 (1-30) x US-10-758-902-5 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 7
US-10-758-902-8
; Sequence 8, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)...(361)
US-10-758-902-8

Alignment Scores:
Pred. No.:              0.00977         Length:         363
Score:                  72.00           Matches:        14
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            45.0%           Indels:         0
DB:                     9               Gaps:           0

US-10-758-902-1 (1-30) x US-10-758-902-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43
```

```
RESULT 8
US-11-010-795-19
; Sequence 19, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  DI, RONG
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
;  TITLE OF INVENTION:  RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
;  FILE REFERENCE: OCIRS 3.0-085
;  CURRENT APPLICATION NUMBER: US/11/010,795
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: 60/529,348
;  PRIOR FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
;   LENGTH: 1360
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (207)..(1145)
US-11-010-795-19

Alignment Scores:
Pred. No.:              5.65            Length:         1360
Score:                  61.00           Matches:        12
Percent Similarity:     68.0%           Conservative:   5
Best Local Similarity:  48.0%           Mismatches:     6
Query Match:            38.1%           Indels:         2
DB:                     16              Gaps:           1

US-10-758-902-1 (1-30) x US-11-010-795-19 (1-1360)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||               :::|||   ||||||:::
Db        276 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 335

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        336 GATCTTCGTAATGAA 350

RESULT 9
US-10-467-009-1
; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
;  APPLICANT: RUTGERS, THE STATE UNIVERSITY
;  TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
;  FILE REFERENCE: OCIRS 3.4-076
;  CURRENT APPLICATION NUMBER: US/10/467,009
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: 60/266,396
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1376
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (225)..(1160)
US-10-467-009-1

Alignment Scores:
Pred. No.:              5.74            Length:         1376
Score:                  61.00           Matches:        12
Percent Similarity:     68.0%           Conservative:   5
Best Local Similarity:  48.0%           Mismatches:     6
Query Match:            38.1%           Indels:         2
DB:                     9               Gaps:           1
```

```
US-10-758-902-1 (1-30) x US-10-467-009-1 (1-1376)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 10
US-09-978-274A-30
; Sequence 30, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 1379
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-30

Alignment Scores:
Pred. No.:              5.76          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-09-978-274A-30 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 11
US-11-106-187-1
; Sequence 1, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  WANG, PINGER
;  TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
;  FILE REFERENCE: OCIRS 3.9-060 CONT
;  CURRENT APPLICATION NUMBER: US/11/106,187
;  CURRENT FILING DATE:  2005-04-14
;  PRIOR APPLICATION NUMBER: US/09/721,047
;  PRIOR FILING DATE: 2000-11-22
;  PRIOR APPLICATION NUMBER: PCT/US99/11301
;  PRIOR FILING DATE: 1999-05-21
;  PRIOR APPLICATION NUMBER: 60/086,374
;  PRIOR FILING DATE: 1998-05-22
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
;   LENGTH: 1379
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (225)..(1163)
US-11-106-187-1

Alignment Scores:
Pred. No.:              5.76          Length:         1379
Score:                  61.00         Matches:        12
Percent Similarity:     68.0%         Conservative:   5
Best Local Similarity:  48.0%         Mismatches:     6
Query Match:            38.1%         Indels:         2
DB:                     13            Gaps:           1

US-10-758-902-1 (1-30) x US-11-106-187-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 12
US-10-301-480-72772/c
; Sequence 72772, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72772
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-72772

Alignment Scores:
Pred. No.:              2.18          Length:         569
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     12            Gaps:           1

US-10-758-902-1 (1-30) x US-10-301-480-72772 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 13
US-10-301-480-72773/c
; Sequence 72773, Application US/10301480
```

```
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72773
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-72773

Alignment Scores:
Pred. No.:              2.18          Length:          569
Score:                  60.50         Matches:         14
Percent Similarity:     40.9%         Conservative:    4
Best Local Similarity:  31.8%         Mismatches:      7
Query Match:            37.8%         Indels:          19
DB:                     12            Gaps:            1

US-10-758-902-1 (1-30) x US-10-301-480-72773 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                        ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 14
US-10-301-480-686181/c
; Sequence 686181, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 686181
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-686181

Alignment Scores:
Pred. No.:              2.18          Length:          569
Score:                  60.50         Matches:         14
Percent Similarity:     40.9%         Conservative:    4
Best Local Similarity:  31.8%         Mismatches:      7
Query Match:            37.8%         Indels:          19
DB:                     12            Gaps:            1

US-10-758-902-1 (1-30) x US-10-301-480-686181 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                        ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 15
US-10-301-480-686182/c
; Sequence 686182, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 686182
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-686182

Alignment Scores:
Pred. No.:              2.18          Length:          569
Score:                  60.50         Matches:         14
Percent Similarity:     40.9%         Conservative:    4
Best Local Similarity:  31.8%         Mismatches:      7
Query Match:            37.8%         Indels:          19
DB:                     12            Gaps:            1

US-10-758-902-1 (1-30) x US-10-301-480-686182 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                        ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 16
US-10-027-632-230755/c
; Sequence 230755, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
```

```
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230755
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230755

Alignment Scores:
Pred. No.:              2.32          Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     6             Gaps:           1

US-10-758-902-1 (1-30) x US-10-027-632-230755 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 17
US-10-027-632-230756/c
; Sequence 230756, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230756
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230756

Alignment Scores:
Pred. No.:              2.32          Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     6             Gaps:           1

US-10-758-902-1 (1-30) x US-10-027-632-230756 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 18
US-10-027-632-230757/c
; Sequence 230757, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230757
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230757

Alignment Scores:
Pred. No.:              2.32          Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     6             Gaps:           1

US-10-758-902-1 (1-30) x US-10-027-632-230757 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 --------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462
```

```
Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 19
US-10-027-632-230755/c
; Sequence 230755, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230755
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230755

Alignment Scores:
Pred. No.:              2.32          Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     7             Gaps:           1

US-10-758-902-1 (1-30) x US-10-027-632-230755 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 ----------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                          ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 20
US-10-027-632-230756/c
; Sequence 230756, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230756
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230756

Alignment Scores:
Pred. No.:              2.32          Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     7             Gaps:           1

US-10-758-902-1 (1-30) x US-10-027-632-230756 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 ----------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                          ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 21
US-10-027-632-230757/c
; Sequence 230757, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230757
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
```

US-10-027-632-230757

Alignment Scores:

Pred. No.:	2.32	Length:	596
Score:	60.50	Matches:	14
Percent Similarity:	40.9%	Conservative:	4
Best Local Similarity:	31.8%	Mismatches:	7
Query Match:	37.8%	Indels:	19
DB:	7	Gaps:	1

US-10-758-902-1 (1-30) x US-10-027-632-230757 (1-596)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu------------------------------ 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 ---------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450
```

RESULT 22
US-10-301-480-572047/c
; Sequence 572047, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 572047
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-572047

Alignment Scores:

Pred. No.:	2.48	Length:	627
Score:	60.50	Matches:	14
Percent Similarity:	40.9%	Conservative:	4
Best Local Similarity:	31.8%	Mismatches:	7
Query Match:	37.8%	Indels:	19
DB:	12	Gaps:	1

US-10-758-902-1 (1-30) x US-10-301-480-572047 (1-627)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu------------------------------ 10
              |||:::|||||||||   |||:::
Db        531 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 472

Qy         11 ---------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        471 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 412

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        411 AGAAACTCCCTA 400
```

RESULT 23
US-10-301-480-1185456/c
; Sequence 1185456, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1185456
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1185456

Alignment Scores:

Pred. No.:	2.48	Length:	627
Score:	60.50	Matches:	14
Percent Similarity:	40.9%	Conservative:	4
Best Local Similarity:	31.8%	Mismatches:	7
Query Match:	37.8%	Indels:	19
DB:	12	Gaps:	1

US-10-758-902-1 (1-30) x US-10-301-480-1185456 (1-627)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu------------------------------ 10
              |||:::|||||||||   |||:::
Db        531 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 472

Qy         11 ---------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        471 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 412

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        411 AGAAACTCCCTA 400
```

RESULT 24
US-10-424-599-70917
; Sequence 70917, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 70917
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3504C.1
US-10-424-599-70917

Alignment Scores:

Pred. No.:	3.67	Length:	526
Score:	59.00	Matches:	17
Percent Similarity:	48.7%	Conservative:	2
Best Local Similarity:	43.6%	Mismatches:	8
Query Match:	36.9%	Indels:	12
DB:	8	Gaps:	2

US-10-758-902-1 (1-30) x US-10-424-599-70917 (1-526)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        311 ACTGTCAACTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 367

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||   |||||||||      |||
Db        368 CAGGCAGAACATGCAGCAGCTGGAGTGGCTCTTAACACTCTTGCAAAAAGAGGTCCC 424
```

RESULT 25
US-10-437-963-43964
; Sequence 43964, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 43964
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_47070C.1
US-10-437-963-43964

Alignment Scores:

Pred. No.:	32.8	Length:	1452
Score:	57.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.6%	Indels:	12
DB:	8	Gaps:	2

US-10-758-902-1 (1-30) x US-10-437-963-43964 (1-1452)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        396 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 452

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        453 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 509
```

RESULT 26
US-09-978-274A-5
; Sequence 5, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-5

Alignment Scores:

Pred. No.:	10.9	Length:	465
Score:	56.00	Matches:	11
Percent Similarity:	72.0%	Conservative:	7
Best Local Similarity:	44.0%	Mismatches:	5
Query Match:	35.0%	Indels:	2
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x US-09-978-274A-5 (1-465)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
              |||||||||:::
Db         67 TCTCTTCGTAATCAA 81
```

RESULT 27
US-10-767-701-6363
; Sequence 6363, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 6363
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41259_1
US-10-767-701-6363

Alignment Scores:

Pred. No.:	17.2	Length:	655
Score:	56.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.0%	Indels:	12
DB:	8	Gaps:	2

US-10-758-902-1 (1-30) x US-10-767-701-6363 (1-655)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        530 ACAGTTAATTTCAAT---GGGGAGATGTTCGAGAGCCCCGCGTTTTGTTCTACTTTGCGG 586

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        587 CAGGCGGAGCATGCGGCAGCTGAGGTAGCGCTCAATGAGTTATCGAAGAGGGGCCCT 643
```

RESULT 28
US-10-425-115-166418
; Sequence 166418, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants

```
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166418
;   LENGTH: 791
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83354C.1
US-10-425-115-166418

Alignment Scores:
Pred. No.:              22.2          Length:         791
Score:                  56.00         Matches:        16
Percent Similarity:     48.7%         Conservative:   3
Best Local Similarity:  41.0%         Mismatches:     8
Query Match:            35.0%         Indels:         12
DB:                     9             Gaps:           2

US-10-758-902-1 (1-30) x US-10-425-115-166418 (1-791)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::|||||||   ||||||   :::|||   |||   |||          ||||||
Db        535 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 591

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        592 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 648

RESULT 29
US-09-978-274A-3
; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 792
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-3

Alignment Scores:
Pred. No.:              22.2          Length:         792
Score:                  56.00         Matches:        11
Percent Similarity:     72.0%         Conservative:   7
Best Local Similarity:  44.0%         Mismatches:     5
Query Match:            35.0%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-09-978-274A-3 (1-792)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                |||||||||:::
Db         67 TCTCTTCGTAATCAA 81

RESULT 30
US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-1

Alignment Scores:
Pred. No.:              28.1          Length:         945
Score:                  56.00         Matches:        11
Percent Similarity:     72.0%         Conservative:   7
Best Local Similarity:  44.0%         Mismatches:     5
Query Match:            35.0%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-09-978-274A-1 (1-945)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::::|||:::   |||   |||         :::|||   ||||||::::::
Db         76 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 135

Qy         20 AspLeuArgAsnGlu 24
                |||||||||:::
Db        136 TCTCTTCGTAATCAA 150

RESULT 31
US-10-128-713A-15
; Sequence 15, Application US/10128713A
; Publication No. US20030170847A1
; GENERAL INFORMATION:
;  APPLICANT: Bramucci, Michael G
;  TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production
;  FILE REFERENCE: CL-1788
;  CURRENT APPLICATION NUMBER: US/10/128,713A
;  CURRENT FILING DATE:  2002-04-22
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Rhodococcus erythropolis
US-10-128-713A-15

Alignment Scores:
Pred. No.:              28.1          Length:         945
Score:                  56.00         Matches:        10
Percent Similarity:     72.7%         Conservative:   6
Best Local Similarity:  45.5%         Mismatches:     6
Query Match:            35.0%         Indels:         0
DB:                     7             Gaps:           0

US-10-758-902-1 (1-30) x US-10-128-713A-15 (1-945)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||:::::         ||||||:::|||:::      :::|||
Db        520 AATCTCGGTGAGGCGTTTCAGCTGACCAACTTCATCCGCGACGTCGGTGAAGACCTCGAC 579

Qy         27 LysGly 28
              :::|||
```

```
Db        580 CGGGGA 585

RESULT 32
US-10-425-115-166417
; Sequence 166417, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166417
;   LENGTH: 1020
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(1020)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83353C.1
US-10-425-115-166417

Alignment Scores:
Pred. No.:              31.1          Length:         1020
Score:                  56.00         Matches:        16
Percent Similarity:     48.7%         Conservative:   3
Best Local Similarity:  41.0%         Mismatches:     8
Query Match:            35.0%         Indels:         12
DB:                     9             Gaps:           2

US-10-758-902-1 (1-30) x US-10-425-115-166417 (1-1020)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        572 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCTACTCTGCGG 628

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                             |||||||||:::|||      |||
Db        629 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 685

RESULT 33
US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 1092
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19

Alignment Scores:
Pred. No.:              34.1          Length:         1092
Score:                  56.00         Matches:        11
Percent Similarity:     72.0%         Conservative:   7
Best Local Similarity:  44.0%         Mismatches:     5
Query Match:            35.0%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-09-978-274A-19 (1-1092)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                 |||||||||:::
Db         67 TCTCTTCGTAATCAA 81

RESULT 34
US-09-978-274A-31
; Sequence 31, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 1368
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-31

Alignment Scores:
Pred. No.:              46.1          Length:         1368
Score:                  56.00         Matches:        12
Percent Similarity:     64.0%         Conservative:   4
Best Local Similarity:  48.0%         Mismatches:     7
Query Match:            35.0%         Indels:         2
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-09-978-274A-31 (1-1368)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCGGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 35
US-10-425-114-31620
; Sequence 31620, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
```

```
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31620
;   LENGTH: 2197
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLB73196E06_FLI
US-10-425-114-31620

Alignment Scores:
Pred. No.:              86.7          Length:        2197
Score:                  56.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.0%         Indels:        12
DB:                     8             Gaps:          2

US-10-758-902-1 (1-30) x US-10-425-114-31620 (1-2197)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db        464 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 520

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        521 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 577

RESULT 36
US-10-425-115-166421
; Sequence 166421, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166421
;   LENGTH: 2380
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83357C.1
US-10-425-115-166421

Alignment Scores:
Pred. No.:              96.5          Length:        2380
Score:                  56.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.0%         Indels:        12
DB:                     9             Gaps:          2

US-10-758-902-1 (1-30) x US-10-425-115-166421 (1-2380)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db        580 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 636

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        637 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 693

RESULT 37
US-10-060-333-3
; Sequence 3, Application US/10060333
; Publication No. US20020115186A1
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL000862DIV
;  CURRENT APPLICATION NUMBER: US/10/060,333
;  CURRENT FILING DATE:  2002-08-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 38844
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-060-333-3

Alignment Scores:
Pred. No.:              4.94e+03      Length:        38844
Score:                  55.50         Matches:       10
Percent Similarity:     48.7%         Conservative:  9
Best Local Similarity:  25.6%         Mismatches:    11
Query Match:            34.7%         Indels:        9
DB:                     6             Gaps:          1

US-10-758-902-1 (1-30) x US-10-060-333-3 (1-38844)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr------------------------ 12
              ||||||::::::   |||:::          |||
Db      38592 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 38651

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::|||||||||   :::      ||||||
Db      38652 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 38708

RESULT 38
US-11-074-697-3
; Sequence 3, Application US/11074697
; Publication No. US20050181414A1
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL000862DIV
;  CURRENT APPLICATION NUMBER: US/11/074,697
;  CURRENT FILING DATE:  2005-03-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 38844
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-074-697-3

Alignment Scores:
Pred. No.:              4.94e+03      Length:        38844
Score:                  55.50         Matches:       10
Percent Similarity:     48.7%         Conservative:  9
Best Local Similarity:  25.6%         Mismatches:    11
Query Match:            34.7%         Indels:        9
DB:                     13            Gaps:          1

US-10-758-902-1 (1-30) x US-11-074-697-3 (1-38844)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr------------------------ 12
              ||||||::::::   |||:::          |||
Db      38592 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 38651

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::|||||||||   :::      ||||||
Db      38652 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 38708

RESULT 39
```

```
US-10-450-763-18022/c
; Sequence 18022, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 790CIP3/US
;  CURRENT APPLICATION NUMBER: US/10/450,763
;  CURRENT FILING DATE:  2003-06-11
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 18022
;   LENGTH: 2139
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (562)..(1398)
;   OTHER INFORMATION: 98% homologous to Homo sapiens mono ATP-binding cassette
;   OTHER INFORMATION: protein,accession number AB013380,Smith-Waterman Score=1341.
US-10-450-763-18022

Alignment Scores:
Pred. No.:              127          Length:         2139
Score:                  55.00        Matches:        8
Percent Similarity:     70.8%        Conservative:   9
Best Local Similarity:  33.3%        Mismatches:     7
Query Match:            34.4%        Indels:         0
DB:                     10           Gaps:           0

US-10-758-902-1 (1-30) x US-10-450-763-18022 (1-2139)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::::|||   |||::::::   |||:::|||:::||||||   :::::::::
Db       1335 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 1276

Qy         27 LysGlyThrPro 30
                |||   |||
Db       1275 TCCGGAGAGCCC 1264

RESULT 40
US-10-343-903-34/c
; Sequence 34, Application US/10343903
; Publication No. US20040224911A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry;
;  APPLICANT:  THORNTON, Michael; RAMKUMAR, Jayalaxmi;
;  APPLICANT:  TANG, Y. Tom; AZIMZAI, Yalda;
;  APPLICANT:  BAUGHN, Mariah R.; YANG, Junming;
;  APPLICANT:  YAO, Monique G.; LAL, Preeti G.;
;  APPLICANT:  CHAWLA, Narinder K.; GANDHI, Ameena R.;
;  APPLICANT:  HAFALIA, April J.A.; NGUYEN, Danniel B.;
;  APPLICANT:  ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
;  APPLICANT:  TRIBOULEY, Catherine M.; LU, Dyung Aina M.;
;  APPLICANT:  XU, Yuming; REDDY, Roopa;
;  APPLICANT:  HERNANDEZ, Roberto; BOROWSKY, Mark L.;
;  APPLICANT:  LO, Terence P.; LU, Yan;
;  APPLICANT:  POLICKY, Jennifer L.; GREENE, Barrie D.;
;  APPLICANT:  SANJANWALA, Madhusudan M.; RAUMANN, Brigette E.;
;  APPLICANT:  BURFORD, Neil; ISON, Craig H.;
;  APPLICANT:  LEE, Ernestine A.; DING, Li;
;  APPLICANT:  DAS, Debopriya; KALLICK, Deborah A.;
;  APPLICANT:  KHAN, Farrah A.; SEILHAMER, Jeffrey J.;
;  TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
;  FILE REFERENCE: PI-0183 USN
;  CURRENT APPLICATION NUMBER: US/10/343,903
;  CURRENT FILING DATE:  2003-02-03
;  PRIOR APPLICATION NUMBER: PCT/US01/24217
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/231,434
;  PRIOR FILING DATE: 2000-09-08
;  PRIOR APPLICATION NUMBER: 60/230,067
;  PRIOR FILING DATE: 2000-08-31
;  PRIOR APPLICATION NUMBER: 60/228,140
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 60/226,410
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: 60/224,456
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: 60/223,269
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PERL Program
; SEQ ID NO 34
;   LENGTH: 2558
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 3105257CB1
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 2523
;   OTHER INFORMATION: a, t, c, g, or other
US-10-343-903-34

Alignment Scores:
Pred. No.:              161          Length:         2558
Score:                  55.00        Matches:        8
Percent Similarity:     70.8%        Conservative:   9
Best Local Similarity:  33.3%        Mismatches:     7
Query Match:            34.4%        Indels:         0
DB:                     9            Gaps:           0

US-10-758-902-1 (1-30) x US-10-343-903-34 (1-2558)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::::|||   |||::::::   |||:::|||:::||||||   :::::::::
Db       1041 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 982

Qy         27 LysGlyThrPro 30
                |||   |||
Db        981 TCCGGAGAGCCC 970

RESULT 41
US-10-750-185-24916/c
; Sequence 24916, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 24916
;   LENGTH: 2776
;   TYPE: DNA
;   ORGANISM: Bovine  19866881045177
US-10-750-185-24916
```

```
Alignment Scores:
Pred. No.:                180          Length:        2776
Score:                    55.00        Matches:       11
Percent Similarity:       59.1%        Conservative:  2
Best Local Similarity:    50.0%        Mismatches:    9
Query Match:              34.4%        Indels:        0
DB:                       10           Gaps:          0

US-10-758-902-1 (1-30) x US-10-750-185-24916 (1-2776)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::     |||||||||         |||:::|||     |||   |||
Db        692 GGGTCAGCCCACTCCATGCCCACCTTCTTTGCCCGGCTCCAGAATGCAAGTGCCATGGGC 633

Qy         29 ThrPro 30
              ||||||
Db        632 ACGCCC 627

RESULT 42
US-10-750-623-24916/c
; Sequence 24916, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 24916
;   LENGTH: 2776
;   TYPE: DNA
;   ORGANISM: Bovine  19866881045177
US-10-750-623-24916

Alignment Scores:
Pred. No.:                180          Length:        2776
Score:                    55.00        Matches:       11
Percent Similarity:       59.1%        Conservative:  2
Best Local Similarity:    50.0%        Mismatches:    9
Query Match:              34.4%        Indels:        0
DB:                       10           Gaps:          0

US-10-758-902-1 (1-30) x US-10-750-623-24916 (1-2776)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::     |||||||||         |||:::|||     |||   |||
Db        692 GGGTCAGCCCACTCCATGCCCACCTTCTTTGCCCGGCTCCAGAATGCAAGTGCCATGGGC 633

Qy         29 ThrPro 30
              ||||||
Db        632 ACGCCC 627

RESULT 43
US-10-424-599-131861
; Sequence 131861, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 131861
;   LENGTH: 1142
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_90078C.1
US-10-424-599-131861

Alignment Scores:
Pred. No.:                67.8         Length:        1142
Score:                    54.50        Matches:       12
Percent Similarity:       58.1%        Conservative:  6
Best Local Similarity:    38.7%        Mismatches:    12
Query Match:              34.1%        Indels:        1
DB:                       8            Gaps:          1

US-10-758-902-1 (1-30) x US-10-424-599-131861 (1-1142)

Qy          1 TyrAsnThrValSerPheAsnLeu---GlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||       :::   ||||||      ||||||   ::::::||||||   |||
Db        328 TACACCTTTCTTGAATTCAACACGCAGGGCGAGGATTTCGACTACCCCGAGTTCCGCGAC 387

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 :::|||:::   :::|||      ||||||
Db        388 CCGATTAGGTCGCCGGTTGCCTGGCCCACGCCG 420

RESULT 44
US-10-425-115-72394/c
; Sequence 72394, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 72394
;   LENGTH: 333
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_166022C.1
US-10-425-115-72394

Alignment Scores:
Pred. No.:                16.1         Length:        333
Score:                    54.00        Matches:       11
Percent Similarity:       59.3%        Conservative:  5
Best Local Similarity:    40.7%        Mismatches:    11
Query Match:              33.8%        Indels:        0
DB:                       9            Gaps:          0

US-10-758-902-1 (1-30) x US-10-425-115-72394 (1-333)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              :::|||      :::   :::||||||   |||      ||||||     :::||||||
Db        100 TTGTCTTGACGTGTCGCTCAGGCCTACAATTATTAAAATTTTATTGCATCAATCAGAAAT 41

Qy         24 GluLeuAlaLysGlyThrPro 30
              :::      ||||||   |||
Db         40 AAAAAAAAGAAAGGGCATCCG 20

RESULT 45
US-09-925-065A-373047
```

```
; Sequence 373047, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 373047
;   LENGTH: 546
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(546)
;   OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-373047

Alignment Scores:
Pred. No.:              31.2          Length:          546
Score:                  54.00         Matches:         10
Percent Similarity:     70.6%         Conservative:    2
Best Local Similarity:  58.8%         Mismatches:      5
Query Match:            33.8%         Indels:          0
DB:                     4             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-373047 (1-546)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||||||||          |||   ||||||   ||||||:::|||:::
Db        111 TCATTTAATCTTCACAACAACTATAACTATCCCCATTTTATAGAGGATGTA 161

RESULT 46
US-09-925-065A-373047
; Sequence 373047, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 373047
;   LENGTH: 546
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(546)
;   OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-373047

Alignment Scores:
Pred. No.:              31.2          Length:          546
Score:                  54.00         Matches:         10
Percent Similarity:     70.6%         Conservative:    2
Best Local Similarity:  58.8%         Mismatches:      5
Query Match:            33.8%         Indels:          0
DB:                     5             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-373047 (1-546)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||||||||          |||   ||||||   ||||||:::|||:::
Db        111 TCATTTAATCTTCACAACAACTATAACTATCCCCATTTTATAGAGGATGTA 161

RESULT 47
US-10-301-480-442950
; Sequence 442950, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 442950
;   LENGTH: 560
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 557, 558, 559, 560
;   OTHER INFORMATION: n = A,T,C or G
US-10-301-480-442950

Alignment Scores:
Pred. No.:              32.3          Length:          560
Score:                  54.00         Matches:         10
Percent Similarity:     70.6%         Conservative:    2
Best Local Similarity:  58.8%         Mismatches:      5
Query Match:            33.8%         Indels:          0
DB:                     12            Gaps:            0

US-10-758-902-1 (1-30) x US-10-301-480-442950 (1-560)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||||||||          |||   ||||||   ||||||:::|||:::
Db        125 TCATTTAATCTTCACAACAACTATAACTATCCCCATTTTATAGAGGATGTA 175

RESULT 48
US-10-301-480-1056359
; Sequence 1056359, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
```

```
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1056359
;   LENGTH: 560
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 557, 558, 559, 560
;   OTHER INFORMATION: n = A,T,C or G
US-10-301-480-1056359

Alignment Scores:
Pred. No.:              32.3          Length:          560
Score:                  54.00         Matches:         10
Percent Similarity:     70.6%         Conservative:    2
Best Local Similarity:  58.8%         Mismatches:      5
Query Match:            33.8%         Indels:          0
DB:                     12            Gaps:            0

US-10-758-902-1 (1-30) x US-10-301-480-1056359 (1-560)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||||||||          |||   ||||||   ||||||:::|||:::
Db        125 TCATTTAATCTTCACAACAACTATAACTATCCCCATTTTATAGAGGATGTA 175

RESULT 49
US-09-925-065A-748607
; Sequence 748607, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748607
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748607

Alignment Scores:
Pred. No.:              33            Length:          569
Score:                  54.00         Matches:         13
Percent Similarity:     59.3%         Conservative:    3
Best Local Similarity:  48.1%         Mismatches:      11
Query Match:            33.8%         Indels:          0
DB:                     4             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-748607 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 50
US-09-925-065A-748608
; Sequence 748608, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748608
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748608

Alignment Scores:
Pred. No.:              33            Length:          569
Score:                  54.00         Matches:         13
Percent Similarity:     59.3%         Conservative:    3
Best Local Similarity:  48.1%         Mismatches:      11
Query Match:            33.8%         Indels:          0
DB:                     4             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-748608 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 51
US-09-925-065A-748609
; Sequence 748609, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748609
```

```
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748609

Alignment Scores:
Pred. No.:              33              Length:         569
Score:                  54.00           Matches:        13
Percent Similarity:     59.3%           Conservative:   3
Best Local Similarity:  48.1%           Mismatches:     11
Query Match:            33.8%           Indels:         0
DB:                     4               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-748609 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 52
US-09-925-065A-748607
; Sequence 748607, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748607
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748607

Alignment Scores:
Pred. No.:              33              Length:         569
Score:                  54.00           Matches:        13
Percent Similarity:     59.3%           Conservative:   3
Best Local Similarity:  48.1%           Mismatches:     11
Query Match:            33.8%           Indels:         0
DB:                     5               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-748607 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 53
US-09-925-065A-748608
; Sequence 748608, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748608
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748608

Alignment Scores:
Pred. No.:              33              Length:         569
Score:                  54.00           Matches:        13
Percent Similarity:     59.3%           Conservative:   3
Best Local Similarity:  48.1%           Mismatches:     11
Query Match:            33.8%           Indels:         0
DB:                     5               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-748608 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              ||||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 54
US-09-925-065A-748609
; Sequence 748609, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748609
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-748609
```

```
Alignment Scores:
Pred. No.:              33              Length:         569
Score:                  54.00           Matches:        13
Percent Similarity:     59.3%           Conservative:   3
Best Local Similarity:  48.1%           Mismatches:     11
Query Match:            33.8%           Indels:         0
DB:                     5               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-748609 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          2 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 61

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         62 TTGAGAAATAAATTGGCAAAG 82

RESULT 55
US-09-925-065A-799267
; Sequence 799267, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799267
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799267

Alignment Scores:
Pred. No.:              33              Length:         570
Score:                  54.00           Matches:        13
Percent Similarity:     59.3%           Conservative:   3
Best Local Similarity:  48.1%           Mismatches:     11
Query Match:            33.8%           Indels:         0
DB:                     4               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-799267 (1-570)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         63 TTGAGAAATAAATTGGCAAAG 83

RESULT 56
US-09-925-065A-799268
; Sequence 799268, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799268
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799268

Alignment Scores:
Pred. No.:              33              Length:         570
Score:                  54.00           Matches:        13
Percent Similarity:     59.3%           Conservative:   3
Best Local Similarity:  48.1%           Mismatches:     11
Query Match:            33.8%           Indels:         0
DB:                     4               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-799268 (1-570)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         63 TTGAGAAATAAATTGGCAAAG 83

RESULT 57
US-09-925-065A-799269
; Sequence 799269, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799269
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799269

Alignment Scores:
Pred. No.:              33              Length:         570
Score:                  54.00           Matches:        13
Percent Similarity:     59.3%           Conservative:   3
Best Local Similarity:  48.1%           Mismatches:     11
```

```
Query Match:            33.8%          Indels:        0
DB:                     4              Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-799269 (1-570)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::       |||     ||||||     ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         63 TTGAGAAATAAATTGGCAAAG 83

RESULT 58
US-09-925-065A-799267
; Sequence 799267, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799267
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799267

Alignment Scores:
Pred. No.:              33             Length:        570
Score:                  54.00          Matches:       13
Percent Similarity:     59.3%          Conservative:  3
Best Local Similarity:  48.1%          Mismatches:    11
Query Match:            33.8%          Indels:        0
DB:                     5              Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-799267 (1-570)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::       |||     ||||||     ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         63 TTGAGAAATAAATTGGCAAAG 83

RESULT 59
US-09-925-065A-799268
; Sequence 799268, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799268
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799268

Alignment Scores:
Pred. No.:              33             Length:        570
Score:                  54.00          Matches:       13
Percent Similarity:     59.3%          Conservative:  3
Best Local Similarity:  48.1%          Mismatches:    11
Query Match:            33.8%          Indels:        0
DB:                     5              Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-799268 (1-570)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::       |||     ||||||     ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         63 TTGAGAAATAAATTGGCAAAG 83

RESULT 60
US-09-925-065A-799269
; Sequence 799269, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 799269
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-799269

Alignment Scores:
Pred. No.:              33             Length:        570
Score:                  54.00          Matches:       13
Percent Similarity:     59.3%          Conservative:  3
Best Local Similarity:  48.1%          Mismatches:    11
Query Match:            33.8%          Indels:        0
DB:                     5              Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-799269 (1-570)
```

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::       |||      ||||||     ||||||:::
Db          3 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 62

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db         63 TTGAGAAATAAATTGGCAAAG 83
```

RESULT 61
US-09-925-065A-891048
; Sequence 891048, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 891048
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-891048

Alignment Scores:

Pred. No.:	34.8	Length:	592
Score:	54.00	Matches:	13
Percent Similarity:	59.3%	Conservative:	3
Best Local Similarity:	48.1%	Mismatches:	11
Query Match:	33.8%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-1 (1-30) x US-09-925-065A-891048 (1-592)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::       |||      ||||||     ||||||:::
Db        162 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 221

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db        222 TTGAGAAATAAATTGGCAAAG 242
```

RESULT 62
US-09-925-065A-891048
; Sequence 891048, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 891048
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-891048

Alignment Scores:

Pred. No.:	34.8	Length:	592
Score:	54.00	Matches:	13
Percent Similarity:	59.3%	Conservative:	3
Best Local Similarity:	48.1%	Mismatches:	11
Query Match:	33.8%	Indels:	0
DB:	5	Gaps:	0

US-10-758-902-1 (1-30) x US-09-925-065A-891048 (1-592)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::       |||      ||||||     ||||||:::
Db        162 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 221

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db        222 TTGAGAAATAAATTGGCAAAG 242
```

RESULT 63
US-09-925-065A-871708
; Sequence 871708, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 871708
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-871708

Alignment Scores:

Pred. No.:	34.8	Length:	593
Score:	54.00	Matches:	13
Percent Similarity:	59.3%	Conservative:	3
Best Local Similarity:	48.1%	Mismatches:	11
Query Match:	33.8%	Indels:	0
DB:	4	Gaps:	0

US-10-758-902-1 (1-30) x US-09-925-065A-871708 (1-593)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::       |||      ||||||     ||||||:::
Db        162 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 221

Qy         21 LeuArgAsnGluLeuAlaLys 27
```

```
              |||||||||:::|||||||||
Db        222 TTGAGAAATAAATTGGCAAAG 242

RESULT 64
US-09-925-065A-871708
; Sequence 871708, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 871708
;   LENGTH: 593
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-871708

Alignment Scores:
Pred. No.:                34.8          Length:          593
Score:                    54.00         Matches:         13
Percent Similarity:       59.3%         Conservative:    3
Best Local Similarity:    48.1%         Mismatches:      11
Query Match:              33.8%         Indels:          0
DB:                       5             Gaps:            0

US-10-758-902-1 (1-30) x US-09-925-065A-871708 (1-593)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||         |||:::         |||      ||||||      ||||||:::
Db        162 TACCCACCTGCTAGTTATGTCACCTGGGAGGGTCCAGAGTACACACACTTCATCAAGGCT 221

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||||||||:::|||||||||
Db        222 TTGAGAAATAAATTGGCAAAG 242

RESULT 65
US-10-425-115-74403/c
; Sequence 74403, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 74403
;   LENGTH: 651
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_167854C.1
US-10-425-115-74403

Alignment Scores:
Pred. No.:                39.5          Length:          651
Score:                    54.00         Matches:         11
Percent Similarity:       66.7%         Conservative:    3
Best Local Similarity:    52.4%         Mismatches:      7
Query Match:              33.8%         Indels:          0
DB:                       9             Gaps:            0

US-10-758-902-1 (1-30) x US-10-425-115-74403 (1-651)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||   |||   :::||||||               :::|||||||||
Db        548 GGCGAAGCGTATGAACCGCCTTGTTACATACAACCTTCTGAAAAGGGAGTGGCAAAAGGT 489

Qy         29 Thr 29
              :::
Db        488 TCC 486

RESULT 66
US-10-424-599-72856
; Sequence 72856, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 72856
;   LENGTH: 1683
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_36803C.1
US-10-424-599-72856

Alignment Scores:
Pred. No.:                140           Length:          1683
Score:                    54.00         Matches:         11
Percent Similarity:       63.6%         Conservative:    3
Best Local Similarity:    50.0%         Mismatches:      8
Query Match:              33.8%         Indels:          0
DB:                       8             Gaps:            0

US-10-758-902-1 (1-30) x US-10-424-599-72856 (1-1683)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              |||      |||      |||      |||   |||   |||:::||||||:::||||||
Db        733 GTAGTTATGAATTTCTTTGAGGAATTGGAACCACCTTTGTTTGTTCAAGACATGAGAAAC 792

Qy         24 GluLeu 25
              :::|||
Db        793 AAGTTG 798

RESULT 67
US-10-010-901-14/c
; Sequence 14, Application US/10010901
; Publication No. US20020098201A1
; GENERAL INFORMATION:
;  APPLICANT: McFadden, Grant
;  TITLE OF INVENTION: NOVEL MYXOMA GENES FOR IMMUNE MODULATION
;  FILE REFERENCE: 50082/009002
;  CURRENT APPLICATION NUMBER: US/10/010,901
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: US/09/615,041
;  PRIOR FILING DATE: 2000-07-12
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 14
;   LENGTH: 903
;   TYPE: DNA
;   ORGANISM: Myxoma Virus
US-10-010-901-14

Alignment Scores:
Pred. No.:              92.7          Length:         903
Score:                  53.00         Matches:        13
Percent Similarity:     51.4%         Conservative:   6
Best Local Similarity:  35.1%         Mismatches:     8
Query Match:            33.1%         Indels:         10
DB:                     6             Gaps:           1

US-10-758-902-1 (1-30) x US-10-010-901-14 (1-903)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp--------- 20
              |||:::||||||:::      ||||||:::  ||||||   ::::::
Db        590 GTAGCGTTTAACGTACACGTCGCGTACGACGCACCCACCAGTGTAAAGTCGGGATTGCAC 531

Qy         21 --------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
                                  :::|||   |||   ||||||||||||
Db        530 GTAAAACGTACCCTGTTTTTATAACAGAATCGTTTAATGAAGGGAACTCCG 480

RESULT 68
US-11-097-143-40124
; Sequence 40124, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157;832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40124
;   LENGTH: 5366
;   TYPE: DNA
;   ORGANISM: DROSOPHILA
US-11-097-143-40124

Alignment Scores:
Pred. No.:              1e+03         Length:         5366
Score:                  53.00         Matches:        10
Percent Similarity:     65.2%         Conservative:   5
Best Local Similarity:  43.5%         Mismatches:     8
Query Match:            33.1%         Indels:         0
DB:                     13            Gaps:           0

US-10-758-902-1 (1-30) x US-11-097-143-40124 (1-5366)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::||||||   ||||||:::|||   :::   :::         ||||||      :::
Db       2292 TCGCTGGGCATGGCCTACGACTATGATTCGATTATGCACTACGCACGGAACACCTTCTCC 2351

Qy         27 LysGlyThr 29
                 |||||||||
Db       2352 AAGGGCACC 2360

RESULT 69
US-11-097-143-40123
; Sequence 40123, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40123
;   LENGTH: 31068
;   TYPE: DNA
;   ORGANISM: DROSOPHILA
US-11-097-143-40123

Alignment Scores:
Pred. No.:              1.04e+04      Length:         31068
Score:                  53.00         Matches:        10
Percent Similarity:     65.2%         Conservative:   5
Best Local Similarity:  43.5%         Mismatches:     8
Query Match:            33.1%         Indels:         0
DB:                     13            Gaps:           0

US-10-758-902-1 (1-30) x US-11-097-143-40123 (1-31068)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::||||||   ||||||:::|||   :::   :::         ||||||      :::
Db      26247 TCGCTGGGCATGGCCTACGACTATGATTCGATTATGCACTACGCACGGAACACCTTCTCC 26306

Qy         27 LysGlyThr 29
                 |||||||||
Db      26307 AAGGGCACC 26315

RESULT 70
US-10-424-599-26095
; Sequence 26095, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
```

```
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 26095
;   LENGTH: 710
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_123565C.1
US-10-424-599-26095

Alignment Scores:
Pred. No.:              82.9          Length:         710
Score:                  52.50         Matches:        13
Percent Similarity:     62.5%         Conservative:   2
Best Local Similarity:  54.2%         Mismatches:     8
Query Match:            32.8%         Indels:         1
DB:                     8             Gaps:           1

US-10-758-902-1 (1-30) x US-10-424-599-26095 (1-710)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              ||||||||||||       |||::::::   ||||||   ||||||   |||   |||
Db        629 TTTAACTTGGGGTTCATTTACCAACACCAAACATTT---CAGGATGCCAGGAAGGAGCAG 685

Qy         26 AlaLysGlyThr 29
                 |||   |||
Db        686 CTCAAGGTCACA 697

RESULT 71
US-10-301-480-451151/c
; Sequence 451151, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 451151
;   LENGTH: 590
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-451151

Alignment Scores:
Pred. No.:              79.8          Length:         590
Score:                  52.00         Matches:        11
Percent Similarity:     57.7%         Conservative:   4
Best Local Similarity:  42.3%         Mismatches:     11
Query Match:            32.5%         Indels:         0
DB:                     12            Gaps:           0

US-10-758-902-1 (1-30) x US-10-301-480-451151 (1-590)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   |||:::|||   |||||||||   |||             ||||||
Db        445 TTTAATATGGTCAATTTCATGCTAGGTGAATTATATACCAATAAGCCTTTCATTACAAAA 386

Qy         21 LeuArgAsnGluLeuAla 26
                 :::   |||:::|||
Db        385 AGTAAAAAGGAAATAGCT 368

RESULT 72
US-10-301-480-1064560/c
; Sequence 1064560, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1064560
;   LENGTH: 590
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-1064560

Alignment Scores:
Pred. No.:              79.8          Length:         590
Score:                  52.00         Matches:        11
Percent Similarity:     57.7%         Conservative:   4
Best Local Similarity:  42.3%         Mismatches:     11
Query Match:            32.5%         Indels:         0
DB:                     12            Gaps:           0

US-10-758-902-1 (1-30) x US-10-301-480-1064560 (1-590)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   |||:::|||   |||||||||   |||             ||||||
Db        445 TTTAATATGGTCAATTTCATGCTAGGTGAATTATATACCAATAAGCCTTTCATTACAAAA 386

Qy         21 LeuArgAsnGluLeuAla 26
                 :::   |||:::|||
Db        385 AGTAAAAAGGAAATAGCT 368

RESULT 73
US-09-925-065A-382110/c
; Sequence 382110, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 382110
;   LENGTH: 593
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-382110

Alignment Scores:
Pred. No.:              80.4          Length:         593
Score:                  52.00         Matches:        11
Percent Similarity:     57.7%         Conservative:   4
Best Local Similarity:  42.3%         Mismatches:     11
Query Match:            32.5%         Indels:         0
```

```
DB:                    4              Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-382110 (1-593)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   |||:::|||   |||||||||   |||           ||||||
Db        445 TTTAATATGGTCAATTTCATGCTAGGTGAATTATATACCAATAAGCCTTTCATTACAAAA 386

Qy         21 LeuArgAsnGluLeuAla 26
                 :::   |||:::|||
Db        385 AGTAAAAAGGAAATAGCT 368

RESULT 74
US-09-925-065A-382110/c
; Sequence 382110, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 382110
;   LENGTH: 593
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-382110

Alignment Scores:
Pred. No.:              80.4          Length:        593
Score:                  52.00         Matches:       11
Percent Similarity:     57.7%         Conservative:  4
Best Local Similarity:  42.3%         Mismatches:    11
Query Match:            32.5%         Indels:        0
DB:                     5             Gaps:          0

US-10-758-902-1 (1-30) x US-09-925-065A-382110 (1-593)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::|||   |||:::|||   |||||||||   |||           ||||||
Db        445 TTTAATATGGTCAATTTCATGCTAGGTGAATTATATACCAATAAGCCTTTCATTACAAAA 386

Qy         21 LeuArgAsnGluLeuAla 26
                 :::   |||:::|||
Db        385 AGTAAAAAGGAAATAGCT 368

RESULT 75
US-10-198-846-11177
; Sequence 11177, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Steinmann, Kathleen
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;  TITLE OF INVENTION:  FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-049
;  CURRENT APPLICATION NUMBER: US/10/198,846
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: 60/306,220
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 14084
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11177
;   LENGTH: 1040
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-198-846-11177

Alignment Scores:
Pred. No.:              170           Length:        1040
Score:                  52.00         Matches:       11
Percent Similarity:     62.5%         Conservative:  4
Best Local Similarity:  45.8%         Mismatches:    9
Query Match:            32.5%         Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-1 (1-30) x US-10-198-846-11177 (1-1040)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              |||   ||||||:::   |||:::   |||:::||||||   :::       |||   |||
Db        518 GTGTTATTTAACATTCTTGAATCTTCAGAGTGGCCAACACTTTTGTTGACTCTTCACAAT 577

Qy         24 GluLeuAlaLys 27
                 |||   |||
Db        578 AACCTATTAAAA 589

RESULT 76
US-10-425-114-25526
; Sequence 25526, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25526
;   LENGTH: 1689
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3912-027-D12_FLI
US-10-425-114-25526

Alignment Scores:
Pred. No.:              325           Length:        1689
Score:                  52.00         Matches:       10
Percent Similarity:     66.7%         Conservative:  4
Best Local Similarity:  47.6%         Mismatches:    7
Query Match:            32.5%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x US-10-425-114-25526 (1-1689)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||   |||   :::||||||           :::|||:::|||
Db       1287 GGCGAAGCATATGAACCGCCTTGTTACATACAACCTTTTGAAAAGGGAGTGGCAGAAGGT 1346

Qy         29 Thr 29
                :::
Db       1347 TCC 1349

RESULT 77
```

```
US-10-425-114-17777
; Sequence 17777, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 17777
;   LENGTH: 1692
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3075-022-B9_FLI
US-10-425-114-17777

Alignment Scores:
Pred. No.:                326           Length:          1692
Score:                    52.00         Matches:         10
Percent Similarity:       66.7%         Conservative:    4
Best Local Similarity:    47.6%         Mismatches:      7
Query Match:              32.5%         Indels:          0
DB:                       8             Gaps:            0

US-10-758-902-1 (1-30) x US-10-425-114-17777 (1-1692)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||   |||   :::||||||           :::|||:::|||
Db       1284 GGCGAAGCATATGAACCGCCTTGTTACATACAACCTTTTGAAAAGGGAGTGGCAGAAGGT 1343

Qy         29 Thr 29
              :::
Db       1344 TCC 1346

RESULT 78
US-10-425-115-68440
; Sequence 68440, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 68440
;   LENGTH: 2622
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_162411C.1
US-10-425-115-68440

Alignment Scores:
Pred. No.:                585           Length:          2622
Score:                    52.00         Matches:         10
Percent Similarity:       66.7%         Conservative:    4
Best Local Similarity:    47.6%         Mismatches:      7
Query Match:              32.5%         Indels:          0
DB:                       9             Gaps:            0

US-10-758-902-1 (1-30) x US-10-425-115-68440 (1-2622)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||   |||   :::||||||           :::|||:::|||
Db       2140 GGCGAAGCATATGAACCGCCTTGTTACATACAACCTTTTGAAAAGGGAGTGGCAGAAGGT 2199

Qy         29 Thr 29
              :::
Db       2200 TCC 2202

RESULT 79
US-10-029-386-16475
; Sequence 16475, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16475
;   LENGTH: 258
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR4.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.48
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.38
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.62
;   OTHER INFORMATION: NT HIT: AF156490.1, EVALUE 5.00e-58
;   OTHER INFORMATION: EST_HUMAN HIT: BI914503.1, EVALUE 6.00e-09
;   OTHER INFORMATION: SWISSPROT HIT: P23574, EVALUE 6.00e-46
US-10-029-386-16475

Alignment Scores:
Pred. No.:                32.6          Length:          258
Score:                    51.50         Matches:         13
Percent Similarity:       52.6%         Conservative:    7
Best Local Similarity:    34.2%         Mismatches:      10
Query Match:              32.2%         Indels:          8
DB:                       7             Gaps:            1

US-10-758-902-1 (1-30) x US-10-029-386-16475 (1-258)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::       |||   |||   ||||||   ||||||:::||| :::||||||
Db         64 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 123

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||:|||||:::       |||
Db        124 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 175

RESULT 80
US-10-029-386-2775
; Sequence 2775, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
```

```
; SEQ ID NO 2775
;   LENGTH: 543
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR4.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.48
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.38
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.62
;   OTHER INFORMATION: NT HIT: AF156490.1, EVALUE 1.00e-57
;   OTHER INFORMATION: EST_HUMAN HIT: BI914503.1, EVALUE 1.00e-08
;   OTHER INFORMATION: SWISSPROT HIT: P23574, EVALUE 2.00e-46
US-10-029-386-2775

Alignment Scores:
Pred. No.:              88.1          Length:         543
Score:                  51.50         Matches:        13
Percent Similarity:     52.6%         Conservative:   7
Best Local Similarity:  34.2%         Mismatches:     10
Query Match:            32.2%         Indels:         8
DB:                     7             Gaps:           1

US-10-758-902-1 (1-30) x US-10-029-386-2775 (1-543)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db        247 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 306

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db        307 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 358

RESULT 81
US-10-149-930-2/c
; Sequence 2, Application US/10149930
; Publication No. US20030215813A1
; GENERAL INFORMATION:
;  APPLICANT: Roberds, Steven L.
;  APPLICANT:  Benjamin, Chris
;  APPLICANT:  Ruble, Cara L.
;  APPLICANT:  Karnovsky, Alla M.
;  TITLE OF INVENTION: Human Ion Channels
;  FILE REFERENCE: PHRM0399
;  CURRENT APPLICATION NUMBER: US/10/149,930
;  CURRENT FILING DATE:  2002-10-21
;  PRIOR APPLICATION NUMBER: 09/460,602
;  PRIOR FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: PCT/US00/33829
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 549
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-149-930-2

Alignment Scores:
Pred. No.:              89.4          Length:         549
Score:                  51.50         Matches:        13
Percent Similarity:     52.6%         Conservative:   7
Best Local Similarity:  34.2%         Mismatches:     10
Query Match:            32.2%         Indels:         8
DB:                     7             Gaps:           1

US-10-758-902-1 (1-30) x US-10-149-930-2 (1-549)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db        488 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 429

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db        428 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 377

RESULT 82
US-09-893-321-1/c
; Sequence 1, Application US/09893321
; Patent No. US20020082407A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Friddle, Carl Johan
;  APPLICANT:  Mathur, Brian
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20020082407A1el Human GABA Receptors and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0195-USA
;  CURRENT APPLICATION NUMBER: US/09/893,321
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: US 60/214,083
;  PRIOR FILING DATE: 2000-06-27
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1398
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-893-321-1

Alignment Scores:
Pred. No.:              311           Length:         1398
Score:                  51.50         Matches:        13
Percent Similarity:     52.6%         Conservative:   7
Best Local Similarity:  34.2%         Mismatches:     10
Query Match:            32.2%         Indels:         8
DB:                     3             Gaps:           1

US-10-758-902-1 (1-30) x US-09-893-321-1 (1-1398)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db       1335 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1276

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db       1275 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1224

RESULT 83
US-10-380-727-48/c
; Sequence 48, Application US/10380727
; Publication No. US20040024183A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.; LEE, Ernestine A.;
;  APPLICANT:  YUE, Henry; LAL, Preeti G.;
;  APPLICANT:  CHAWLA, Narinder K.; BAUGHN, Mariah R.;
;  APPLICANT:  WARREN, Bridget A.; LEE, Sally;
;  APPLICANT:  SANJANWALA, Madhu S.; YAO, Monique G.;
;  APPLICANT:  RAMKUMAR, Jayalaxmi; THORNTON, Michael;
;  APPLICANT:  GANDHI, Ameena R.; POLICKY, Jennifer L.;
;  APPLICANT:  ELLIOTT, Vicki S.; ARVIZU, Chandra;
;  APPLICANT:  RAUMANN, Brigitte E.; BRUNS, Christopher M.;
;  APPLICANT:  NAINA, Amir; HAFALIA, April J.A.;
;  APPLICANT:  NGUYEN, Danniel B.; XU, Yuming;
;  APPLICANT:  LU, Dyung Aina M.; ISON, Craig H.;
;  APPLICANT:  GRIFFIN, Jennifer A.; REDDY, Roopa M.;
;  APPLICANT:  BURFORD, Neil
;  TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
;  FILE REFERENCE: PI-0217 USN
;  CURRENT APPLICATION NUMBER: US/10/380,727
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: PCT/US01/28938
;  PRIOR FILING DATE: 2001-09-14
;  PRIOR APPLICATION NUMBER: US 60/241,700
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: US 60/240,540
```

; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/239,057
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/236,882
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,842
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,685
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 48
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040024183A1 7476283CB1
US-10-380-727-48

Alignment Scores:

Pred. No.:	326	Length:	1446
Score:	51.50	Matches:	13
Percent Similarity:	52.6%	Conservative:	7
Best Local Similarity:	34.2%	Mismatches:	10
Query Match:	32.2%	Indels:	8
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-10-380-727-48 (1-1446)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db       1383 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1324

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db       1323 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1272
```

RESULT 84
US-10-092-900A-7/c
; Sequence 7, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev,, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 7
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1426)
US-10-092-900A-7

Alignment Scores:

Pred. No.:	328	Length:	1455
Score:	51.50	Matches:	13
Percent Similarity:	52.6%	Conservative:	7
Best Local Similarity:	34.2%	Mismatches:	10
Query Match:	32.2%	Indels:	8
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-10-092-900A-7 (1-1455)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db       1365 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1306

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db       1305 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1254
```

RESULT 85
US-10-092-900A-3/c
; Sequence 3, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.

```
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Guo, Xiaojia Sasha
;  APPLICANT:  Tchernev,, Velizar T.
;  APPLICANT:  Fernandes, Elma R.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Liu, Yi
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Leite, Mario W.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Alsobrook, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-290C
;  CURRENT APPLICATION NUMBER: US/10/092,900A
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: USSN 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/283,675
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: USSN 60/338,092
;  PRIOR FILING DATE: 2001-12-03
;  PRIOR APPLICATION NUMBER: USSN 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/274,191
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/325,681
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: USSN 60/304,354
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: USSN 60/279,995
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: USSN 60/294,899
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: USSN 60/287,424
;  PRIOR FILING DATE: 2001-04-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 3
;   LENGTH: 1457
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (9)..(1425)
US-10-092-900A-3

Alignment Scores:
Pred. No.:              329          Length:        1457
Score:                  51.50        Matches:       13
Percent Similarity:     52.6%        Conservative:  7
Best Local Similarity:  34.2%        Mismatches:    10
Query Match:            32.2%        Indels:        8
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-10-092-900A-3 (1-1457)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db       1364 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1305

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                    :::   :::||||||:::      |||
Db       1304 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1253

RESULT 86
US-11-096-568A-15041/c
; Sequence 15041, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides E
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15041
;   LENGTH: 1562
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ceres Seq. ID no. 12341687
US-11-096-568A-15041

Alignment Scores:
Pred. No.:              361          Length:        1562
Score:                  51.50        Matches:       12
Percent Similarity:     65.2%        Conservative:  3
Best Local Similarity:  52.2%        Mismatches:    7
Query Match:            32.2%        Indels:        1
DB:                     16           Gaps:          1

US-10-758-902-1 (1-30) x US-11-096-568A-15041 (1-1562)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||:::     |||      :::||||||     |||   |||
Db       1378 AATCTGGGAGAAGCCCACCGGCCACCACCCAGCTTGCAGGAT---AATAATAGACTGAAG 1322

Qy         27 LysGlyThr 29
              :::|||||||
Db       1321 CAGGGTACA 1313

RESULT 87
US-09-893-321-5/c
; Sequence 5, Application US/09893321
; Patent No. US20020082407A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Friddle, Carl Johan
;  APPLICANT:  Mathur, Brian
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20020082407A1el Human GABA Receptors and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0195-USA
;  CURRENT APPLICATION NUMBER: US/09/893,321
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: US 60/214,083
;  PRIOR FILING DATE: 2000-06-27
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1568
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-893-321-5

Alignment Scores:
Pred. No.:              363          Length:        1568
Score:                  51.50        Matches:       13
Percent Similarity:     52.6%        Conservative:  7
Best Local Similarity:  34.2%        Mismatches:    10
Query Match:            32.2%        Indels:        8
DB:                     3            Gaps:          1

US-10-758-902-1 (1-30) x US-09-893-321-5 (1-1568)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
```

```
Db       1452 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1393

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                    :::   :::||||||:::      |||
Db       1392 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1341
```

RESULT 88
US-10-482-834A-99/c
; Sequence 99, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hillary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 1672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-834A-99

Alignment Scores:

Pred. No.:	395	Length:	1672
Score:	51.50	Matches:	13
Percent Similarity:	52.6%	Conservative:	7
Best Local Similarity:	34.2%	Mismatches:	10
Query Match:	32.2%	Indels:	8
DB:	10	Gaps:	1

US-10-758-902-1 (1-30) x US-10-482-834A-99 (1-1672)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db       1442 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1383

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                    :::   :::||||||:::      |||
Db       1382 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1331
```

RESULT 89
US-10-482-834A-100/c
; Sequence 100, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hillary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 1672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-834A-100

Alignment Scores:

Pred. No.:	395	Length:	1672
Score:	51.50	Matches:	13
Percent Similarity:	52.6%	Conservative:	7
Best Local Similarity:	34.2%	Mismatches:	10
Query Match:	32.2%	Indels:	8
DB:	10	Gaps:	1

US-10-758-902-1 (1-30) x US-10-482-834A-100 (1-1672)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db       1442 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1383

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                    :::   :::||||||:::      |||
Db       1382 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1331
```

RESULT 90
US-10-437-963-34100
; Sequence 34100, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 34100
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2355)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38148C.1
US-10-437-963-34100

Alignment Scores:

Pred. No.:	624	Length:	2355
Score:	51.50	Matches:	11
Percent Similarity:	59.3%	Conservative:	5
Best Local Similarity:	40.7%	Mismatches:	8
Query Match:	32.2%	Indels:	3
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-10-437-963-34100 (1-2355)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||   :::|||      ||||||      ::::::||||||      :::|||:::
Db        814 AACCTTAATCAAGCAATGTCGTATCCACCACTGATGGAGGATTTGGGGCGCCAACTCAGC 873

Qy         27 Lys---------GlyThrPro 30
              |||         |||   |||
Db        874 AAGAAATGTGGTGGTTTACCT 894
```

RESULT 91
US-09-818-657-1/c
; Sequence 1, Application US/09818657

```
; Publication No. US20030077773A1
; GENERAL INFORMATION:
;  APPLICANT: BRANDON, Rhonda et al.
;  TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL001006-CIP
;  CURRENT APPLICATION NUMBER: US/09/818,657
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: 09/730,002
;  PRIOR FILING DATE: 2000-12-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2819
;   TYPE: DNA
;   ORGANISM: Human
US-09-818-657-1

Alignment Scores:
Pred. No.:                794             Length:         2819
Score:                    51.50           Matches:        13
Percent Similarity:       52.6%           Conservative:   7
Best Local Similarity:    34.2%           Mismatches:     10
Query Match:              32.2%           Indels:         8
DB:                       3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-818-657-1 (1-2819)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::       |||   |||   ||||||   ||||||:::||| :::|||||
Db       1455 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1396

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db       1395 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1344

RESULT 92
US-11-136-623-1/c
; Sequence 1, Application US/11136623
; Publication No. US20050221437A1
; GENERAL INFORMATION:
;  APPLICANT: BRANDON, Rhonda, et al.
;  TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL001006-CIPCON
;  CURRENT APPLICATION NUMBER: US/11/136,623
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: 09/730,002
;  PRIOR FILING DATE: 2000-12-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2819
;   TYPE: DNA
;   ORGANISM: Human
US-11-136-623-1

Alignment Scores:
Pred. No.:                794             Length:         2819
Score:                    51.50           Matches:        13
Percent Similarity:       52.6%           Conservative:   7
Best Local Similarity:    34.2%           Mismatches:     10
Query Match:              32.2%           Indels:         8
DB:                       13              Gaps:           1

US-10-758-902-1 (1-30) x US-11-136-623-1 (1-2819)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::       |||   |||   ||||||   ||||||:::||| :::|||||
Db       1455 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1396

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db       1395 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1344

RESULT 93
US-09-818-657-3/c
; Sequence 3, Application US/09818657
; Publication No. US20030077773A1
; GENERAL INFORMATION:
;  APPLICANT: BRANDON, Rhonda et al.
;  TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL001006-CIP
;  CURRENT APPLICATION NUMBER: US/09/818,657
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: 09/730,002
;  PRIOR FILING DATE: 2000-12-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 82938
;   TYPE: DNA
;   ORGANISM: Human
US-09-818-657-3

Alignment Scores:
Pred. No.:                7.25e+04        Length:         82938
Score:                    51.50           Matches:        13
Percent Similarity:       52.6%           Conservative:   7
Best Local Similarity:    34.2%           Mismatches:     10
Query Match:              32.2%           Indels:         8
DB:                       3               Gaps:           1

US-10-758-902-1 (1-30) x US-09-818-657-3 (1-82938)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::       |||   |||   ||||||   ||||||:::||| :::|||||
Db      81869 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 81810

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db      81809 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 81758

RESULT 94
US-11-136-623-3/c
; Sequence 3, Application US/11136623
; Publication No. US20050221437A1
; GENERAL INFORMATION:
;  APPLICANT: BRANDON, Rhonda, et al.
;  TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL001006-CIPCON
;  CURRENT APPLICATION NUMBER: US/11/136,623
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: 09/730,002
;  PRIOR FILING DATE: 2000-12-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 82938
;   TYPE: DNA
;   ORGANISM: Human
US-11-136-623-3

Alignment Scores:
Pred. No.:                7.25e+04        Length:         82938
Score:                    51.50           Matches:        13
Percent Similarity:       52.6%           Conservative:   7
Best Local Similarity:    34.2%           Mismatches:     10
Query Match:              32.2%           Indels:         8
DB:                       13              Gaps:           1
```

```
US-10-758-902-1 (1-30) x US-11-136-623-3 (1-82938)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::  :::     |||  |||  ||||||  ||||||:::||| :::|||||
Db      81869 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 81810

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                   :::  :::||||||:::      |||
Db      81809 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 81758

RESULT 95
US-11-117-187-204
; Sequence 204, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
;  APPLICANT: PREUSS, DAPHNE
;  APPLICANT:  COPENHAVER, GREGORY
;  TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
;  FILE REFERENCE: ARCD:309US
;  CURRENT APPLICATION NUMBER: US/11/117,187
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: US/09/531,120
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,219
;  PRIOR FILING DATE: 1999-03-18
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 204
;   LENGTH: 109974
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-11-117-187-204

Alignment Scores:
Pred. No.:              1.06e+05        Length:         109974
Score:                  51.50           Matches:        10
Percent Similarity:     69.6%           Conservative:   6
Best Local Similarity:  43.5%           Mismatches:     4
Query Match:            32.2%           Indels:         3
DB:                     15              Gaps:           1

US-10-758-902-1 (1-30) x US-11-117-187-204 (1-109974)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAsp---------LeuArgAsnGluLeuAlaLys 27
              |||  :::|||||||||||||   ::::::         ||||||:::  ::::::
Db      23327 GCCGAGAAGTATCCTACCTTCTTTGAAGAACTCCTCACACTGAGAAGTTCAATCAGTTCG 23386

Qy         28 GlyThrPro 30
              |||||||||
Db      23387 GGAACCCCG 23395

RESULT 96
US-10-767-701-18898
; Sequence 18898, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 18898
;   LENGTH: 460
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3480-009-P1-K1-F12
US-10-767-701-18898

Alignment Scores:
Pred. No.:              87*             Length:         460
Score:                  51.00           Matches:        8
Percent Similarity:     70.0%           Conservative:   6
Best Local Similarity:  40.0%           Mismatches:     6
Query Match:            31.9%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-10-767-701-18898 (1-460)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              :::  |||  ||||||||||||:::     ::::::|||:::  :::   ||||||
Db         25 CATGTCGTCGACTTCAACCTTGGCGACGGCATACAGTGGCCATCGCTCATGTCAGACCTT 84

RESULT 97
US-09-925-065A-826328
; Sequence 826328, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:. Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 826328
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-826328

Alignment Scores:
Pred. No.:              98.5            Length:         505
Score:                  51.00           Matches:        10
Percent Similarity:     66.7%           Conservative:   6
Best Local Similarity:  41.7%           Mismatches:     8
Query Match:            31.9%           Indels:         0
DB:                     4               Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-826328 (1-505)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::  :::|||          :::  :::||||||||||||
Db        228 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 287

Qy         27 LysGlyThrPro 30
              :::||||||||
Db        288 AGAGGGACACCA 299

RESULT 98
US-09-925-065A-826329
; Sequence 826329, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
```

```
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 826329
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-826329

Alignment Scores:
Pred. No.:              98.5          Length:         505
Score:                  51.00         Matches:        10
Percent Similarity:     66.7%         Conservative:   6
Best Local Similarity:  41.7%         Mismatches:     8
Query Match:            31.9%         Indels:         0
DB:                     4             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-826329 (1-505)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::   :::|||            :::   :::||||||||||||
Db        228 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 287

Qy         27 LysGlyThrPro 30
              :::|||||||||
Db        288 AGAGGGACACCA 299

RESULT 99
US-09-925-065A-826328
; Sequence 826328, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 826328
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-826328

Alignment Scores:
Pred. No.:              98.5          Length:         505
Score:                  51.00         Matches:        10
Percent Similarity:     66.7%         Conservative:   6
Best Local Similarity:  41.7%         Mismatches:     8
Query Match:            31.9%         Indels:         0
DB:                     5             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-826328 (1-505)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::   :::|||            :::   :::||||||||||||
Db        228 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 287

Qy         27 LysGlyThrPro 30
              :::|||||||||
Db        288 AGAGGGACACCA 299

RESULT 100
US-09-925-065A-826329
; Sequence 826329, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 826329
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-826329

Alignment Scores:
Pred. No.:              98.5          Length:         505
Score:                  51.00         Matches:        10
Percent Similarity:     66.7%         Conservative:   6
Best Local Similarity:  41.7%         Mismatches:     8
Query Match:            31.9%         Indels:         0
DB:                     5             Gaps:           0

US-10-758-902-1 (1-30) x US-09-925-065A-826329 (1-505)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||:::   :::|||            :::   :::||||||||||||
Db        228 AGTCTGCAGGAGAGTCTGAAGTACATGCCACTTCCTGAAGTGATCAGGAATGAACTGGGG 287

Qy         27 LysGlyThrPro 30
              :::|||||||||
Db        288 AGAGGGACACCA 299


Search completed: September 18, 2006, 21:17:44
Job time : 367.715 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 20:23:47 ; Search time 53.6313 Seconds
(without alignments)
1471.519 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2330496 seqs, 876882855 residues

Total number of hits satisfying chosen parameters: 4660992

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_18092006_162720_11806/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10758902_@CGN_1_1_306_@runat_18092006_162720_11806 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	57	35.6	2392	6	US-10-449-902-13635	Sequence 13635, A
	2	55.5	34.7	1000	8	US-11-266-748A-293743	Sequence 293743,
c	3	55.5	34.7	1000	8	US-11-266-748A-345172	Sequence 345172,
	4	55.5	34.7	1000	8	US-11-266-748A-405859	Sequence 405859,
c	5	55.5	34.7	1000	8	US-11-266-748A-476905	Sequence 476905,
c	6	55	34.4	1142	8	US-11-266-748A-185242	Sequence 185242,
c	7	55	34.4	3873	8	US-11-266-748A-22343	Sequence 22343, A
	8	54	33.8	3828	9	US-11-218-305-1179	Sequence 1179, Ap
c	9	53	33.1	875	8	US-11-266-748A-36243	Sequence 36243, A
	10	52	32.5	1000	8	US-11-266-748A-199596	Sequence 199596,
c	11	52	32.5	1612	9	US-11-056-355B-79603	Sequence 79603, A
	12	52	32.5	1837	9	US-11-218-305-1178	Sequence 1178, Ap
c	13	51.5	32.2	1562	9	US-11-056-355B-5323	Sequence 5323, Ap
c	14	51.5	32.2	1562	9	US-11-056-355B-8326	Sequence 8326, Ap
	15	51.5	32.2	1779	8	US-11-266-748A-356267	Sequence 356267,
c	16	51.5	32.2	1779	8	US-11-266-748A-439646	Sequence 439646,
	17	51.5	32.2	3155	6	US-10-449-902-16834	Sequence 16834, A
	18	51.5	32.2	3173	6	US-10-449-902-15622	Sequence 15622, A
	19	51	31.9	6449	7	US-11-299-286-69	Sequence 69, Appl
	20	51	31.9	194534	6	US-10-540-898-458	Sequence 458, App
c	21	51	31.9	4647455	6	US-10-641-321-205	Sequence 205, App
c	22	50	31.2	598	7	US-11-292-078-9579	Sequence 9579, Ap
c	23	50	31.2	1350	9	US-11-218-305-4673	Sequence 4673, Ap
c	24	50	31.2	1847	9	US-11-218-305-4675	Sequence 4675, Ap
	25	50	31.2	2172	6	US-10-449-902-22294	Sequence 22294, A
c	26	50	31.2	2455	9	US-11-056-355B-77422	Sequence 77422, A
c	27	50	31.2	2458	9	US-11-056-355B-107356	Sequence 107356,
c	28	50	31.2	2458	9	US-11-056-355B-118595	Sequence 118595,
c	29	50	31.2	2482	6	US-10-953-349-10942	Sequence 10942, A
c	30	50	31.2	2482	9	US-11-056-355B-45708	Sequence 45708, A
c	31	50	31.2	5166	9	US-11-218-305-4674	Sequence 4674, Ap
c	32	50	31.2	24231	6	US-10-540-898-353	Sequence 353, App
c	33	49	30.6	1006	8	US-11-266-748A-364364	Sequence 364364,
c	34	49	30.6	1006	8	US-11-266-748A-388269	Sequence 388269,
	35	49	30.6	1006	8	US-11-266-748A-447743	Sequence 447743,
	36	49	30.6	1118	8	US-11-216-545-3180	Sequence 3180, Ap
	37	49	30.6	1344	8	US-11-217-529-4610	Sequence 4610, Ap
	38	49	30.6	1439	9	US-11-174-307B-4567	Sequence 4567, Ap
c	39	49	30.6	1647	8	US-11-216-545-2350	Sequence 2350, Ap
	40	49	30.6	2010	8	US-11-266-748A-188310	Sequence 188310,
	41	49	30.6	3879	8	US-11-266-748A-75195	Sequence 75195, A
	42	49	30.6	3879	8	US-11-266-748A-108778	Sequence 108778,
c	43	49	30.6	3879	8	US-11-266-748A-128006	Sequence 128006,
	44	49	30.6	7561	8	US-11-289-102-42	Sequence 42, Appl
	45	48.5	30.3	607	7	US-11-292-078-3562	Sequence 3562, Ap
	46	48.5	30.3	939	8	US-11-217-529-75584	Sequence 75584, A
	47	48.5	30.3	2231	8	US-11-266-748A-186724	Sequence 186724,
	48	48	30.0	398	8	US-11-266-748A-36729	Sequence 36729, A
	49	48	30.0	401	8	US-11-266-748A-7702	Sequence 7702, Ap
	50	48	30.0	724	8	US-11-266-748A-358244	Sequence 358244,
c	51	48	30.0	724	8	US-11-266-748A-441623	Sequence 441623,
c	52	48	30.0	967	8	US-11-266-748A-370782	Sequence 370782,
	53	48	30.0	967	8	US-11-266-748A-454161	Sequence 454161,
c	54	48	30.0	1077	6	US-10-374-780A-1447	Sequence 1447, Ap
	55	48	30.0	1288	8	US-11-266-748A-364704	Sequence 364704,
	56	48	30.0	1288	8	US-11-266-748A-388331	Sequence 388331,
c	57	48	30.0	1288	8	US-11-266-748A-448083	Sequence 448083,
	58	48	30.0	1404	8	US-11-266-748A-188021	Sequence 188021,
	59	48	30.0	2130	8	US-11-217-529-264	Sequence 264, App
	60	48	30.0	2139	8	US-11-217-529-75693	Sequence 75693, A
c	61	48	30.0	2209	8	US-11-266-748A-61640	Sequence 61640, A
c	62	48	30.0	3045	8	US-11-266-748A-30799	Sequence 30799, A
c	63	48	30.0	4161	9	US-11-218-305-24120	Sequence 24120, A
	64	48	30.0	5640	9	US-11-218-305-18783	Sequence 18783, A
c	65	48	30.0	7347	6	US-10-536-606-17	Sequence 17, Appl
c	66	48	30.0	687411	6	US-10-540-898-26	Sequence 26, Appl
	67	48	30.0	1130575	6	US-10-833-833-125	Sequence 125, App
c	68	47.5	29.7	1000	8	US-11-266-748A-202256	Sequence 202256,
	69	47.5	29.7	1803	6	US-10-471-571A-4685	Sequence 4685, Ap
	70	47.5	29.7	15056	7	US-11-206-135-3	Sequence 3, Appli
	71	47.5	29.7	75762	9	US-11-021-837-38	Sequence 38, Appl
	72	47	29.4	327	6	US-10-488-619-181	Sequence 181, App
c	73	47	29.4	548	7	US-11-292-078-2755	Sequence 2755, Ap
	74	47	29.4	763	8	US-11-266-748A-363915	Sequence 363915,
c	75	47	29.4	763	8	US-11-266-748A-447294	Sequence 447294,
	76	47	29.4	833	8	US-11-266-748A-33176	Sequence 33176, A
	77	47	29.4	833	8	US-11-266-748A-231941	Sequence 231941,
c	78	47	29.4	868	8	US-11-266-748A-415251	Sequence 415251,
c	79	47	29.4	1000	8	US-11-266-748A-202167	Sequence 202167,
c	80	47	29.4	2183	8	US-11-293-697-977	Sequence 977, App

81	47	29.4	2355	8	US-11-217-529-77943	Sequence 77943, A
82	47	29.4	2658	8	US-11-217-529-521	Sequence 521, App
c 83	47	29.4	3072	9	US-11-218-305-12860	Sequence 12860, A
84	47	29.4	4628	6	US-10-511-937-2809	Sequence 2809, Ap
85	47	29.4	5458	8	US-11-266-748A-56811	Sequence 56811, A
86	47	29.4	6534	6	US-10-713-648A-47	Sequence 47, Appl
87	47	29.4	8093	6	US-10-713-648A-30	Sequence 30, Appl
88	47	29.4	17719	8	US-11-266-748A-24960	Sequence 24960, A
c 89	47	29.4	48509	6	US-10-539-228-510	Sequence 510, App
90	47	29.4	184242	8	US-11-266-748A-29043	Sequence 29043, A
c 91	47	29.4	319486	8	US-11-266-748A-22833	Sequence 22833, A
92	47	29.4	4647455	6	US-10-641-321-205	Sequence 205, App
c 93	46.5	29.1	872	8	US-11-266-748A-366769	Sequence 366769,
94	46.5	29.1	872	8	US-11-266-748A-450148	Sequence 450148,
95	46.5	29.1	1749	9	US-11-348-413-11970	Sequence 11970, A
96	46.5	29.1	1761	9	US-11-348-413-13488	Sequence 13488, A
c 97	46.5	29.1	2131	9	US-11-218-305-5435	Sequence 5435, Ap
98	46.5	29.1	85920	6	US-10-669-920-938	Sequence 938, App
c 99	46.5	29.1	130414	6	US-10-833-833-34	Sequence 34, Appl
c 100	46	28.7	404	8	US-11-266-748A-302904	Sequence 302904,

ALIGNMENTS

```
RESULT 1
US-10-449-902-13635
; Sequence 13635, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13635
;   LENGTH: 2392
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK110983
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-13635

Alignment Scores:
Pred. No.:                6.12          Length:          2392
Score:                    57.00         Matches:         16
Percent Similarity:       48.7%         Conservative:    3
Best Local Similarity:    41.0%         Mismatches:      8
Query Match:              35.6%         Indels:          12
DB:                       6             Gaps:            2

US-10-758-902-1 (1-30) x US-10-449-902-13635 (1-2392)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        471 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 527

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        528 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 584

RESULT 2
US-11-266-748A-293743
; Sequence 293743, Application US/11266748A
```

```
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 293743
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-293743

Alignment Scores:
Pred. No.:                3.69          Length:          1000
Score:                    55.50         Matches:         10
Percent Similarity:       48.7%         Conservative:    9
Best Local Similarity:    25.6%         Mismatches:      11
Query Match:              34.7%         Indels:          9
DB:                       8             Gaps:            1

US-10-758-902-1 (1-30) x US-11-266-748A-293743 (1-1000)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr---------------------- 12
              ||||||::::::   |||:::            |||
Db        344 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 403

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::|||||||||   :::      ||||||
Db        404 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 460

RESULT 3
US-11-266-748A-345172/c
; Sequence 345172, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
```

```
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 345172
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-345172

Alignment Scores:
Pred. No.:              3.69          Length:        1000
Score:                  55.50         Matches:       10
Percent Similarity:     48.7%         Conservative:  9
Best Local Similarity:  25.6%         Mismatches:    11
Query Match:            34.7%         Indels:        9
DB:                     8             Gaps:          1

US-10-758-902-1 (1-30) x US-11-266-748A-345172 (1-1000)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr----------------------- 12
              ||||||::::::   |||:::           |||
Db        657 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 598

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::|||||||||   :::      ||||||
Db        597 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 541

RESULT 4
US-11-266-748A-405859
; Sequence 405859, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 405859
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-405859

Alignment Scores:
Pred. No.:              3.69          Length:        1000
Score:                  55.50         Matches:       10
Percent Similarity:     48.7%         Conservative:  9
Best Local Similarity:  25.6%         Mismatches:    11
Query Match:            34.7%         Indels:        9
DB:                     8             Gaps:          1

US-10-758-902-1 (1-30) x US-11-266-748A-405859 (1-1000)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr----------------------- 12
              ||||||::::::   |||:::           |||
Db        344 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 403

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::|||||||||   :::      ||||||
Db        404 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 460

RESULT 5
US-11-266-748A-476905/c
; Sequence 476905, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 476905
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-476905

Alignment Scores:
Pred. No.:              3.69          Length:        1000
Score:                  55.50         Matches:       10
Percent Similarity:     48.7%         Conservative:  9
Best Local Similarity:  25.6%         Mismatches:    11
Query Match:            34.7%         Indels:        9
DB:                     8             Gaps:          1

US-10-758-902-1 (1-30) x US-11-266-748A-476905 (1-1000)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr----------------------- 12
              ||||||::::::   |||:::           |||
Db        657 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 598

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::|||||||||   :::      ||||||
Db        597 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 541

RESULT 6
US-11-266-748A-185242/c
```

```
; Sequence 185242, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185242
;   LENGTH: 1142
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-185242

Alignment Scores:
Pred. No.:              5.41          Length:        1142
Score:                  55.00         Matches:       8
Percent Similarity:     70.8%         Conservative:  9
Best Local Similarity:  33.3%         Mismatches:    7
Query Match:            34.4%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x US-11-266-748A-185242 (1-1142)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ::::::|||   |||::::::   |||:::|||:::||||||   :::::::::
Db        553 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 494

Qy         27 LysGlyThrPro 30
                 |||   |||
Db        493 TCCGGAGAGCCC 482

RESULT 7
US-11-266-748A-22343/c
; Sequence 22343, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22343
;   LENGTH: 3873
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-22343

Alignment Scores:
Pred. No.:              26.4          Length:        3873
Score:                  55.00         Matches:       8
Percent Similarity:     70.8%         Conservative:  9
Best Local Similarity:  33.3%         Mismatches:    7
Query Match:            34.4%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x US-11-266-748A-22343 (1-3873)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ::::::|||   |||::::::   |||:::|||:::||||||   :::::::::
Db       1311 CATGTGGGCACTGCCCATCAGCAGCCCTCCTTTGTACAGGACAGAAAGCACGATCAGGTT 1252

Qy         27 LysGlyThrPro 30
                 |||   |||
Db       1251 TCCGGAGAGCCC 1240

RESULT 8
US-11-218-305-1179
; Sequence 1179, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1179
;   LENGTH: 3828
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-1179

Alignment Scores:
Pred. No.:              39.5          Length:        3828
Score:                  54.00         Matches:       11
Percent Similarity:     66.7%         Conservative:  3
Best Local Similarity:  52.4%         Mismatches:    7
Query Match:            33.8%         Indels:        0
DB:                     9             Gaps:          0

US-10-758-902-1 (1-30) x US-11-218-305-1179 (1-3828)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||   |||   :::||||||                :::||||||||||
Db       1634 GGCGAAGCGTATGAACCGCCTTGTTACATACAACCTTCTGAAAAGGGAGTGGCAAAAGGT 1693
```

```
Qy          29 Thr 29
               :::
Db        1694 TCC 1696

RESULT 9
US-11-266-748A-36243/c
; Sequence 36243, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36243
;   LENGTH: 875
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-36243

Alignment Scores:
Pred. No.:              8.85          Length:          875
Score:                  53.00         Matches:         11
Percent Similarity:     65.4%         Conservative:    6
Best Local Similarity:  42.3%         Mismatches:      9
Query Match:            33.1%         Indels:          0
DB:                     8             Gaps:            0

US-10-758-902-1 (1-30) x US-11-266-748A-36243 (1-875)

Qy           2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
               :::|||:::|||       |||   |||   |||   :::|||:::|||||||||   :::
Db         859 GACACCCTTAGTCCAATGCTGTGTGAAAACTACCATTTTCCTTCCTTCATCCAATCTGTA 800

Qy          22 ArgAsnGluLeuAlaLys 27
                     ||||||:::
Db         799 AATAAGCACCTTGCTAGA 782

RESULT 10
US-11-266-748A-199596
; Sequence 199596, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 199596
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-199596

Alignment Scores:
Pred. No.:              16            Length:          1000
Score:                  52.00         Matches:         8
Percent Similarity:     72.2%         Conservative:    5
Best Local Similarity:  44.4%         Mismatches:      5
Query Match:            32.5%         Indels:          0
DB:                     8             Gaps:            0

US-10-758-902-1 (1-30) x US-11-266-748A-199596 (1-1000)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle 18
               |||:::|||:::   ::::::.    |||   |||||||||   |||||||:::
Db         273 TATTCAACTATTCTTTATTCATTCAGTGAAAATTATGAATATAAAACATTTCTT 326

RESULT 11
US-11-056-355B-79603/c
; Sequence 79603, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 79603
;   LENGTH: 1612
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1612)
;   OTHER INFORMATION: Ceres Seq. ID no. 12652097
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1612)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14314755
;   OTHER INFORMATION: as cited in SEQ ID NO 59919
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1612)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13597574
;   OTHER INFORMATION: as cited in SEQ ID NO 64677
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1612)
```

```
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13597843
;   OTHER INFORMATION: as cited in SEQ ID NO 64850
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1612)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13597678
;   OTHER INFORMATION: as cited in SEQ ID NO 65375
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1612)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13596180
;   OTHER INFORMATION: as cited in SEQ ID NO 67941
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1612)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13591190
;   OTHER INFORMATION: as cited in SEQ ID NO 68044
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1612)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13595961
;   OTHER INFORMATION: as cited in SEQ ID NO 68223
US-11-056-355B-79603

Alignment Scores:
Pred. No.:                29.7          Length:          1612
Score:                    52.00         Matches:         9
Percent Similarity:       92.9%         Conservative:    4
Best Local Similarity:    64.3%         Mismatches:      1
Query Match:              32.5%         Indels:          0
DB:                       9             Gaps:            0

US-10-758-902-1 (1-30) x US-11-056-355B-79603 (1-1612)

Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::|||||||||||||:::|||:::::::||||||
Db        433 CCCTTCTTCCTTCAAGATCTTCGTCATGAAGTCTCGAAAGGG 392

RESULT 12
US-11-218-305-1178
; Sequence 1178, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1178
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-1178

Alignment Scores:
Pred. No.:                35.2          Length:          1837
Score:                    52.00         Matches:         10
Percent Similarity:       66.7%         Conservative:    4
Best Local Similarity:    47.6%         Mismatches:      7
Query Match:              32.5%         Indels:          0
DB:                       9             Gaps:            0

US-10-758-902-1 (1-30) x US-11-218-305-1178 (1-1837)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
```

```
              ||||||||||||||||   |||   :::||||||              :::|||:::|||
Db       1385 GGCGAAGCATATGAACCGCCTTGTTACATACAACCTTTTGAAAAGGGAGTGGCAGAAGGT 1444

Qy         29 Thr 29
              :::
Db       1445 TCC 1447

RESULT 13
US-11-056-355B-5323/c
; Sequence 5323, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 5323
;   LENGTH: 1562
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ceres Seq. ID no. 12341687
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12609146
;   OTHER INFORMATION: as cited in SEQ ID NO 52118
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14316158
;   OTHER INFORMATION: as cited in SEQ ID NO 52413
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13594056
;   OTHER INFORMATION: as cited in SEQ ID NO 55691
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13638136
;   OTHER INFORMATION: as cited in SEQ ID NO 58644
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13596868
;   OTHER INFORMATION: as cited in SEQ ID NO 62806
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12587035
;   OTHER INFORMATION: as cited in SEQ ID NO 63605
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14301886
;   OTHER INFORMATION: as cited in SEQ ID NO 64201
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13595885
;   OTHER INFORMATION: as cited in SEQ ID NO 69265
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
```

```
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12566239
;   OTHER INFORMATION: as cited in SEQ ID NO 0
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13599119
;   OTHER INFORMATION: as cited in SEQ ID NO 0
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14308987
;   OTHER INFORMATION: as cited in SEQ ID NO 0
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 15179992
;   OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-5323

Alignment Scores:
Pred. No.:              35.2          Length:         1562
Score:                  51.50         Matches:        12
Percent Similarity:     65.2%         Conservative:   3
Best Local Similarity:  52.2%         Mismatches:     7
Query Match:            32.2%         Indels:         1
DB:                     9             Gaps:           1

US-10-758-902-1 (1-30) x US-11-056-355B-5323 (1-1562)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||:::     |||      :::||||||     |||   |||
Db       1378 AATCTGGGAGAAGCCCACCGGCCACCACCCAGCTTGCAGGAT---AATAATAGACTGAAG 1322

Qy         27 LysGlyThr 29
              :::|||||||
Db       1321 CAGGGTACA 1313

RESULT 14
US-11-056-355B-8326/c
; Sequence 8326, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 8326
;   LENGTH: 1562
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ceres Seq. ID no. 12341687
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12609146
;   OTHER INFORMATION: as cited in SEQ ID NO 52118
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14316158
;   OTHER INFORMATION: as cited in SEQ ID NO 52413
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13594056
;   OTHER INFORMATION: as cited in SEQ ID NO 55691
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13638136
;   OTHER INFORMATION: as cited in SEQ ID NO 58644
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13596868
;   OTHER INFORMATION: as cited in SEQ ID NO 62806
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12587035
;   OTHER INFORMATION: as cited in SEQ ID NO 63605
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14301886
;   OTHER INFORMATION: as cited in SEQ ID NO 64201
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13595885
;   OTHER INFORMATION: as cited in SEQ ID NO 69265
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12566239
;   OTHER INFORMATION: as cited in SEQ ID NO 0
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13599119
;   OTHER INFORMATION: as cited in SEQ ID NO 0
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14308987
;   OTHER INFORMATION: as cited in SEQ ID NO 0
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1562)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 15179992
;   OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-8326

Alignment Scores:
Pred. No.:              35.2          Length:         1562
Score:                  51.50         Matches:        12
Percent Similarity:     65.2%         Conservative:   3
Best Local Similarity:  52.2%         Mismatches:     7
Query Match:            32.2%         Indels:         1
DB:                     9             Gaps:           1

US-10-758-902-1 (1-30) x US-11-056-355B-8326 (1-1562)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||:::     |||      :::||||||     |||   |||
Db       1378 AATCTGGGAGAAGCCCACCGGCCACCACCCAGCTTGCAGGAT---AATAATAGACTGAAG 1322

Qy         27 LysGlyThr 29
              :::|||||||
Db       1321 CAGGGTACA 1313

RESULT 15
US-11-266-748A-356267
; Sequence 356267, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
```

```
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 356267
;   LENGTH: 1779
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (19)..(19)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (54)..(54)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (898)..(898)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-356267

Alignment Scores:
Pred. No.:                41.6          Length:          1779
Score:                    51.50         Matches:         13
Percent Similarity:       52.6%         Conservative:    7
Best Local Similarity:    34.2%         Mismatches:      10
Query Match:              32.2%         Indels:          8
DB:                       8             Gaps:            1

US-10-758-902-1 (1-30) x US-11-266-748A-356267 (1-1779)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   |||||||:::||| :::|||||
Db        343 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 402

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db        403 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 454

RESULT 16
US-11-266-748A-439646/c
; Sequence 439646, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 439646
;   LENGTH: 1779
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (882)..(882)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1726)..(1726)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1761)..(1761)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-439646

Alignment Scores:
Pred. No.:                41.6          Length:          1779
Score:                    51.50         Matches:         13
Percent Similarity:       52.6%         Conservative:    7
Best Local Similarity:    34.2%         Mismatches:      10
Query Match:              32.2%         Indels:          8
DB:                       8             Gaps:            1

US-10-758-902-1 (1-30) x US-11-266-748A-439646 (1-1779)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   |||||||:::||| :::|||||
Db       1437 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1378

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                        :::   :::||||||:::      |||
Db       1377 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1326

RESULT 17
US-10-449-902-16834
; Sequence 16834, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
```

```
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16834
;   LENGTH: 3155
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK098997
;   DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-16834

Alignment Scores:
Pred. No.:              87.6          Length:         3155
Score:                  51.50         Matches:        11
Percent Similarity:     59.3%         Conservative:   5
Best Local Similarity:  40.7%         Mismatches:     8
Query Match:            32.2%         Indels:         3
DB:                     6             Gaps:           1

US-10-758-902-1 (1-30) x US-10-449-902-16834 (1-3155)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||   :::|||      ||||||      ::::::||||||     :::|||:::
Db       1120 AACCTTAATCAAGCAATGTCGTATCCACCACTGATGGAGGATTTGGGGCGCCAACTCAGC 1179

Qy         27 Lys---------GlyThrPro 30
              |||         |||   |||
Db       1180 AAGAAATGTGGTGGTTTACCT 1200

RESULT 18
US-10-449-902-15622
; Sequence 15622, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15622
;   LENGTH: 3173
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK066140
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-15622

Alignment Scores:
Pred. No.:              88.3          Length:         3173
Score:                  51.50         Matches:        11
Percent Similarity:     59.3%         Conservative:   5
Best Local Similarity:  40.7%         Mismatches:     8
Query Match:            32.2%         Indels:         3
DB:                     6             Gaps:           1

US-10-758-902-1 (1-30) x US-10-449-902-15622 (1-3173)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||   :::|||      ||||||      ::::::||||||     :::|||:::
Db       1138 AACCTTAATCAAGCAATGTCGTATCCACCACTGATGGAGGATTTGGGGCGCCAACTCAGC 1197

Qy         27 Lys---------GlyThrPro 30
              |||         |||   |||
Db       1198 AAGAAATGTGGTGGTTTACCT 1218

RESULT 19
US-11-299-286-69
; Sequence 69, Application US/11299286
; Publication No. US20060183137A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/11/299,286
;  CURRENT FILING DATE:  2005-12-09
;  PRIOR APPLICATION NUMBER: US/09/938,842
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 69
;   LENGTH: 6449
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-11-299-286-69

Alignment Scores:
Pred. No.:              273           Length:         6449
Score:                  51.00         Matches:        11
Percent Similarity:     68.2%         Conservative:   4
Best Local Similarity:  50.0%         Mismatches:     7
Query Match:            31.9%         Indels:         0
DB:                     7             Gaps:           0

US-10-758-902-1 (1-30) x US-11-299-286-69 (1-6449)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              |||:::|||   |||   ::::::|||   |||      ||||||   :::   ||||||
Db       3057 TTCTCTCTGAGTGAGGAGTTCAAGTATGTCACTGTTCGACAAGATGAGAAGATGGAACTG 3116

Qy         26 AlaLys 27
              ||||||
Db       3117 GCAAAG 3122

RESULT 20
US-10-540-898-458
; Sequence 458, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: CHIR0056-101 (PP023367.0003)
;  CURRENT APPLICATION NUMBER: US/10/540,898
;  CURRENT FILING DATE:  2005-06-27
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 458
;   LENGTH: 194534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(194534)
;   OTHER INFORMATION: n = A,T,C or G
US-10-540-898-458
```

```
Alignment Scores:
Pred. No.:                2.28e+04        Length:         194534
Score:                    51.00           Matches:        12
Percent Similarity:       63.6%           Conservative:   2
Best Local Similarity:    54.5%           Mismatches:     8
Query Match:              31.9%           Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-1 (1-30) x US-10-540-898-458 (1-194534)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              |||:::  |||||||||  |||  |||  ||||||  :::      ||||||
Db      64117 GTGGCTCTCAATCTTGGCTGGGCATCAGAATCACCCACGCTGCTTTACAAACTGAGGCCT 64176

Qy         24 GluLeu 25
              ||||||
Db      64177 GAGCTA 64182

RESULT 21
US-10-641-321-205/c
; Sequence 205, Application US/10641321
; Publication No. US20060183128A1
; GENERAL INFORMATION:
;  APPLICANT: Berlin, Kurt
;  APPLICANT:  Olek, Alexander
;  APPLICANT:  Beck, Stephan
;  APPLICANT:  Hildmann, Thomas
;  APPLICANT:  Lewin, Jorn
;  APPLICANT:  Novik, Karen
;  TITLE OF INVENTION: Methods and Compositions for Differentiating Tissues or Cell Type
;  TITLE OF INVENTION:  Epigenetic Markers
;  FILE REFERENCE: 47675-49
;  CURRENT APPLICATION NUMBER: US/10/641,321
;  CURRENT FILING DATE:  2003-08-12
;  NUMBER OF SEQ ID NOS: 221
; SEQ ID NO 205
;   LENGTH: 4647455
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (4267840)
;   OTHER INFORMATION: unknown base
US-10-641-321-205

Alignment Scores:
Pred. No.:                1.21e+06        Length:         4647455
Score:                    51.00           Matches:        11
Percent Similarity:       73.3%           Conservative:   0
Best Local Similarity:    73.3%           Mismatches:     4
Query Match:              31.9%           Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-1 (1-30) x US-10-641-321-205 (1-4647455)

Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              |||||||||  |||  |||||||||  ||||||  ||||||
Db    2726981 CCCACCTTCCACCAGAGCCTCAGGAACGTGCTGGCAACAGGGACC 2726937

RESULT 22
US-11-292-078-9579/c
; Sequence 9579, Application US/11292078
; Publication No. US20060195941A1
; GENERAL INFORMATION:
;  APPLICANT: Deikman, Jill
;  APPLICANT:  Feng, Paul C.C.
;  APPLICANT:  Fincher, Karen L.
;  APPLICANT:  Ziegler, Todd E.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 16517.346 - 38-21(52274)C
;  CURRENT APPLICATION NUMBER: US/11/292,078
;  CURRENT FILING DATE:  2005-12-02
;  PRIOR APPLICATION NUMBER: US 10/021,323
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: US 60/255,619
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 9579
;   LENGTH: 598
;   TYPE: DNA
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3828-024-Q6-K6-D7
US-11-292-078-9579

Alignment Scores:
Pred. No.:                19              Length:         598
Score:                    50.00           Matches:        10
Percent Similarity:       61.5%           Conservative:   6
Best Local Similarity:    38.5%           Mismatches:     10
Query Match:              31.2%           Indels:         0
DB:                       7               Gaps:           0

US-10-758-902-1 (1-30) x US-11-292-078-9579 (1-598)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||  |||  :::     |||  :::|||:::     |||     |||:::|||
Db        227 TATGTTACCACCAACATCACTCTTCACAAGGCTCATAGCAGACCCGAACTTATCGAGGAC 168

Qy         21 LeuArgAsnGluLeuAla 26
                :::|||:::||||||
Db        167 TGGCAAAATCAACTTGCA 150

RESULT 23
US-11-218-305-4673/c
; Sequence 4673, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4673
;   LENGTH: 1350
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-4673

Alignment Scores:
Pred. No.:                54.5            Length:         1350
Score:                    50.00           Matches:        10
Percent Similarity:       70.6%           Conservative:   2
Best Local Similarity:    58.8%           Mismatches:     5
Query Match:              31.2%           Indels:         0
DB:                       9               Gaps:           0

US-10-758-902-1 (1-30) x US-11-218-305-4673 (1-1350)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||  |||:::|||||||||      ||||||      :::|||||||||
Db       1194 GAGCAGTACCAATACCCAACATCTTGACAGGACTTCAGTTCTGAATTGGCT 1144

RESULT 24
US-11-218-305-4675/c
; Sequence 4675, Application US/11218305
; Publication No. US20060141495A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4675
;   LENGTH: 1847
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-4675

Alignment Scores:
Pred. No.:              81.9          Length:          1847
Score:                  50.00         Matches:         10
Percent Similarity:     70.6%         Conservative:    2
Best Local Similarity:  58.8%         Mismatches:      5
Query Match:            31.2%         Indels:          0
DB:                     9             Gaps:            0

US-10-758-902-1 (1-30) x US-11-218-305-4675 (1-1847)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||   |||:::|||||||||       ||||||      :::|||||||||
Db       1691 GAGCAGTACCAATACCCAACATCTTGACAGGACTTCAGTTCTGAATTGGCT 1641

RESULT 25
US-10-449-902-22294
; Sequence 22294, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22294
;   LENGTH: 2172
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK072485
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-22294

Alignment Scores:
Pred. No.:              101           Length:          2172
Score:                  50.00         Matches:         7
Percent Similarity:     72.2%         Conservative:    6
Best Local Similarity:  38.9%         Mismatches:      5
Query Match:            31.2%         Indels:          0
DB:                     6             Gaps:            0

US-10-758-902-1 (1-30) x US-10-449-902-22294 (1-2172)

Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              |||:::||||||   |||:::   ||||||      :::::::::   |||:::
Db       1118 TACGACTACCCGGAGTTCGTCGCCGACCTGACGACGCAGGTGTCGAACGGGTCG 1171

RESULT 26
US-11-056-355B-77422/c
; Sequence 77422, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 77422
;   LENGTH: 2455
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2455)
;   OTHER INFORMATION: Ceres Seq. ID no. 12576356
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2455)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13598023
;   OTHER INFORMATION: as cited in SEQ ID NO 66487
US-11-056-355B-77422

Alignment Scores:
Pred. No.:              119           Length:          2455
Score:                  50.00         Matches:         8
Percent Similarity:     92.3%         Conservative:    4
Best Local Similarity:  61.5%         Mismatches:      1
Query Match:            31.2%         Indels:          0
DB:                     9             Gaps:            0

US-10-758-902-1 (1-30) x US-11-056-355B-77422 (1-2455)

Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::::::::|||||||||||||   :::|||||||||||||
Db       253 TTTGATTTTCCGACATTTATTTTGGAATTGCGTAACGAA 215

RESULT 27
US-11-056-355B-107356/c
; Sequence 107356, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 107356
;   LENGTH: 2458
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2458)
;   OTHER INFORMATION: Ceres Seq. ID no. 13646820
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2458)
```

; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13598023
; OTHER INFORMATION: as cited in SEQ ID NO 66487
US-11-056-355B-107356

Alignment Scores:

Pred. No.:	119	Length:	2458
Score:	50.00	Matches:	8
Percent Similarity:	92.3%	Conservative:	4
Best Local Similarity:	61.5%	Mismatches:	1
Query Match:	31.2%	Indels:	0
DB:	9	Gaps:	0

US-10-758-902-1 (1-30) x US-11-056-355B-107356 (1-2458)

```
Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::::::::|||||||||||||   :::||||||||||||
Db        280 TTTGATTTTCCGACATTTATTTTGGAATTGCGTAACGAA 242
```

RESULT 28
US-11-056-355B-118595/c
; Sequence 118595, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 118595
; LENGTH: 2458
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2458)
; OTHER INFORMATION: Ceres Seq. ID no. 13646820
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2458)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13598023
; OTHER INFORMATION: as cited in SEQ ID NO 66487
US-11-056-355B-118595

Alignment Scores:

Pred. No.:	119	Length:	2458
Score:	50.00	Matches:	8
Percent Similarity:	92.3%	Conservative:	4
Best Local Similarity:	61.5%	Mismatches:	1
Query Match:	31.2%	Indels:	0
DB:	9	Gaps:	0

US-10-758-902-1 (1-30) x US-11-056-355B-118595 (1-2458)

```
Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::::::::|||||||||||||   :::||||||||||||
Db        280 TTTGATTTTCCGACATTTATTTTGGAATTGCGTAACGAA 242
```

RESULT 29
US-10-953-349-10942/c
; Sequence 10942, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10942
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10942

Alignment Scores:

Pred. No.:	120	Length:	2482
Score:	50.00	Matches:	8
Percent Similarity:	92.3%	Conservative:	4
Best Local Similarity:	61.5%	Mismatches:	1
Query Match:	31.2%	Indels:	0
DB:	6	Gaps:	0

US-10-758-902-1 (1-30) x US-10-953-349-10942 (1-2482)

```
Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::::::::|||||||||||||   :::||||||||||||
Db        280 TTTGATTTTCCGACATTTATTTTGGAATTGCGTAACGAA 242
```

RESULT 30
US-11-056-355B-45708/c
; Sequence 45708, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 45708
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2482)
; OTHER INFORMATION: Ceres Seq. ID no. 14309739
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2482)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13598023
; OTHER INFORMATION: as cited in SEQ ID NO 66487
US-11-056-355B-45708

Alignment Scores:

Pred. No.:	120	Length:	2482
Score:	50.00	Matches:	8
Percent Similarity:	92.3%	Conservative:	4
Best Local Similarity:	61.5%	Mismatches:	1
Query Match:	31.2%	Indels:	0
DB:	9	Gaps:	0

US-10-758-902-1 (1-30) x US-11-056-355B-45708 (1-2482)

```
Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              :::::::::|||||||||||||   :::||||||||||||
Db        280 TTTGATTTTCCGACATTTATTTTGGAATTGCGTAACGAA 242
```

RESULT 31
US-11-218-305-4674/c
; Sequence 4674, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.

```
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4674
;   LENGTH: 5166
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-4674

Alignment Scores:
Pred. No.:              311          Length:         5166
Score:                  50.00        Matches:        10
Percent Similarity:     70.6%        Conservative:   2
Best Local Similarity:  58.8%        Mismatches:     5
Query Match:            31.2%        Indels:         0
DB:                     9            Gaps:           0

US-10-758-902-1 (1-30) x US-11-218-305-4674 (1-5166)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||   |||:::|||||||||      ||||||      :::|||||||||
Db       1069 GAGCAGTACCAATACCCAACATCTTGACAGGACTTCAGTTCTGAATTGGCT 1019

RESULT 32
US-10-540-898-353/c
; Sequence 353, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: CHIR0056-101 (PP023367.0003)
;  CURRENT APPLICATION NUMBER: US/10/540,898
;  CURRENT FILING DATE:  2005-06-27
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 353
;   LENGTH: 24231
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(24231)
;   OTHER INFORMATION: n = A,T,C or G
US-10-540-898-353

Alignment Scores:
Pred. No.:              2.32e+03     Length:         24231
Score:                  50.00        Matches:        13
Percent Similarity:     50.0%        Conservative:   0
Best Local Similarity:  50.0%        Mismatches:     3
Query Match:            31.2%        Indels:         10
DB:                     6            Gaps:           1

US-10-758-902-1 (1-30) x US-10-540-898-353 (1-24231)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              ||||||   ||||||||||||                                ||||||
Db       6466 TCCTTTGGCCTTGGCGAGGCT----------------------------AGGAATCGC 6437

Qy         25 LeuAlaLysGlyThrPro 30
              ||||||   ||||||||
Db       6436 CTTGCGCCAGGAACCCCA 6419

RESULT 33
US-11-266-748A-364364/c
; Sequence 364364, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 364364
;   LENGTH: 1006
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-364364

Alignment Scores:
Pred. No.:              56.6         Length:         1006
Score:                  49.00        Matches:        13
Percent Similarity:     58.3%        Conservative:   1
Best Local Similarity:  54.2%        Mismatches:     10
Query Match:            30.6%        Indels:         0
DB:                     8            Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-364364 (1-1006)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              |||||||||   ||||||         |||||||||         |||||||||   |||
Db        962 TTCAATCTGGTGGAAGCCCCCAGAGGCCCCACCTTCCCTCATACATTGCGGAACATGTTA 903

Qy         26 AlaLysGlyThr 29
              :::   |||
Db        902 TCAGGGGAGACC 891

RESULT 34
US-11-266-748A-388269/c
; Sequence 388269, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
```

```
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 388269
;   LENGTH: 1006
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-388269

Alignment Scores:
Pred. No.:                56.6          Length:          1006
Score:                    49.00         Matches:         13
Percent Similarity:       58.3%         Conservative:    1
Best Local Similarity:    54.2%         Mismatches:      10
Query Match:              30.6%         Indels:          0
DB:                       8             Gaps:            0

US-10-758-902-1 (1-30) x US-11-266-748A-388269 (1-1006)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              |||||||||  ||||||          |||||||||          |||||||||  |||
Db        962 TTCAATCTGGTGGAAGCCCCCAGAGGCCCCACCTTCCCTCATACATTGCGGAACATGTTA 903

Qy         26 AlaLysGlyThr 29
              :::  |||
Db        902 TCAGGGGAGACC 891

RESULT 35
US-11-266-748A-447743
; Sequence 447743, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 447743
;   LENGTH: 1006
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-447743

Alignment Scores:
Pred. No.:                56.6          Length:          1006
Score:                    49.00         Matches:         13
Percent Similarity:       58.3%         Conservative:    1
Best Local Similarity:    54.2%         Mismatches:      10
Query Match:              30.6%         Indels:          0
DB:                       8             Gaps:            0

US-10-758-902-1 (1-30) x US-11-266-748A-447743 (1-1006)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              |||||||||  ||||||          |||||||||          |||||||||  |||
Db         45 TTCAATCTGGTGGAAGCCCCCAGAGGCCCCACCTTCCCTCATACATTGCGGAACATGTTA 104

Qy         26 AlaLysGlyThr 29
              :::  |||
Db        105 TCAGGGGAGACC 116

RESULT 36
US-11-216-545-3180
; Sequence 3180, Application US/11216545
; Publication No. US20060135758A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO Technology, LLC
;  APPLICANT:  McLaird, Paul L
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Soybeans.
;  FILE REFERENCE: 38-21 (53659)B
;  CURRENT APPLICATION NUMBER: US/11/216,545
;  CURRENT FILING DATE:  2005-08-31
;  PRIOR APPLICATION NUMBER: US 60/606,062
;  PRIOR FILING DATE: 2004-08-31
;  NUMBER OF SEQ ID NOS: 8783
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3180
;   LENGTH: 1118
;   TYPE: DNA
;   ORGANISM: Glycine max
US-11-216-545-3180

Alignment Scores:
Pred. No.:                64.9          Length:          1118
Score:                    49.00         Matches:         11
Percent Similarity:       63.3%         Conservative:    8
Best Local Similarity:    36.7%         Mismatches:      7
Query Match:              30.6%         Indels:          4
DB:                       8             Gaps:            1

US-10-758-902-1 (1-30) x US-11-216-545-3180 (1-1118)

Qy          2 AsnThrValSerPheAsnLeuGly----------GluAlaTyrGluTyrProThrPhe 17
              :::|||::::::|||:::|||                |||||   |||:::|||
Db        717 GATACACTTGCATTTTCCTTGGCACCTCATCCACCCGAAGCTGAAGAATTTCCTGCAGTT 776

Qy         18 IleGlnAspLeuArgAsnGluLeuAlaLys 27
              :::|||:::   ||||||   :::|||
Db        777 TGTAGAGATATTGTGAATGAATACTCAAAG 806

RESULT 37
US-11-217-529-4610
; Sequence 4610, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
```

```
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4610
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4610

Alignment Scores:
Pred. No.:              82.4          Length:         1344
Score:                  49.00         Matches:        9
Percent Similarity:     59.4%         Conservative:   10
Best Local Similarity:  28.1%         Mismatches:     5
Query Match:            30.6%         Indels:         8
DB:                     8             Gaps:           1

US-10-758-902-1 (1-30) x US-11-217-529-4610 (1-1344)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyr------------------------ProThr 16
              |||:::   :::   :::   ::::::|||                        ||||||
Db        547 TCATACGAAATATTTCAATTACACGATTATCCAGAAGCCATTAACGACTTATTGCCGACA 606

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||::::::||||||::::::|||:::      |||
Db        607 TTTCTAGAAGATCTTAAAAGTGAAATTTACCATGGC 642

RESULT 38
US-11-174-307B-4567
; Sequence 4567, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 4567
;   LENGTH: 1439
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1439)
;   OTHER INFORMATION: Ceres cDNA ID no. 21995806
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1439)
;   OTHER INFORMATION: Ceres CLONE  ID no. 472079
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1439)
;   OTHER INFORMATION: Also known as  Ceres CDNA ID no. 25087993
US-11-174-307B-4567

Alignment Scores:
Pred. No.:              90.1          Length:         1439
Score:                  49.00         Matches:        11
Percent Similarity:     63.3%         Conservative:   8
Best Local Similarity:  36.7%         Mismatches:     7
Query Match:            30.6%         Indels:         4
DB:                     9             Gaps:           1

US-10-758-902-1 (1-30) x US-11-174-307B-4567 (1-1439)

Qy          2 AsnThrValSerPheAsnLeuGly-----------GluAlaTyrGluTyrProThrPhe 17
              :::|||::::::|||:::|||                ||||||   |||:::|||
Db        498 GATACACTTGCATTTTCCTTGGCACCTCATCCACCCGAAGCTGAAGAATTTCCTGCAGTT 557

Qy         18 IleGlnAspLeuArgAsnGluLeuAlaLys 27
                :::|||:::   ||||||   :::|||
Db        558 TGTAGAGATATTGTGAATGAATACTCAAAG 587

RESULT 39
US-11-216-545-2350/c
; Sequence 2350, Application US/11216545
; Publication No. US20060135758A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO Technology, LLC
;  APPLICANT:  McLaird, Paul L
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Soybeans.
;  FILE REFERENCE: 38-21 (53659)B
;  CURRENT APPLICATION NUMBER: US/11/216,545
;  CURRENT FILING DATE:  2005-08-31
;  PRIOR APPLICATION NUMBER: US 60/606,062
;  PRIOR FILING DATE: 2004-08-31
;  NUMBER OF SEQ ID NOS: 8783
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2350
;   LENGTH: 1647
;   TYPE: DNA
;   ORGANISM: Glycine max
US-11-216-545-2350

Alignment Scores:
Pred. No.:              107           Length:         1647
Score:                  49.00         Matches:        10
Percent Similarity:     63.6%         Conservative:   4
Best Local Similarity:  45.5%         Mismatches:     8
Query Match:            30.6%         Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-1 (1-30) x US-11-216-545-2350 (1-1647)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              |||       |||       |||       |||   |||   |||:::||||||:::|||:::
Db        906 GTAGTTATGAATTTCTTTGAGGAGTTGGAGCCACCTTTGTTTGTTCAAGACATGAGATCC 847

Qy         24 GluLeu 25
              :::|||
Db        846 AAGTTG 841

RESULT 40
US-11-266-748A-188310
; Sequence 188310, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
```

; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 188310
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-188310

Alignment Scores:

Pred. No.:	139	Length:	2010
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-188310 (1-2010)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::          |||
Db        887 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 946

Qy         25 LeuAlaLysGlyThr 29
                 |||:::   |||
Db        947 TTTGCCCGAGACACC 961
```

RESULT 41
US-11-266-748A-75195
; Sequence 75195, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75195
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3353)..(3367)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3385)..(3399)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-75195

Alignment Scores:

Pred. No.:	326	Length:	3879
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-75195 (1-3879)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::          |||
Db       1312 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 1371

Qy         25 LeuAlaLysGlyThr 29
                 |||:::   |||
Db       1372 TTTGCCCGAGACACC 1386
```

RESULT 42
US-11-266-748A-108778
; Sequence 108778, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 108778
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3353)..(3367)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3385)..(3399)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-108778

```
Alignment Scores:
Pred. No.:                326             Length:         3879
Score:                    49.00           Matches:        10
Percent Similarity:       60.0%           Conservative:   5
Best Local Similarity:    40.0%           Mismatches:     10
Query Match:              30.6%           Indels:         0
DB:                       8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-108778 (1-3879)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||       ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       1312 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 1371

Qy         25 LeuAlaLysGlyThr 29
                 |||:::   |||
Db       1372 TTTGCCCGAGACACC 1386

RESULT 43
US-11-266-748A-128006/c
; Sequence 128006, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128006
;   LENGTH: 3879
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (481)..(495)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (513)..(527)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-128006

Alignment Scores:
Pred. No.:                326             Length:         3879
Score:                    49.00           Matches:        10
Percent Similarity:       60.0%           Conservative:   5
Best Local Similarity:    40.0%           Mismatches:     10
Query Match:              30.6%           Indels:         0
DB:                       8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-128006 (1-3879)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||       ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       2568 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 2509

Qy         25 LeuAlaLysGlyThr 29
                 |||:::   |||
Db       2508 TTTGCCCGAGACACC 2494

RESULT 44
US-11-289-102-42
; Sequence 42, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Hyerim
;  APPLICANT:  Shaw, Peter M.
;  APPLICANT:  Clark, Edwin
;  TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
;  TITLE OF INVENTION:  MICROTUBULE-STABILIZING AGENTS
;  FILE REFERENCE: 10338 NP
;  CURRENT APPLICATION NUMBER: US/11/289,102
;  CURRENT FILING DATE:  2005-11-29
;  PRIOR APPLICATION NUMBER: US 60/631,993
;  PRIOR FILING DATE: 2004-11-30
;  NUMBER OF SEQ ID NOS: 395
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
;   LENGTH: 7561
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-289-102-42

Alignment Scores:
Pred. No.:                776             Length:         7561
Score:                    49.00           Matches:        10
Percent Similarity:       60.0%           Conservative:   5
Best Local Similarity:    40.0%           Mismatches:     10
Query Match:              30.6%           Indels:         0
DB:                       8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-289-102-42 (1-7561)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||       ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5477 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5536

Qy         25 LeuAlaLysGlyThr 29
                 |||:::   |||
Db       5537 TTTGCCCGAGACACC 5551

RESULT 45
US-11-292-078-3562
; Sequence 3562, Application US/11292078
; Publication No. US20060195941A1
; GENERAL INFORMATION:
;  APPLICANT: Deikman, Jill
;  APPLICANT:  Feng, Paul C.C.
;  APPLICANT:  Fincher, Karen L.
;  APPLICANT:  Ziegler, Todd E.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 16517.346 - 38-21(52274)C
;  CURRENT APPLICATION NUMBER: US/11/292,078
;  CURRENT FILING DATE:  2005-12-02
;  PRIOR APPLICATION NUMBER: US 10/021,323
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: US 60/255,619
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 3562
;   LENGTH: 607
;   TYPE: DNA
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
```

```
;   NAME/KEY: unsure
;   LOCATION: (1)..(607)
;   OTHER INFORMATION: unsure at all n locations
;   OTHER INFORMATION: Clone ID: LIB3825-027-Q6-K6-H1
US-11-292-078-3562

Alignment Scores:
Pred. No.:                36.2          Length:          607
Score:                    48.50         Matches:         12
Percent Similarity:       64.3%         Conservative:    6
Best Local Similarity:    42.9%         Mismatches:      9
Query Match:              30.3%         Indels:          1
DB:                       7             Gaps:            1

US-10-758-902-1 (1-30) x US-11-292-078-3562 (1-607)

Qy           4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu---Arg 22
               :::   |||   ||||||:::   |||:::  ||||||  ::::::   |||   |||
Db         189 ATACAATTCAAGCTTGGAGATTATTATGATGATCCTACTGTCCTGAGATATTTAGAAAGG 248

Qy          23 AsnGluLeuAlaLysGlyThrPro 30
                 |||   |||   |||:::|||
Db         249 CTTGAGGGAGCAGGTGGTTCACCC 272

RESULT 46
US-11-217-529-75584
; Sequence 75584, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75584
;   LENGTH: 939
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-75584

Alignment Scores:
Pred. No.:                63.8          Length:          939
Score:                    48.50         Matches:         11
Percent Similarity:       48.3%         Conservative:    3
Best Local Similarity:    37.9%         Mismatches:      6
Query Match:              30.3%         Indels:          9
DB:                       8             Gaps:            1

US-10-758-902-1 (1-30) x US-11-217-529-75584 (1-939)

Qy           2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
               |||   |||   :::|||                                 |||||||||:::
Db          61 AACGTTGTCAAATATAATACG-------------------------ATTCAGGATATC 93

Qy          22 ArgAsnGluLeuAlaLysGlyThrPro 30
               ||||||:::         |||||||||
Db          94 AGGAACAAATATGTTACTGGTACGCCT 120

RESULT 47
US-11-266-748A-186724
; Sequence 186724, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 186724
;   LENGTH: 2231
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2174)..(2187)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-186724

Alignment Scores:
Pred. No.:                196           Length:          2231
Score:                    48.50         Matches:         10
Percent Similarity:       62.5%         Conservative:    5
Best Local Similarity:    41.7%         Mismatches:      6
Query Match:              30.3%         Indels:          3
DB:                       8             Gaps:            1

US-10-758-902-1 (1-30) x US-11-266-748A-186724 (1-2231)

Qy           7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
               |||:::|||   :::||||||||||||||   :::         :::   ||||||   |||
Db         475 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 534

Qy          24 GluLeuAlaLys 27
                  :::   |||
Db         535 GTGATCAAGAAA 546

RESULT 48
US-11-266-748A-36729
; Sequence 36729, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
```

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36729
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-36729

Alignment Scores:

Pred. No.:	25.8	Length:	398
Score:	48.00	Matches:	10
Percent Similarity:	68.2%	Conservative:	5
Best Local Similarity:	45.5%	Mismatches:	5
Query Match:	30.0%	Indels:	2
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-266-748A-36729 (1-398)

```
Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   ||||||   :::|||||||         :::|||||||   |||:::::::::|||
Db        187 GGATCGGCCTACACATTCCCAACC------CATGAGCTCAGGCTGGAGGTGAGCCAGGGA 240

Qy         29 ThrPro 30
                |||
Db        241 GAGCCA 246
```

RESULT 49
US-11-266-748A-7702
; Sequence 7702, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7702
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-7702

Alignment Scores:

Pred. No.:	26.1	Length:	401
Score:	48.00	Matches:	9
Percent Similarity:	68.4%	Conservative:	4
Best Local Similarity:	47.4%	Mismatches:	6
Query Match:	30.0%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-7702 (1-401)

```
Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
                :::|||   :::   ||||||   :::||||||||||||   :::|||      |||
Db         64 CAAGCCCCACAAGTGCCCACATTGCTCCAAGACCTTCGCCAACAGCTCCTACCTGGC 120
```

RESULT 50
US-11-266-748A-358244
; Sequence 358244, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 358244
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-358244

Alignment Scores:

Pred. No.:	56.1	Length:	724
Score:	48.00	Matches:	8
Percent Similarity:	63.2%	Conservative:	4
Best Local Similarity:	42.1%	Mismatches:	7
Query Match:	30.0%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-358244 (1-724)

```
Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                |||   ||||||   |||:::      :::|||   ::::::|||   |||   |||
Db        632 TATTTTTACCCCATGTTCCTGGATCCAATAAGACAGGATATTGCTAATGGATAACCC 688
```

RESULT 51
US-11-266-748A-441623/c
; Sequence 441623, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 441623
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-441623

Alignment Scores:

Pred. No.:	56.1	Length:	724
Score:	48.00	Matches:	8
Percent Similarity:	63.2%	Conservative:	4
Best Local Similarity:	42.1%	Mismatches:	7
Query Match:	30.0%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-441623 (1-724)

```
Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||   ||||||   |||:::      :::|||   ::::::|||   |||   |||
Db         93 TATTTTTACCCCATGTTCCTGGATCCAATAAGACAGGATATTGCTAATGGATAACCC 37
```

RESULT 52
US-11-266-748A-370782/c
; Sequence 370782, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 370782
; LENGTH: 967
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (311)..(311)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (491)..(513)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (938)..(938)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-370782

Alignment Scores:

Pred. No.:	81.7	Length:	967
Score:	48.00	Matches:	10
Percent Similarity:	50.0%	Conservative:	4
Best Local Similarity:	35.7%	Mismatches:	14
Query Match:	30.0%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-370782 (1-967)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||||||||:::   ||||||      |||   |||   |||       :::
Db        479 TACAACACTCTAGGTTTTAATTCAAAGGAAAAATATATATATAATAAACTGGTTTACACC 420

Qy         21 LeuArgAsnGluLeuAlaLysGly 28
              |||   ::::::         |||
Db        419 CTTGGGTCAGACTGTTGCCTGGGA 396
```

RESULT 53
US-11-266-748A-454161
; Sequence 454161, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 454161
; LENGTH: 967

```
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (30)..(30)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (455)..(477)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (657)..(657)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (695)..(695)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-454161

Alignment Scores:
Pred. No.:              81.7          Length:        967
Score:                  48.00         Matches:       10
Percent Similarity:     50.0%         Conservative:  4
Best Local Similarity:  35.7%         Mismatches:    14
Query Match:            30.0%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x US-11-266-748A-454161 (1-967)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||||||||:::   ||||||    |||  |||  |||       :::
Db        489 TACAACACTCTAGGTTTTAATTCAAAGGAAAAATATATATATAATAAACTGGTTTACACC 548

Qy         21 LeuArgAsnGluLeuAlaLysGly 28
              |||   ::::::         |||
Db        549 CTTGGGTCAGACTGTTGCCTGGGA 572

RESULT 54
US-10-374-780A-1447/c
; Sequence 1447, Application US/10374780A
; Publication No. US20060162006A9
; GENERAL INFORMATION:
;  APPLICANT: Sherman, Bradley K
;  APPLICANT:  Riechmann, Jose Luis
;  APPLICANT:  Jiang, Cai-Zhong
;  APPLICANT:  Heard, Jacqueline E
;  APPLICANT:  Haake, Volker
;  APPLICANT:  Creelman, Robert A
;  APPLICANT:  Ratcliffe, Oliver
;  APPLICANT:  Adam, Luc J
;  APPLICANT:  Reuber, T. Lynne
;  APPLICANT:  Keddie, James
;  APPLICANT:  Broun, Pierre E
;  APPLICANT:  Pilgrim, Marsha L
;  APPLICANT:  Dubell III, Arnold T
;  APPLICANT:  Pineda, Omaira
;  APPLICANT:  Yu, Guo-Liang
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
;  FILE REFERENCE: MBI-0047 CIP
;  CURRENT APPLICATION NUMBER: US/10/374,780A
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: 09/837,944
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: 60/310,847
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 09/934,455
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: 60/336,049
;  PRIOR FILING DATE: 2001-11-19
;  PRIOR APPLICATION NUMBER: 60/338,692
;  PRIOR FILING DATE: 2001-12-11
;  PRIOR APPLICATION NUMBER: 10/171,468
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: 10/225,066
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 10/225,067
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 10/225,068
;  PRIOR FILING DATE: 2002-08-09
;  NUMBER OF SEQ ID NOS: 2906
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1447
;   LENGTH: 1077
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G1140
US-10-374-780A-1447

Alignment Scores:
Pred. No.:              94            Length:        1077
Score:                  48.00         Matches:       11
Percent Similarity:     66.7%         Conservative:  7
Best Local Similarity:  40.7%         Mismatches:    7
Query Match:            30.0%         Indels:        2
DB:                     6             Gaps:          1

US-10-758-902-1 (1-30) x US-10-374-780A-1447 (1-1077)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||:::|||   |||   |||||||||:::::::::::   |||:::         |||
Db        755 TACAGTACACATTCTAAGAATCTGGGGAAATCACATCAGCAGCCTTCTATT------GAT 702

Qy         21 LeuArgAsnGluLeuAlaLys 27
              |||       |||   :::|||
Db        701 TTGAATGGAGAGCAGAGCAAA 681

RESULT 55
US-11-266-748A-364704
; Sequence 364704, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 364704
;   LENGTH: 1288
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (145)..(161)
```

```
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-364704

Alignment Scores:
Pred. No.:                119           Length:         1288
Score:                    48.00         Matches:        9
Percent Similarity:       68.4%         Conservative:   4
Best Local Similarity:    47.4%         Mismatches:     6
Query Match:              30.0%         Indels:         0
DB:                       8             Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-364704 (1-1288)

Qy          10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
               :::|||   :::   ||||||   :::||||||||||||   :::|||      |||
Db        1041 CAAGCCCCACAAGTGCCCACATTGCTCCAAGACCTTCGCCAACAGCTCCTACCTGGC 1097

RESULT 56
US-11-266-748A-388331
; Sequence 388331, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 388331
;   LENGTH: 1288
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (145)..(161)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-388331

Alignment Scores:
Pred. No.:                119           Length:         1288
Score:                    48.00         Matches:        9
Percent Similarity:       68.4%         Conservative:   4
Best Local Similarity:    47.4%         Mismatches:     6
Query Match:              30.0%         Indels:         0
DB:                       8             Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-388331 (1-1288)

Qy          10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
               :::|||   :::   ||||||   :::||||||||||||   :::|||      |||
Db        1041 CAAGCCCCACAAGTGCCCACATTGCTCCAAGACCTTCGCCAACAGCTCCTACCTGGC 1097

RESULT 57
US-11-266-748A-448083/c
; Sequence 448083, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 448083
;   LENGTH: 1288
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1128)..(1144)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-448083

Alignment Scores:
Pred. No.:                119           Length:         1288
Score:                    48.00         Matches:        9
Percent Similarity:       68.4%         Conservative:   4
Best Local Similarity:    47.4%         Mismatches:     6
Query Match:              30.0%         Indels:         0
DB:                       8             Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-448083 (1-1288)

Qy          10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
               :::|||   :::   ||||||   :::||||||||||||   :::|||      |||
Db         248 CAAGCCCCACAAGTGCCCACATTGCTCCAAGACCTTCGCCAACAGCTCCTACCTGGC 192

RESULT 58
US-11-266-748A-188021
; Sequence 188021, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
```

```
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 188021
;   LENGTH: 1404
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (80)..(96)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-188021

Alignment Scores:
Pred. No.:              133          Length:         1404
Score:                  48.00        Matches:        9
Percent Similarity:     68.4%        Conservative:   4
Best Local Similarity:  47.4%        Mismatches:     6
Query Match:            30.0%        Indels:         0
DB:                     8            Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-188021 (1-1404)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              :::|||   :::   ||||||   :::||||||||||||   :::|||      |||
Db        966 CAAGCCCCACAAGTGCCCACATTGCTCCAAGACCTTCGCCAACAGCTCCTACCTGGC 1022

RESULT 59
US-11-217-529-264
; Sequence 264, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 264
;   LENGTH: 2130
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-264

Alignment Scores:
Pred. No.:              228          Length:         2130
Score:                  48.00        Matches:        13
Percent Similarity:     58.1%        Conservative:   5
Best Local Similarity:  41.9%        Mismatches:     7
Query Match:            30.0%        Indels:         6
DB:                     8            Gaps:           2

US-10-758-902-1 (1-30) x US-11-217-529-264 (1-2130)

Qy          2 AsnThrValSerPhe------AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||::::::::::|||      ||||||||||||      ||||||   ||||||   :::

Db        571 AACTCCATCAATTTCTCCAAAAATCTCGGTGAACAAAAGGAATACATTACCTTCACCAAA 630

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                        |||      :::|||   |||

Db        631 ------------GAGCAACTGGAAGGCGTTCCC 651

RESULT 60
US-11-217-529-75693
; Sequence 75693, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75693
;   LENGTH: 2139
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-75693

Alignment Scores:
Pred. No.:              229          Length:         2139
Score:                  48.00        Matches:        13
Percent Similarity:     58.1%        Conservative:   5
Best Local Similarity:  41.9%        Mismatches:     7
Query Match:            30.0%        Indels:         6
DB:                     8            Gaps:           2

US-10-758-902-1 (1-30) x US-11-217-529-75693 (1-2139)

Qy          2 AsnThrValSerPhe------AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||::::::::::|||      ||||||||||||      ||||||   ||||||   :::

Db        571 AACTCTATTAATTTTTCTAAGAATCTGGGAGAACAAAAGGAATACATCACTTTCACCAAA 630

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                        |||      :::|||   |||

Db        631 ------------GAACAATTGGAAGGTGTGCCG 651

RESULT 61
US-11-266-748A-61640/c
; Sequence 61640, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
```

```
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61640
;   LENGTH: 2209
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-61640

Alignment Scores:
Pred. No.:              239           Length:          2209
Score:                  48.00         Matches:         11
Percent Similarity:     48.1%         Conservative:    2
Best Local Similarity:  40.7%         Mismatches:      4
Query Match:            30.0%         Indels:          10
DB:                     8             Gaps:            1

US-10-758-902-1 (1-30) x US-11-266-748A-61640 (1-2209)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGlu--------------------------- 24
              ||||||   |||:::||||||      |||:::
Db       1022 TACCCCCTATTTGTGCAAGACTGTGCAAATCAGTGTCAAGTGTGTGCAGCTGGCCTGGAG 963

Qy         25 ---LeuAlaLysGlyThrPro 30
                ||||||   |||||||||
Db        962 GGGCTGGCCCTGGGGACTCCC 942

RESULT 62
US-11-266-748A-30799/c
; Sequence 30799, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30799
;   LENGTH: 3045
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-30799

Alignment Scores:
Pred. No.:              362           Length:          3045
Score:                  48.00         Matches:         11
Percent Similarity:     48.1%         Conservative:    2
Best Local Similarity:  40.7%         Mismatches:      4
Query Match:            30.0%         Indels:          10
DB:                     8             Gaps:            1

US-10-758-902-1 (1-30) x US-11-266-748A-30799 (1-3045)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGlu--------------------------- 24
              ||||||   |||:::||||||      |||:::
Db        906 TACCCCCTATTTGTGCAAGACTGTGCAAATCAGTGTCAAGTGTGTGCAGCTGGCCTGGAG 847

Qy         25 ---LeuAlaLysGlyThrPro 30
                ||||||   |||||||||
Db        846 GGGCTGGCCCTGGGGACTCCC 826

RESULT 63
US-11-218-305-24120/c
; Sequence 24120, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24120
;   LENGTH: 4161
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-24120

Alignment Scores:
Pred. No.:              543           Length:          4161
Score:                  48.00         Matches:         7
Percent Similarity:     70.6%         Conservative:    5
Best Local Similarity:  41.2%         Mismatches:      5
Query Match:            30.0%         Indels:          0
DB:                     9             Gaps:            0

US-10-758-902-1 (1-30) x US-11-218-305-24120 (1-4161)

Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||:::||||||   |||:::   ||||||      ::::::   :::|||
Db       1424 TACGACTACCCGGAGTTCGTCGCCGACCTGGCCAAGCAGGTGAAGCAGGGG 1374

RESULT 64
US-11-218-305-18783
; Sequence 18783, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18783
;   LENGTH: 5640
;   TYPE: DNA
;   ORGANISM: Zea mays
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (79)..(79)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (88)..(88)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (104)..(104)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (149)..(149)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (185)..(185)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (213)..(213)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (223)..(223)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (275)..(275)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-18783

Alignment Scores:
Pred. No.:                806           Length:          5640
Score:                    48.00         Matches:         7
Percent Similarity:       81.2%         Conservative:    6
Best Local Similarity:    43.8%         Mismatches:      3
Query Match:              30.0%         Indels:          0
DB:                       9             Gaps:            0

US-10-758-902-1 (1-30) x US-11-218-305-18783 (1-5640)

Qy          13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
               :::::::|||    |||:::   :::||||||::::::   |||||||||
Db        1380 CAGTGGCCTGCCTTTGTTGATGAGCTCCGCCATGACGCAGCCAAGGGA 1427

RESULT 65
US-10-536-606-17/c
; Sequence 17, Application US/10536606
; Publication No. US20060171959A1
; GENERAL INFORMATION:
;  APPLICANT: Cosson et al.
;  TITLE OF INVENTION: VIRULENCE GENES, PROTEINS, AND THEIR USE
;  FILE REFERENCE: 25421-502NATL
;  CURRENT APPLICATION NUMBER: US/10/536,606
;  CURRENT FILING DATE:  2005-05-26
;  PRIOR APPLICATION NUMBER: PCT/CH2003/00836
;  PRIOR FILING DATE: 2003-12-19
;  PRIOR APPLICATION NUMBER: 10/324,967
;  PRIOR FILING DATE: 2002-12-19
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 7347
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-10-536-606-17

Alignment Scores:
Pred. No.:                1.14e+03      Length:          7347
Score:                    48.00         Matches:         8
Percent Similarity:       66.7%         Conservative:    4
Best Local Similarity:    44.4%         Mismatches:      6
Query Match:              30.0%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-1 (1-30) x US-10-536-606-17 (1-7347)

Qy           8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
               ||||||:::          |||||||||   ::::::|||:::|||      |||
Db        5001 CTGGGTCAGCAGCAGCCGTACCCCACTGTCGTCGAGGATATGCGCCAGGCGCTC 4948

RESULT 66
US-10-540-898-26/c
; Sequence 26, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: CHIR0056-101 (PP023367.0003)
;  CURRENT APPLICATION NUMBER: US/10/540,898
;  CURRENT FILING DATE:  2005-06-27
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 687411
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(687411)
;   OTHER INFORMATION: n = A,T,C or G
US-10-540-898-26

Alignment Scores:
Pred. No.:                3.94e+05      Length:          687411
Score:                    48.00         Matches:         8
Percent Similarity:       73.7%         Conservative:    6
Best Local Similarity:    42.1%         Mismatches:      5
Query Match:              30.0%         Indels:          0
DB:                       6             Gaps:            0

US-10-758-902-1 (1-30) x US-10-540-898-26 (1-687411)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
               :::|||   |||:::|||:::      |||:::|||   :::|||:::|||   |||
Db      618175 TTCAACAAAGTCAATTTTCATTTTTTTGAAAGCTACATTTTTCCTTCCTTTTATCAA 618119

RESULT 67
US-10-833-833-125
; Sequence 125, Application US/10833833
; Publication No. US20060194210A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  APPLICANT:  Lai, Albert
;  APPLICANT:  Tse, Christin
;  APPLICANT:  Fattaey, Ali
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-038001
;  CURRENT APPLICATION NUMBER: US/10/833,833
;  CURRENT FILING DATE:  2004-04-27
;  NUMBER OF SEQ ID NOS: 175
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125
;   LENGTH: 1130575
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)  (1130575)
```

```
;   OTHER INFORMATION: n = A, C, G, or T/U
US-10-833-833-125

Alignment Scores:
Pred. No.:              7.23e+05        Length:         1130575
Score:                  48.00           Matches:        11
Percent Similarity:     61.9%           Conservative:   2
Best Local Similarity:  52.4%           Mismatches:     8
Query Match:            30.0%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x US-10-833-833-125 (1-1130575)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              |||   ||||||       |||||||||:::|||||||||      |||      :::
Db      89387 CTGTGTGAAGCAATATACCTACCCACCTTCTTACAGGACCTGAGCCTGGAGCAAGGAAGG 89446

Qy         28 Gly 28
              |||
Db      89447 GGT 89449

RESULT 68
US-11-266-748A-202256/c
; Sequence 202256, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 202256
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-202256

Alignment Scores:
Pred. No.:              105             Length:         1000
Score:                  47.50           Matches:        12
Percent Similarity:     56.0%           Conservative:   2
Best Local Similarity:  48.0%           Mismatches:     6
Query Match:            29.7%           Indels:         5
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-266-748A-202256 (1-1000)

Qy          4 ValSerPheAsnLeuGlyGluAla----------TyrGluTyrProThrPheIle 18
              |||      |||||||||||||||          |||   :::|||:::
Db        634 GTGAAAGGAAATCTGGGAGAAGCAAAAGAGGTTTCTTGTTATAGATTTCCTAGCACTCAT 575

Qy         19 GlnAspLeuArgAsn 23
              ||||||||||||
Db        574 TCTGATTTAAGAAAT 560

RESULT 69
US-10-471-571A-4685
; Sequence 4685, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4685
;   LENGTH: 1803
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-4685

Alignment Scores:
Pred. No.:              226             Length:         1803
Score:                  47.50           Matches:        11
Percent Similarity:     57.7%           Conservative:   4
Best Local Similarity:  42.3%           Mismatches:     10
Query Match:            29.7%           Indels:         1
DB:                     6               Gaps:           1

US-10-758-902-1 (1-30) x US-10-471-571A-4685 (1-1803)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle---GlnAspLeuArgAsn 23
              :::|||||||||   |||   |||:::   |||      :::      ||||||:::
Db       1087 GCATTTAATTTAGCAGAACAATATCAATGCCCTGTTATAGTTCTAAGTGATTTGCAATTA 1146

Qy         24 GluLeuAlaLysGlyThr 29
              |||   |||   |||
Db       1147 TCTTTAGGTAAACAAACT 1164

RESULT 70
US-11-206-135-3
; Sequence 3, Application US/11206135
; Publication No. US20060188479A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, De Chao
;  APPLICANT:  Henderson, Daniel
;  TITLE OF INVENTION: Adenovirus Vectors Containing Cell
;  TITLE OF INVENTION:  Status-Specific Response Elements and Methods of Use Thereof
;  FILE REFERENCE: CELL-014; 122.1
;  CURRENT APPLICATION NUMBER: US/11/206,135
;  CURRENT FILING DATE:  2005-08-18
;  PRIOR APPLICATION NUMBER: US/10/938,227
;  PRIOR FILING DATE: 2004-09-09
;  PRIOR APPLICATION NUMBER: 60/099,791
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/392,822
;  PRIOR FILING DATE: 1999-09-09
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 15056
;   TYPE: DNA
;   ORGANISM: H. sapiens
US-11-206-135-3

Alignment Scores:
Pred. No.:              3.56e+03        Length:         15056
Score:                  47.50           Matches:        12
Percent Similarity:     53.8%           Conservative:   2
Best Local Similarity:  46.2%           Mismatches:     9
Query Match:            29.7%           Indels:         3
```

```
DB:                    7             Gaps:          1

US-10-758-902-1 (1-30) x US-11-206-135-3 (1-15056)

Qy          8 LeuGlyGluAlaTyrGluTyrPro---------ThrPheIleGlnAspLeuArgAsnGlu 24
              |||||||||       |||||||||         ||||||:::|||        :::
Db      10390 CTGGGAGAAGACATGGAATACCCATGGCTTCTCACCTTCCTCCAGTCCAGTGGGCACCAT 10449

Qy         25 LeuAlaLysGlyThrPro 30
              |||      |||   |||
Db      10450 TTATGCCTAGGACACCCA 10467

RESULT 71
US-11-021-837-38
; Sequence 38, Application US/11021837
; Publication No. US20060140972A1
; GENERAL INFORMATION:
;  APPLICANT: Alm, Richard
;  APPLICANT:  Manning, Paul
;  APPLICANT:  Mclaughlin, Robert
;  APPLICANT:  MacCormack, Kathleen
;  TITLE OF INVENTION: Staphlococcus Saprophyticus Nucleic Acids and Polypeptides
;  FILE REFERENCE: 101324-US
;  CURRENT APPLICATION NUMBER: US/11/021,837
;  CURRENT FILING DATE:  2004-12-23
;  PRIOR APPLICATION NUMBER: US 60/533534
;  PRIOR FILING DATE: 2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/600680
;  PRIOR FILING DATE: 2003-08-31
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
;   LENGTH: 75762
;   TYPE: DNA
;   ORGANISM: Staphylococcus saprophyticus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (9659)..(9659)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (75142)..(75142)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-021-837-38

Alignment Scores:
Pred. No.:              2.9e+04       Length:        75762
Score:                  47.50         Matches:       11
Percent Similarity:     57.7%         Conservative:  4
Best Local Similarity:  42.3%         Mismatches:    10
Query Match:            29.7%         Indels:        1
DB:                     9             Gaps:          1

US-10-758-902-1 (1-30) x US-11-021-837-38 (1-75762)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIle---GlnAspLeuArgAsn 23
              :::|||||||||   |||   |||:::   |||      :::      ||||||:::
Db       5299 GCTTTTAATTTGGCTGAACAATATCAATGTCCAGTCATAGTATTAAGTGATTTACAACTT 5358

Qy         24 GluLeuAlaLysGlyThr 29
                 |||   |||   |||
Db       5359 TCATTAGGTAAACAAACG 5376

RESULT 72
US-10-488-619-181
; Sequence 181, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 181
;   LENGTH: 327
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-488-619-181

Alignment Scores:
Pred. No.:              30.4          Length:        327
Score:                  47.00         Matches:       8
Percent Similarity:     50.0%         Conservative:  3
Best Local Similarity:  36.4%         Mismatches:    11
Query Match:            29.4%         Indels:        0
DB:                     6             Gaps:          0

US-10-758-902-1 (1-30) x US-10-488-619-181 (1-327)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              ||||||:::         ||||||   |||   |||:::   |||      :::
Db        105 TTTAATATTTCATCTACATATGAATTACCACATTTTGTGTATGACTTTAATTCCTACTTT 164

Qy         26 AlaLys 27
                 |||
Db        165 AAAAAA 170

RESULT 73
US-11-292-078-2755/c
; Sequence 2755, Application US/11292078
; Publication No. US20060195941A1
; GENERAL INFORMATION:
;  APPLICANT: Deikman, Jill
;  APPLICANT:  Feng, Paul C.C.
;  APPLICANT:  Fincher, Karen L.
;  APPLICANT:  Ziegler, Todd E.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 16517.346 - 38-21(52274)C
;  CURRENT APPLICATION NUMBER: US/11/292,078
;  CURRENT FILING DATE:  2005-12-02
;  PRIOR APPLICATION NUMBER: US 10/021,323
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: US 60/255,619
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 2755
;   LENGTH: 548
;   TYPE: DNA
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3825-017-Q1-N6-E1
US-11-292-078-2755

Alignment Scores:
Pred. No.:              59.4          Length:        548
Score:                  47.00         Matches:       7
Percent Similarity:     84.6%         Conservative:  4
Best Local Similarity:  53.8%         Mismatches:    2
Query Match:            29.4%         Indels:        0
DB:                     7             Gaps:          0

US-10-758-902-1 (1-30) x US-11-292-078-2755 (1-548)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyr 14
              ||||||:::   :::|||:::|||:::   |||||||||
Db        171 AATACATTGTTGTATAATATAGGTGATATTTACGAGTAC 133

RESULT 74
US-11-266-748A-363915
; Sequence 363915, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
```

; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 363915
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-363915

Alignment Scores:

Pred. No.:	91.3	Length:	763
Score:	47.00	Matches:	9
Percent Similarity:	68.8%	Conservative:	2
Best Local Similarity:	56.2%	Mismatches:	5
Query Match:	29.4%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-363915 (1-763)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||   :::|||||||||   ||||||   |||:::   |||
Db         97 GAAGTCCCCGTATACATTCAAGATTCCCGAAATCCACTCTCCGCTGGA 144
```

RESULT 75
US-11-266-748A-447294/c
; Sequence 447294, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 447294
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-447294

Alignment Scores:

Pred. No.:	91.3	Length:	763
Score:	47.00	Matches:	9
Percent Similarity:	68.8%	Conservative:	2
Best Local Similarity:	56.2%	Mismatches:	5
Query Match:	29.4%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-447294 (1-763)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||   :::|||||||||   ||||||   |||:::   |||
Db        667 GAAGTCCCCGTATACATTCAAGATTCCCGAAATCCACTCTCCGCTGGA 620
```

RESULT 76
US-11-266-748A-33176
; Sequence 33176, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33176
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-33176

Alignment Scores:

Pred. No.:	102	Length:	833
Score:	47.00	Matches:	9
Percent Similarity:	68.8%	Conservative:	2
Best Local Similarity:	56.2%	Mismatches:	5
Query Match:	29.4%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-33176 (1-833)

```
Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||      :::|||||||||||||||   ||||||      :::|||
```

```
Db         72 CCCGAGAGCCTGCAGGACCTTCGGAACCATCTGGCGTCTGACTCTCCT 119

RESULT 77
US-11-266-748A-231941
; Sequence 231941, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 231941
;   LENGTH: 833
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-231941

Alignment Scores:
Pred. No.:              102          Length:         833
Score:                  47.00        Matches:        9
Percent Similarity:     68.8%        Conservative:   2
Best Local Similarity:  56.2%        Mismatches:     5
Query Match:            29.4%        Indels:         0
DB:                     8            Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-231941 (1-833)

Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||      :::|||||||||||||||||   ||||||      :::|||
Db         72 CCCGAGAGCCTGCAGGACCTTCGGAACCATCTGGCGTCTGACTCTCCT 119

RESULT 78
US-11-266-748A-415251/c
; Sequence 415251, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 415251
;   LENGTH: 868
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-415251

Alignment Scores:
Pred. No.:              108          Length:         868
Score:                  47.00        Matches:        7
Percent Similarity:     59.1%        Conservative:   6
Best Local Similarity:  31.8%        Mismatches:     9
Query Match:            29.4%        Indels:         0
DB:                     8            Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-415251 (1-868)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::|||      :::   ||||||      ::::::   :::   ||||||:::
Db        797 AACATGGGCACTGAGTTTTACTATCCCTGTGCAGTCAAACCAATGTCAAACGAGATTTGT 738

Qy         27 LysGly 28
              |||
Db        737 AATGGG 732

RESULT 79
US-11-266-748A-202167/c
; Sequence 202167, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 202167
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-202167

Alignment Scores:
```

```
Pred. No.:              130           Length:         1000
Score:                  47.00         Matches:        8
Percent Similarity:     50.0%         Conservative:   3
Best Local Similarity:  36.4%         Mismatches:     11
Query Match:            29.4%         Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-202167 (1-1000)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              ||||||:::         ||||||  |||  |||:::  |||     :::
Db        830 TTTAATATTTCATCTACATATGAATTACCACATTTTGTGTATGACTTTAATTCCTACTTT 771

Qy         26 AlaLys 27
                |||
Db        770 AAAAAA 765

RESULT 80
US-11-293-697-977/c
; Sequence 977, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 977
;   LENGTH: 2183
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-977

Alignment Scores:
Pred. No.:              357           Length:         2183
Score:                  47.00         Matches:        8
Percent Similarity:     50.0%         Conservative:   3
Best Local Similarity:  36.4%         Mismatches:     11
Query Match:            29.4%         Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-1 (1-30) x US-11-293-697-977 (1-2183)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              ||||||:::         ||||||  |||  |||:::  |||     :::
Db       2013 TTTAATATTTCATCTACATATGAATTACCACATTTTGTGTATGACTTTAATTCCTACTTT 1954

Qy         26 AlaLys 27
                |||
Db       1953 AAAAAA 1948

RESULT 81
US-11-217-529-77943
; Sequence 77943, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77943
;   LENGTH: 2355
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77943

Alignment Scores:
Pred. No.:              394           Length:         2355
Score:                  47.00         Matches:        8
Percent Similarity:     68.4%         Conservative:   5
Best Local Similarity:  42.1%         Mismatches:     6
Query Match:            29.4%         Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-1 (1-30) x US-11-217-529-77943 (1-2355)

Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||   ||||||   ||||||:::|||:::::::::   |||   :::     |||
Db       1507 TATCTTTATCCCTTGTTCATCAGGGATATTCAGAGCGTATTGAAACAAAATAATCCA 1563

RESULT 82
US-11-217-529-521
; Sequence 521, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 521
;   LENGTH: 2658
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-521

Alignment Scores:
Pred. No.:              462           Length:         2658
Score:                  47.00         Matches:        9
Percent Similarity:     59.1%         Conservative:   4
Best Local Similarity:  40.9%         Mismatches:     9
Query Match:            29.4%         Indels:         0
DB:                     8             Gaps:           0

US-10-758-902-1 (1-30) x US-11-217-529-521 (1-2658)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              ||||||  ||||||  |||  :::  |||::::::|||  |||:::
Db        610 TTAGGAACAGCGTATCGCTACAAGAGTCTCATTGAAGAACTCTCAAACAAATATCCCACA 669

Qy         28 GlyThr 29
                |||
Db        670 TCTACT 675

RESULT 83
US-11-218-305-12860/c
; Sequence 12860, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
```

```
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12860
;   LENGTH: 3072
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-12860

Alignment Scores:
Pred. No.:              557             Length:         3072
Score:                  47.00           Matches:        10
Percent Similarity:     56.2%           Conservative:   8
Best Local Similarity:  31.2%           Mismatches:     10
Query Match:            29.4%           Indels:         4
DB:                     9               Gaps:           1

US-10-758-902-1 (1-30) x US-11-218-305-12860 (1-3072)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyr----------ProThr 16
              :::   ::::::||||||:::   |||:::         :::            |||
Db        325 TTTAGGTCGATTAGCTTCCATTTTGGACAAGGCGCACTGTTTTGCTGTGTGTGCCCTGAA*266

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||:::|||:::   |||   ||||||      |||
Db        265 TTTGTCCAGAATCCCCGTGAAGAATTAATGCTTGGT 230

RESULT 84
US-10-511-937-2809
; Sequence 2809, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2809
;   LENGTH: 4628
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-2809

Alignment Scores:
Pred. No.:              948             Length:         4628
Score:                  47.00           Matches:        9
Percent Similarity:     68.8%           Conservative:   2
Best Local Similarity:  56.2%           Mismatches:     5
Query Match:            29.4%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x US-10-511-937-2809 (1-4628)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||   :::|||||||||   ||||||   |||:::   |||
Db        995 GAAGTCCCCGTATACATTCAAGATTCCCGAAATCCACTTTCCGCTGGA 1042

RESULT 85
US-11-266-748A-56811
; Sequence 56811, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56811
;   LENGTH: 5458
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-56811

Alignment Scores:
Pred. No.:              1.17e+03        Length:         5458
Score:                  47.00           Matches:        9
Percent Similarity:     68.8%           Conservative:   2
Best Local Similarity:  56.2%           Mismatches:     5
Query Match:            29.4%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-56811 (1-5458)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||   :::|||||||||   ||||||   |||:::   |||
Db       1808 GAAGTCCCCGTATACATTCAAGATTCCCGAAATCCACTTTCCGCTGGA 1855

RESULT 86
US-10-713-648A-47
; Sequence 47, Application US/10713648A
; Publication No. US20060107344A1
; GENERAL INFORMATION:
;  APPLICANT: POSCO
;  APPLICANT:  POSTECH
;  APPLICANT:  An, Gynheung
;  APPLICANT:  Ryu, Choong-Hwan
;  APPLICANT:  Han, Jong-Jin
;  APPLICANT:  Kang, Hong-Gyu
;  APPLICANT:  An, Kyungsook
;  TITLE OF INVENTION: ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
;  TITLE OF INVENTION:  MUTAGENESIS OF RICE
;  FILE REFERENCE: 20010-04USA
;  CURRENT APPLICATION NUMBER: US/10/713,648A
```

```
;  CURRENT FILING DATE:  2003-11-14
;  PRIOR APPLICATION NUMBER: 60/427,166
;  PRIOR FILING DATE: 2002-11-15
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
;   LENGTH: 6534
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: line 1C-109-51 coding sequence
US-10-713-648A-47

Alignment Scores:
Pred. No.:              1.48e+03        Length:         6534
Score:                  47.00           Matches:        10
Percent Similarity:     68.2%           Conservative:   5
Best Local Similarity:  45.5%           Mismatches:     7
Query Match:            29.4%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x US-10-713-648A-47 (1-6534)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              |||:::|||   |||   ::::::|||   :::      ||||||   :::   ||||||
Db       3157 TTTTCACTCAGTGAAGAATTCAAGTATGTCAGTGTTAGACAAGATGAGAAAATGGAGCTG 3216

Qy         26 AlaLys 27
              ||||||
Db       3217 GCTAAG 3222

RESULT 87
US-10-713-648A-30
; Sequence 30, Application US/10713648A
; Publication No. US20060107344A1
; GENERAL INFORMATION:
;  APPLICANT: POSCO
;  APPLICANT:  POSTECH
;  APPLICANT:  An, Gynheung
;  APPLICANT:  Ryu, Choong-Hwan
;  APPLICANT:  Han, Jong-Jin
;  APPLICANT:  Kang, Hong-Gyu
;  APPLICANT:  An, Kyungsook
;  TITLE OF INVENTION: ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
;  TITLE OF INVENTION:  MUTAGENESIS OF RICE
;  FILE REFERENCE: 20010-04USA
;  CURRENT APPLICATION NUMBER: US/10/713,648A
;  CURRENT FILING DATE:  2003-11-14
;  PRIOR APPLICATION NUMBER: 60/427,166
;  PRIOR FILING DATE: 2002-11-15
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 8093
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: line 1C-109-51 - genomic DNA without T-DNA insert
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6570)...(6571)
;   OTHER INFORMATION: location in genomic DNA where T-DNA was inserted
;   OTHER INFORMATION: to create line 1C-109-51
US-10-713-648A-30

Alignment Scores:
Pred. No.:              1.96e+03        Length:         8093
Score:                  47.00           Matches:        10
Percent Similarity:     68.2%           Conservative:   5
Best Local Similarity:  45.5%           Mismatches:     7
Query Match:            29.4%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x US-10-713-648A-30 (1-8093)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              |||:::|||   |||   ::::::|||   :::      ||||||   :::   ||||||
Db       4309 TTTTCACTCAGTGAAGAATTCAAGTATGTCAGTGTTAGACAAGATGAGAAAATGGAGCTG 4368

Qy         26 AlaLys 27
              ||||||
Db       4369 GCTAAG 4374

RESULT 88
US-11-266-748A-24960
; Sequence 24960, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24960
;   LENGTH: 17719
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-24960

Alignment Scores:
Pred. No.:              5.42e+03        Length:         17719
Score:                  47.00           Matches:        8
Percent Similarity:     50.0%           Conservative:   3
Best Local Similarity:  36.4%           Mismatches:     11
Query Match:            29.4%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-24960 (1-17719)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              ||||||:::       ||||||   |||   |||:::   |||      :::
Db      16058 TTTAATATTTCATCTACATATGAATTACCACATTTTGTGTATGACTTTAATTCCTACTTT 16117

Qy         26 AlaLys 27
                 |||
Db      16118 AAAAAA 16123

RESULT 89
US-10-539-228-510/c
; Sequence 510, Application US/10539228
; Publication No. US20060154250A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc S. Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: CHIR0052-101 (PP023370.0003)
;  CURRENT APPLICATION NUMBER: US/10/539,228
;  CURRENT FILING DATE:  2005-06-17
;  PRIOR APPLICATION NUMBER: US 10/322,281
;  PRIOR FILING DATE: 2002-12-18
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 510
;   LENGTH: 48509
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(48509)
;   OTHER INFORMATION: n = A,T,C or G
US-10-539-228-510

Alignment Scores:
Pred. No.:              2e+04          Length:         48509
Score:                  47.00          Matches:        9
Percent Similarity:     68.8%          Conservative:   2
Best Local Similarity:  56.2%          Mismatches:     5
Query Match:            29.4%          Indels:         0
DB:                     6              Gaps:           0

US-10-758-902-1 (1-30) x US-10-539-228-510 (1-48509)

Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||      :::|||||||||||||||||   ||||||      :::|||
Db       9837 CCCGAGAGCCTGCAGGACCTTCGGAACCATCTGGCGTCTGACTCTCCT 9790

RESULT 90
US-11-266-748A-29043
; Sequence 29043, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29043
;   LENGTH: 184242
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-29043

Alignment Scores:
Pred. No.:              1.12e+05       Length:         184242
Score:                  47.00          Matches:        11
Percent Similarity:     60.0%          Conservative:   1
Best Local Similarity:  55.0%          Mismatches:     8
Query Match:            29.4%          Indels:         0
DB:                     8              Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-29043 (1-184242)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              |||      |||      ||||||   |||   |||||||||   :::   |||||||||
Db     173796 GAGGGCCCAGAGGACACAACCTTCCACCAGAGCCTCAGGAACATGATGGTGAAAGGGACC 173855

RESULT 91
US-11-266-748A-22833/c
; Sequence 22833, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22833
;   LENGTH: 319486
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-22833

Alignment Scores:
Pred. No.:              2.26e+05       Length:         319486
Score:                  47.00          Matches:        11
Percent Similarity:     60.0%          Conservative:   1
Best Local Similarity:  55.0%          Mismatches:     8
Query Match:            29.4%          Indels:         0
DB:                     8              Gaps:           0

US-10-758-902-1 (1-30) x US-11-266-748A-22833 (1-319486)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              |||      |||      ||||||   |||   |||||||||   :::   |||||||||
Db      42820 GAGGGCCCAGAGGACACAACCTTCCACCAGAGCCTCAGGAACATGATGGTGAAAGGGACC 42761

RESULT 92
US-10-641-321-205
; Sequence 205, Application US/10641321
; Publication No. US20060183128A1
; GENERAL INFORMATION:
;  APPLICANT: Berlin, Kurt
;  APPLICANT:  Olek, Alexander
;  APPLICANT:  Beck, Stephan
;  APPLICANT:  Hildmann, Thomas
```

```
;  APPLICANT:  Lewin, Jorn
;  APPLICANT:  Novik, Karen
;  TITLE OF INVENTION: Methods and Compositions for Differentiating Tissues or Cell Type
;  TITLE OF INVENTION:  Epigenetic Markers
;  FILE REFERENCE: 47675-49
;  CURRENT APPLICATION NUMBER: US/10/641,321
;  CURRENT FILING DATE:  2003-08-12
;  NUMBER OF SEQ ID NOS: 221
; SEQ ID NO 205
;   LENGTH: 4647455
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (4267840)
;   OTHER INFORMATION: unknown base
US-10-641-321-205

Alignment Scores:
Pred. No.:              3.72e+06        Length:         4647455
Score:                  47.00           Matches:        11
Percent Similarity:     60.0%           Conservative:   1
Best Local Similarity:  55.0%           Mismatches:     8
Query Match:            29.4%           Indels:         0
DB:                     6               Gaps:           0

US-10-758-902-1 (1-30) x US-10-641-321-205 (1-4647455)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              |||      |||      ||||||  |||  |||||||||   :::   |||||||||
Db    1262979 GAGGGCCCAGAGGACACAACCTTCCACCAGAGCCTCAGGAACATGATGGTGAAAGGGACC 1263038

RESULT 93
US-11-266-748A-366769/c
; Sequence 366769, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 366769
;   LENGTH: 872
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-366769

Alignment Scores:
Pred. No.:              134             Length:         872
Score:                  46.50           Matches:        11
Percent Similarity:     59.1%           Conservative:   2
Best Local Similarity:  50.0%           Mismatches:     4
Query Match:            29.1%           Indels:         5
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-266-748A-366769 (1-872)

Qy          7 AsnLeuGlyGluAla--------------TyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||||||||||||              |||   :::|||:::         ||||||
Db        489 AATCTGGGAGAAGCAAAAGAGGTTTCTTGTTATAGATTTCCTAGCACTCATTCTGATTTA 430

Qy         22 ArgAsn 23
              ||||||
Db        429 AGAAAT 424

RESULT 94
US-11-266-748A-450148
; Sequence 450148, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 450148
;   LENGTH: 872
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-450148

Alignment Scores:
Pred. No.:              134             Length:         872
Score:                  46.50           Matches:        11
Percent Similarity:     59.1%           Conservative:   2
Best Local Similarity:  50.0%           Mismatches:     4
Query Match:            29.1%           Indels:         5
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-266-748A-450148 (1-872)

Qy          7 AsnLeuGlyGluAla--------------TyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||||||||||||              |||   :::|||:::         ||||||
Db        384 AATCTGGGAGAAGCAAAAGAGGTTTCTTGTTATAGATTTCCTAGCACTCATTCTGATTTA 443

Qy         22 ArgAsn 23
              ||||||
Db        444 AGAAAT 449

RESULT 95
US-11-348-413-11970
; Sequence 11970, Application US/11348413
; Publication No. US20060160121A1
```

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 11970
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1749)
; OTHER INFORMATION: WAN01UO65; ORF; 00000000000001; Cluster contains WAN01UBIU
; OTHER INFORMATION: :SR1_3462_Glim2.02::Glimmer 2.02 orf prediction:SR1:AF2693
; OTHER INFORMATION: 35
US-11-348-413-11970

Alignment Scores:

Pred. No.:	331	Length:	1749
Score:	46.50	Matches:	11
Percent Similarity:	59.3%	Conservative:	5
Best Local Similarity:	40.7%	Mismatches:	10
Query Match:	29.1%	Indels:	1
DB:	9	Gaps:	1

US-10-758-902-1 (1-30) x US-11-348-413-11970 (1-1749)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::||||||:::      ||||||        |||:::      |||      ||||||
Db       1657 TTTAACACATTAGAT---AATTTGAATATTAAATATCAATTAGCTACTAGCGCGCAAGAT 1713

Qy         21 LeuArgAsnGluLeuAlaLys 27
              :::   ||||||:::   |||
Db       1714 GTTTATAATGAAATTAAAAAA 1734
```

RESULT 96
US-11-348-413-13488
; Sequence 13488, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 13488
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1761)
; OTHER INFORMATION: WAN01UPIX; ORF; 00000000011100; Cluster contains WAN01OQ2Z
; OTHER INFORMATION: :SE0967::putative 2-oxoacid ferredoxin oxidoreductase alph
; OTHER INFORMATION: a subunit:ATCC12228:NC_004461.1
US-11-348-413-13488

Alignment Scores:

Pred. No.:	333	Length:	1761
Score:	46.50	Matches:	11
Percent Similarity:	57.7%	Conservative:	4
Best Local Similarity:	42.3%	Mismatches:	10
Query Match:	29.1%	Indels:	1
DB:	9	Gaps:	1

US-10-758-902-1 (1-30) x US-11-348-413-13488 (1-1761)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThr---PheIleGlnAspLeuArgAsn 23
              :::|||||||||   |||   |||:::   |||         :::   ||||||:::
Db       1042 GCATTTAATTTAGCTGAAGAATACCAATGTCCAGTCATTCTGTTAAGTGATTTACAATTA 1101

Qy         24 GluLeuAlaLysGlyThr 29
                 |||   |||   |||
Db       1102 TCATTAGGAAAACAAACT 1119
```

RESULT 97
US-11-218-305-5435/c
; Sequence 5435, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5435
; LENGTH: 2131
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-5435

Alignment Scores:

Pred. No.:	427	Length:	2131
Score:	46.50	Matches:	13
Percent Similarity:	47.2%	Conservative:	4
Best Local Similarity:	36.1%	Mismatches:	10
Query Match:	29.1%	Indels:	9
DB:	9	Gaps:	2

US-10-758-902-1 (1-30) x US-11-218-305-5435 (1-2131)

```
Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp--------- 20
              :::      :::||||||      |||      ||||||      |||:::
Db       1474 ATAAAAATTTCATTGGGTCATCAATATAATTCTCCTACATTAGAACAAAACTAACCGCAC 1415

Qy         21 --------------LeuArgAsnGluLeuAlaLys---GlyThrPro 30
                           :::||||||||||||   |||   |||   |||
Db       1414 TTCATAAATGGCAAGATGAGAAATGAATTAATGAAACATGGATTACCT 1367
```

RESULT 98
US-10-669-920-938
; Sequence 938, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER

```
;  FILE REFERENCE: 20366-066001
;  CURRENT APPLICATION NUMBER: US/10/669,920
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/004,113
;  PRIOR FILING DATE: 2001-10-23
;  PRIOR APPLICATION NUMBER: US 10/052,482
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 09/997,722
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: US 10/034,650
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: US 10/085,117
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: US 10/087,192
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 10/322,281
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: US 10/322,696
;  PRIOR FILING DATE: 2002-12-17
;  NUMBER OF SEQ ID NOS: 1441
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 938
;   LENGTH: 85920
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-669-920-938

Alignment Scores:
Pred. No.:              5.16e+04        Length:         85920
Score:                  46.50           Matches:        10
Percent Similarity:     68.0%           Conservative:   7
Best Local Similarity:  40.0%           Mismatches:     7
Query Match:            29.1%           Indels:         1
DB:                     6               Gaps:           1

US-10-758-902-1 (1-30) x US-10-669-920-938 (1-85920)

Qy          6 PheAsnLeuGlyGluAlaTyrGlu---TyrProThrPheIleGlnAspLeuArgAsnGlu 24
              ||||||:::      ::::::|||   |||||||||   :::      |||:::||||||
Db      27223 TTCAATATACACAGATCCCATGAAGCATATCCAACTCTTTTATTTCAGTTACAAAATGAA 27282

Qy         25 LeuAlaLysGlyThr 29
              :::   :::   |||
Db      27283 ATTCCTGAATGAACT 27297

RESULT 99
US-10-833-833-34/c
; Sequence 34, Application US/10833833
; Publication No. US20060194210A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  APPLICANT:  Lai, Albert
;  APPLICANT:  Tse, Christin
;  APPLICANT:  Fattaey, Ali
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-038001
;  CURRENT APPLICATION NUMBER: US/10/833,833
;  CURRENT FILING DATE:  2004-04-27
;  NUMBER OF SEQ ID NOS: 175
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 130414
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-833-833-34

Alignment Scores:
Pred. No.:              8.83e+04        Length:         130414
Score:                  46.50           Matches:        12
Percent Similarity:     44.4%           Conservative:   4
Best Local Similarity:  33.3%           Mismatches:     13
Query Match:            29.1%           Indels:         7

DB:                     6               Gaps:           1

US-10-758-902-1 (1-30) x US-10-833-833-34 (1-130414)

Qy          2 AsnThrValSerPhe--------------------AsnLeuGlyGluAlaTyrGluTyr 14
              ||||||:::||||||                    |||            :::   :::
Db     103805 AATACAATATCTTTCCCCATCATTCTTTAATTTCCAAATTTTTCAGTTCTCCACCCCTTC 103746

Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||   |||      |||:::   |||          ||||||
Db     103745 CCCACCATCATACACCCCTTAAAAGCAGAGAGACTAAGTCTTACTCCT 103698

RESULT 100
US-11-266-748A-302904/c
; Sequence 302904, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 302904
;   LENGTH: 404
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (39)..(39)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (64)..(64)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (67)..(67)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (77)..(77)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (80)..(81)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (137)..(137)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
```

; LOCATION: (232)..(232)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (259)..(259)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (265)..(265)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (307)..(307)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (337)..(337)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-302904

Alignment Scores:

Pred. No.:	60.8	Length:	404
Score:	46.00	Matches:	9
Percent Similarity:	57.7%	Conservative:	6
Best Local Similarity:	34.6%	Mismatches:	11
Query Match:	28.7%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-266-748A-302904 (1-404)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||       :::      |||   |||:::|||   |||:::   :::
Db        361 TCACTTTACCTTGGGGGTAAATTTNCCCTTCCTAAGTTCCTGCAGAAACTGAAGNATCAA 302

Qy         25 LeuAlaLysGlyThrPro 30
                 :::|||:::|||
Db        301 TAACCACGGGGAAGCCCA 284
```

Search completed: September 18, 2006, 20:48:28
Job time : 530.631 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 17:40:57 ; Search time 1579.94 Seconds
(without alignments)
1665.017 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 86534536 seqs, 29229259966 residues

Total number of hits satisfying chosen parameters: 173069072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_18092006_162713_11674/app_query.fasta_1
-DB=Pending_Patents_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10758902_@CGN_1_1_10839_@runat_18092006_162713_11674 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pna/PCTUSA_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pna/PCTUSB_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pna/PCTUSC_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pna/US075_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pna/US076_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pna/US077_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pna/US078_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pna/US079_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pna/US080_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pna/US081_COMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pna/US082_COMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pna/US083_COMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pna/US084_COMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pna/US085_COMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pna/US086_COMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pna/US087_COMB.seq:*
17: /EMC_Celerra_SIDS3/ptodata/2/pna/US088_COMB.seq:*
18: /EMC_Celerra_SIDS3/ptodata/2/pna/US089_COMB.seq:*
19: /EMC_Celerra_SIDS3/ptodata/2/pna/US090_COMB.seq:*
20: /EMC_Celerra_SIDS3/ptodata/2/pna/US091_COMB.seq:*
21: /EMC_Celerra_SIDS3/ptodata/2/pna/US092_COMB.seq:*
22: /EMC_Celerra_SIDS3/ptodata/2/pna/US093_COMB.seq:*
23: /EMC_Celerra_SIDS3/ptodata/2/pna/US094_COMB.seq:*
24: /EMC_Celerra_SIDS3/ptodata/2/pna/US095A_COMB.seq:*
25: /EMC_Celerra_SIDS3/ptodata/2/pna/US095B_COMB.seq:*
26: /EMC_Celerra_SIDS3/ptodata/2/pna/US095C_COMB.seq:*
27: /EMC_Celerra_SIDS3/ptodata/2/pna/US096A_COMB.seq:*
28: /EMC_Celerra_SIDS3/ptodata/2/pna/US096B_COMB.seq:*
29: /EMC_Celerra_SIDS3/ptodata/2/pna/US096C_COMB.seq:*
30: /EMC_Celerra_SIDS3/ptodata/2/pna/US097A_COMB.seq:*
31: /EMC_Celerra_SIDS3/ptodata/2/pna/US097B_COMB.seq:*
32: /EMC_Celerra_SIDS3/ptodata/2/pna/US098A_COMB.seq:*
33: /EMC_Celerra_SIDS3/ptodata/2/pna/US098B_COMB.seq:*
34: /EMC_Celerra_SIDS3/ptodata/2/pna/US099A_COMB.seq:*
35: /EMC_Celerra_SIDS3/ptodata/2/pna/US099B_COMB.seq:*
36: /EMC_Celerra_SIDS3/ptodata/2/pna/US099C_COMB.seq:*
37: /EMC_Celerra_SIDS3/ptodata/2/pna/US099D_COMB.seq:*
38: /EMC_Celerra_SIDS3/ptodata/2/pna/US099E_COMB.seq:*
39: /EMC_Celerra_SIDS3/ptodata/2/pna/US100A_COMB.seq:*
40: /EMC_Celerra_SIDS3/ptodata/2/pna/US100B_COMB.seq:*
41: /EMC_Celerra_SIDS3/ptodata/2/pna/US101_COMB.seq:*
42: /EMC_Celerra_SIDS3/ptodata/2/pna/US102A_COMB.seq:*
43: /EMC_Celerra_SIDS3/ptodata/2/pna/US102B_COMB.seq:*
44: /EMC_Celerra_SIDS3/ptodata/2/pna/US103A_COMB.seq:*
45: /EMC_Celerra_SIDS3/ptodata/2/pna/US103B_COMB.seq:*
46: /EMC_Celerra_SIDS3/ptodata/2/pna/US103C_COMB.seq:*
47: /EMC_Celerra_SIDS3/ptodata/2/pna/US103D_COMB.seq:*
48: /EMC_Celerra_SIDS3/ptodata/2/pna/US103E_COMB.seq:*
49: /EMC_Celerra_SIDS3/ptodata/2/pna/US103F_COMB.seq:*
50: /EMC_Celerra_SIDS3/ptodata/2/pna/US104_COMB.seq:*
51: /EMC_Celerra_SIDS3/ptodata/2/pna/US105_COMB.seq:*
52: /EMC_Celerra_SIDS3/ptodata/2/pna/US106A_COMB.seq:*
53: /EMC_Celerra_SIDS3/ptodata/2/pna/US106B_COMB.seq:*
54: /EMC_Celerra_SIDS3/ptodata/2/pna/US107A_COMB.seq:*
55: /EMC_Celerra_SIDS3/ptodata/2/pna/US107B_COMB.seq:*
56: /EMC_Celerra_SIDS3/ptodata/2/pna/US107C_COMB.seq:*
57: /EMC_Celerra_SIDS3/ptodata/2/pna/US107D_COMB.seq:*
58: /EMC_Celerra_SIDS3/ptodata/2/pna/US107E_COMB.seq:*
59: /EMC_Celerra_SIDS3/ptodata/2/pna/US107F_COMB.seq:*
60: /EMC_Celerra_SIDS3/ptodata/2/pna/US107G_COMB.seq:*
61: /EMC_Celerra_SIDS3/ptodata/2/pna/US108_COMB.seq:*
62: /EMC_Celerra_SIDS3/ptodata/2/pna/US109A_COMB.seq:*
63: /EMC_Celerra_SIDS3/ptodata/2/pna/US109B_COMB.seq:*
64: /EMC_Celerra_SIDS3/ptodata/2/pna/US109C_COMB.seq:*
65: /EMC_Celerra_SIDS3/ptodata/2/pna/US110A_COMB.seq:*
66: /EMC_Celerra_SIDS3/ptodata/2/pna/US110B_COMB.seq:*
67: /EMC_Celerra_SIDS3/ptodata/2/pna/US110C_COMB.seq:*
68: /EMC_Celerra_SIDS3/ptodata/2/pna/US110D_COMB.seq:*
69: /EMC_Celerra_SIDS3/ptodata/2/pna/US111A_COMB.seq:*
70: /EMC_Celerra_SIDS3/ptodata/2/pna/US111B_COMB.seq:*
71: /EMC_Celerra_SIDS3/ptodata/2/pna/US112A_COMB.seq:*
72: /EMC_Celerra_SIDS3/ptodata/2/pna/US112B_COMB.seq:*
73: /EMC_Celerra_SIDS3/ptodata/2/pna/US113A_COMB.seq:*
74: /EMC_Celerra_SIDS3/ptodata/2/pna/US113B_COMB.seq:*
75: /EMC_Celerra_SIDS3/ptodata/2/pna/US114_COMB.seq:*
76: /EMC_Celerra_SIDS3/ptodata/2/pna/US117_COMB.seq:*
77: /EMC_Celerra_SIDS3/ptodata/2/pna/US600_COMB.seq:*
78: /EMC_Celerra_SIDS3/ptodata/2/pna/US601_COMB.seq:*
79: /EMC_Celerra_SIDS3/ptodata/2/pna/US602A_COMB.seq:*
80: /EMC_Celerra_SIDS3/ptodata/2/pna/US602B_COMB.seq:*
81: /EMC_Celerra_SIDS3/ptodata/2/pna/US603_COMB.seq:*
82: /EMC_Celerra_SIDS3/ptodata/2/pna/US604A_COMB.seq:*
83: /EMC_Celerra_SIDS3/ptodata/2/pna/US604B_COMB.seq:*
84: /EMC_Celerra_SIDS3/ptodata/2/pna/US605_COMB.seq:*
85: /EMC_Celerra_SIDS3/ptodata/2/pna/US606_COMB.seq:*
86: /EMC_Celerra_SIDS3/ptodata/2/pna/US607_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	100.0	2404	66	US-11-084-080-15	Sequence 15, Appl
2	160	100.0	2404	66	US-11-084-080-19	Sequence 19, Appl
3	160	100.0	2404	66	US-11-084-080-21	Sequence 21, Appl
4	160	100.0	2404	66	US-11-084-080-23	Sequence 23, Appl

	5	160	100.0	2431	66	US-11-084-080-27 Sequence 27, Appl
	6	111	69.4	65	60	US-10-758-902-5 Sequence 5, Appli
	7	72	45.0	363	60	US-10-758-902-8 Sequence 8, Appli
	8	64	40.0	499	33	US-09-865-439A-77852 Sequence 77852, A
	9	64	40.0	499	79	US-60-207-458-121994 Sequence 121994,
	10	61	38.1	1195	12	US-08-342-786-1 Sequence 1, Appli
	11	61	38.1	1360	65	US-11-010-795-19 Sequence 19, Appl
	12	61	38.1	1376	1	PCT-US02-02792-1 Sequence 1, Appli
	13	61	38.1	1376	50	US-10-467-009-1 Sequence 1, Appli
	14	61	38.1	1379	14	US-08-501-253-1 Sequence 1, Appli
	15	61	38.1	1379	37	US-09-978-274A-30 Sequence 30, Appl
	16	61	38.1	1379	69	US-11-106-187-1 Sequence 1, Appli
c	17	60.5	37.8	569	44	US-10-301-480-72772 Sequence 72772, A
c	18	60.5	37.8	569	44	US-10-301-480-72773 Sequence 72773, A
c	19	60.5	37.8	569	44	US-10-301-480-686181 Sequence 686181,
c	20	60.5	37.8	569	44	US-10-301-480-686182 Sequence 686182,
c	21	60.5	37.8	569	45	US-10-301-480A-448841 Sequence 448841,
c	22	60.5	37.8	569	45	US-10-301-480A-448842 Sequence 448842,
c	23	60.5	37.8	569	46	US-10-301-480B-448841 Sequence 448841,
c	24	60.5	37.8	569	46	US-10-301-480B-448842 Sequence 448842,
c	25	60.5	37.8	569	47	US-10-301-480C-448841 Sequence 448841,
c	26	60.5	37.8	569	47	US-10-301-480C-448842 Sequence 448842,
c	27	60.5	37.8	596	27	US-09-634-306B-230755 Sequence 230755,
c	28	60.5	37.8	596	27	US-09-634-306B-230756 Sequence 230756,
c	29	60.5	37.8	596	27	US-09-634-306B-230757 Sequence 230757,
c	30	60.5	37.8	596	39	US-10-027-632-230755 Sequence 230755,
c	31	60.5	37.8	596	39	US-10-027-632-230756 Sequence 230756,
c	32	60.5	37.8	596	39	US-10-027-632-230757 Sequence 230757,
c	33	60.5	37.8	627	44	US-10-301-480-572047 Sequence 572047,
c	34	60.5	37.8	627	44	US-10-301-480-1185456 Sequence 1185456,
c	35	60.5	37.8	627	45	US-10-301-480A-948116 Sequence 948116,
c	36	60.5	37.8	627	46	US-10-301-480B-948116 Sequence 948116,
c	37	60.5	37.8	627	47	US-10-301-480C-948116 Sequence 948116,
	38	59	36.9	442	26	US-09-565-240-46864 Sequence 46864, A
	39	59	36.9	442	71	US-11-239-610A-46864 Sequence 46864, A
	40	59	36.9	526	50	US-10-424-599-70917 Sequence 70917, A
	41	59	36.9	532	28	US-09-654-617-12060 Sequence 12060, A
	42	59	36.9	532	28	US-09-684-016-12060 Sequence 12060, A
	43	59	36.9	561	33	US-09-865-439A-77772 Sequence 77772, A
	44	59	36.9	561	79	US-60-207-458-121914 Sequence 121914,
	45	59	36.9	699	23	US-09-474-435A-65250 Sequence 65250, A
	46	59	36.9	20509	32	US-09-803-736-1196 Sequence 1196, Ap
c	47	58	36.2	251	26	US-09-565-306-10375 Sequence 10375, A
c	48	58	36.2	251	74	US-11-353-150-10375 Sequence 10375, A
c	49	58	36.2	286	22	US-09-394-745-4271 Sequence 4271, Ap
	50	58	36.2	496	79	US-60-207-458-24805 Sequence 24805, A
	51	58	36.2	1195	9	US-08-049-075-1 Sequence 1, Appli
	52	57.5	35.9	678	50	US-10-417-884-3648 Sequence 3648, Ap
	53	57.5	35.9	678	50	US-10-417-884A-3648 Sequence 3648, Ap
	54	57.5	35.9	14560	77	US-60-068-217-948 Sequence 948, App
	55	57	35.6	431	22	US-09-304-517A-250010 Sequence 250010,
	56	57	35.6	431	23	US-09-440-687-9039 Sequence 9039, Ap
	57	57	35.6	431	27	US-09-615-606A-28851 Sequence 28851, A
	58	57	35.6	431	38	US-09-985-678-250010 Sequence 250010,
	59	57	35.6	431	71	US-11-239-591A-9039 Sequence 9039, Ap
	60	57	35.6	431	78	US-60-144-084-39395 Sequence 39395, A
	61	57	35.6	526	28	US-09-654-617-415334 Sequence 415334,
	62	57	35.6	526	28	US-09-669-817A-6666 Sequence 6666, Ap
	63	57	35.6	526	28	US-09-684-016-415334 Sequence 415334,
	64	57	35.6	549	22	US-09-371-146A-250010 Sequence 250010,
	65	57	35.6	1452	50	US-10-437-963-43964 Sequence 43964, A
c	66	57	35.6	1501	32	US-09-815-264-3642 Sequence 3642, Ap
	67	57	35.6	2392	50	US-10-449-902-13635 Sequence 13635, A
c	68	57	35.6	5443	27	US-09-620-392-68993 Sequence 68993, A
	69	57	35.6	15153	27	US-09-620-392-44492 Sequence 44492, A
	70	57	35.6	57600	30	US-09-702-134-8583 Sequence 8583, Ap
	71	57	35.6	57600	32	US-09-815-264-68788 Sequence 68788, A
	72	56.5	35.3	1236	3	PCT-US06-06593-19 Sequence 19, Appl
	73	56.5	35.3	1236	74	US-11-361-092-19 Sequence 19, Appl
c	74	56.5	35.3	152372	3	PCT-US06-06593-171 Sequence 171, App
c	75	56.5	35.3	152372	74	US-11-361-092-171 Sequence 171, App
	76	56	35.0	295	22	US-09-304-517A-12197 Sequence 12197, A
	77	56	35.0	295	22	US-09-371-146A-12197 Sequence 12197, A
	78	56	35.0	295	38	US-09-985-678-12197 Sequence 12197, A
	79	56	35.0	301	22	US-09-304-517A-9966 Sequence 9966, Ap
	80	56	35.0	301	22	US-09-371-146A-9966 Sequence 9966, Ap
	81	56	35.0	301	38	US-09-985-678-9966 Sequence 9966, Ap
	82	56	35.0	308	22	US-09-304-517A-12223 Sequence 12223, A
	83	56	35.0	308	22	US-09-371-146A-12223 Sequence 12223, A
	84	56	35.0	308	28	US-09-654-617-288444 Sequence 288444,
	85	56	35.0	308	28	US-09-684-016-288444 Sequence 288444,
	86	56	35.0	308	38	US-09-985-678-12223 Sequence 12223, A
	87	56	35.0	465	37	US-09-978-274A-5 Sequence 5, Appli
	88	56	35.0	474	21	US-09-270-849B-89668 Sequence 89668, A
	89	56	35.0	655	60	US-10-767-701-6363 Sequence 6363, Ap
	90	56	35.0	791	50	US-10-425-115-166418 Sequence 166418,
	91	56	35.0	792	37	US-09-978-274A-3 Sequence 3, Appli
	92	56	35.0	882	16	US-08-715-074A-1 Sequence 1, Appli
	93	56	35.0	945	1	PCT-US02-15033A-15 Sequence 15, Appl
	94	56	35.0	945	37	US-09-978-274A-1 Sequence 1, Appli
	95	56	35.0	1020	50	US-10-425-115-166417 Sequence 166417,
	96	56	35.0	1092	37	US-09-978-274A-19 Sequence 19, Appl
	97	56	35.0	1149	23	US-09-404-520-27610 Sequence 27610, A
	98	56	35.0	1149	23	US-09-404-520B-27610 Sequence 27610, A
	99	56	35.0	1368	37	US-09-978-274A-31 Sequence 31, Appl
	100	56	35.0	2197	42	US-10-219-999-29690 Sequence 29690, A

ALIGNMENTS

```
RESULT 1
US-11-084-080-15
; Sequence 15, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-15

Alignment Scores:
Pred. No.:                1.18e-17        Length:          2404
Score:                    160.00          Matches:         30
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       66              Gaps:            0

US-10-758-902-1 (1-30) x US-11-084-080-15 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 884

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
```

```
                    ||||||||||||||||||||||||||||||
Db        885 TTGCGCAATGAATTGGCTAAGGGCACACCA 914

RESULT 2
US-11-084-080-19
; Sequence 19, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Alignment Scores:
Pred. No.:              1.18e-17      Length:          2404
Score:                  160.00        Matches:         30
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            100.0%        Indels:          0
DB:                     66            Gaps:            0

US-10-758-902-1 (1-30) x US-11-084-080-19 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1643 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1702

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db       1703 TTGCGCAATGAATTGGCTAAGGGCACACCA 1732

RESULT 3
US-11-084-080-21
; Sequence 21, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-21

Alignment Scores:
Pred. No.:              1.18e-17      Length:          2404
Score:                  160.00        Matches:         30
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            100.0%        Indels:          0
DB:                     66            Gaps:            0

US-10-758-902-1 (1-30) x US-11-084-080-21 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 191

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        192 TTGCGCAATGAATTGGCTAAGGGCACACCA 221

RESULT 4
US-11-084-080-23
; Sequence 23, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Alignment Scores:
Pred. No.:              1.18e-17      Length:          2404
Score:                  160.00        Matches:         30
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            100.0%        Indels:          0
DB:                     66            Gaps:            0

US-10-758-902-1 (1-30) x US-11-084-080-23 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        950 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1009
```

```
Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db       1010 TTGCGCAATGAATTGGCTAAGGGCACACCA 1039

RESULT 5
US-11-084-080-27
; Sequence 27, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 2431
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-011
US-11-084-080-27

Alignment Scores:
Pred. No.:              1.2e-17       Length:        2431
Score:                  160.00        Matches:       30
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            100.0%        Indels:        0
DB:                     66            Gaps:          0

US-10-758-902-1 (1-30) x US-11-084-080-27 (1-2431)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 911

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||
Db        912 TTGCGCAATGAATTGGCTAAGGGCACACCA 941

RESULT 6
US-10-758-902-5
; Sequence 5, Application US/10758902
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-5

Alignment Scores:
Pred. No.:              1.19e-10      Length:        65
Score:                  111.00        Matches:       21
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            69.4%         Indels:        0
DB:                     60            Gaps:          0

US-10-758-902-1 (1-30) x US-10-758-902-5 (1-65)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGGCCTACGAGTATCCCACTTTTATACAAGATTTGCGCAACGAACTCGCTAAAGGA 60

Qy         29 Thr 29
              |||
Db         61 ACC 63

RESULT 7
US-10-758-902-8
; Sequence 8, Application US/10758902
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Bougainvillaea Spectabilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)...(361)
US-10-758-902-8

Alignment Scores:
Pred. No.:              0.0253        Length:        363
Score:                  72.00         Matches:       14
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            45.0%         Indels:        0
DB:                     60            Gaps:          0

US-10-758-902-1 (1-30) x US-10-758-902-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCA 43

RESULT 8
US-09-865-439A-77852
; Sequence 77852, Application US/09865439A
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  APPLICANT:  Hardeman, Kristine J.
;  APPLICANT:  La Rosa, Thomas J.
;  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(51936)B
```

; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 77852
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3606-018-Q6-N6-H4
US-09-865-439A-77852

Alignment Scores:

Pred. No.:	1.23	Length:	499
Score:	64.00	Matches:	12
Percent Similarity:	73.7%	Conservative:	2
Best Local Similarity:	63.2%	Mismatches:	5
Query Match:	40.0%	Indels:	0
DB:	33	Gaps:	0

US-10-758-902-1 (1-30) x US-09-865-439A-77852 (1-499)

```
Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::|||||||||||||   ||||||      :::|||||||||   |||
Db        157 GAGCAGTACCAATACCCAACATTTTGACAGGACTTCAATTCTGAATTGGCTGCTGGG 213
```

RESULT 9
US-60-207-458-121994
; Sequence 121994, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 121994
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3606-018-Q6-N6-H4
US-60-207-458-121994

Alignment Scores:

Pred. No.:	1.23	Length:	499
Score:	64.00	Matches:	12
Percent Similarity:	73.7%	Conservative:	2
Best Local Similarity:	63.2%	Mismatches:	5
Query Match:	40.0%	Indels:	0
DB:	79	Gaps:	0

US-10-758-902-1 (1-30) x US-60-207-458-121994 (1-499)

```
Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::|||||||||||||   ||||||      :::|||||||||   |||
Db    .    157 GAGCAGTACCAATACCCAACATTTTGACAGGACTTCAATTCTGAATTGGCTGCTGGG 213
```

RESULT 10
US-08-342-786-1
; Sequence 1, Application US/08342786
; GENERAL INFORMATION:
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Kim, Man-Keun
; TITLE OF INVENTION: A Novel Expression Vector for Phytolacca
; TITLE OF INVENTION: Antiviral Protein
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Ave.
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,786
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/147,024
; FILING DATE: 01-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/08862
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)527-7700
; TELEFAX: (212)753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Phytolacca americana L.
; IMMEDIATE SOURCE:
; CLONE: PAP
US-08-342-786-1

Alignment Scores:

Pred. No.:	15	Length:	1195
Score:	61.00	Matches:	12
Percent Similarity:	68.0%	Conservative:	5
Best Local Similarity:	48.0%	Mismatches:	6
Query Match:	38.1%	Indels:	2
DB:	12	Gaps:	1

US-10-758-902-1 (1-30) x US-08-342-786-1 (1-1195)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              |||||||||||||||
Db        162 GATCTTCGTAATGAA 176
```

RESULT 11
US-11-010-795-19
; Sequence 19, Application US/11010795
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.

```
;  APPLICANT:  DI, RONG
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
;  TITLE OF INVENTION:  RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
;  FILE REFERENCE: OCIRS 3.0-085
;  CURRENT APPLICATION NUMBER: US/11/010,795
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: 60/529,348
;  PRIOR FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
;   LENGTH: 1360
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (207)..(1145)
US-11-010-795-19

Alignment Scores:
Pred. No.:              17.9          Length:        1360
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     65            Gaps:          1

US-10-758-902-1 (1-30) x US-11-010-795-19 (1-1360)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        276 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 335

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        336 GATCTTCGTAATGAA 350

RESULT 12
PCT-US02-02792-1
; Sequence 1, Application PC/TUS0202792
; GENERAL INFORMATION:
;  APPLICANT: RUTGERS, THE STATE UNIVERSITY
;  TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
;  FILE REFERENCE: OCIRS 3.4-076
;  CURRENT APPLICATION NUMBER: PCT/US02/02792
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: 60/266,396
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1376
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (225)..(1160)
PCT-US02-02792-1

Alignment Scores:
Pred. No.:              18.2          Length:        1376
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     1             Gaps:          1

US-10-758-902-1 (1-30) x PCT-US02-02792-1 (1-1376)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 13
US-10-467-009-1
; Sequence 1, Application US/10467009
; GENERAL INFORMATION:
;  APPLICANT: RUTGERS, THE STATE UNIVERSITY
;  TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
;  FILE REFERENCE: OCIRS 3.4-076
;  CURRENT APPLICATION NUMBER: US/10/467,009
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: 60/266,396
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1376
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (225)..(1160)
US-10-467-009-1

Alignment Scores:
Pred. No.:              18.2          Length:        1376
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     50            Gaps:          1

US-10-758-902-1 (1-30) x US-10-467-009-1 (1-1376)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 14
US-08-501-253-1
; Sequence 1, Application US/08501253
;  GENERAL INFORMATION:
;    APPLICANT:  Uckun, Fatih
;    APPLICANT:  Tumer, Nilgun
;    TITLE OF INVENTION:  Biotherapeutic Agents Comprising
;    TITLE OF INVENTION:  Recombinant PAp and PAP Mutants
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  90 South 7th Street, 3100 Norwest Center
;      CITY:  Minneapolis
;      STATE:  MM
;      COUNTRY:  US
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/501,253
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M.
;      REGISTRATION NUMBER:  33,924
;      REFERENCE/DOCKET NUMBER:  600.323US01
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1379 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  225..1163
US-08-501-253-1

Alignment Scores:
Pred. No.:              18.2          Length:        1379
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     14            Gaps:          1

US-10-758-902-1 (1-30) x US-08-501-253-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 15
US-09-978-274A-30
; Sequence 30, Application US/09978274A
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 1379
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-30

Alignment Scores:
Pred. No.:              18.2          Length:        1379
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     37            Gaps:          1

US-10-758-902-1 (1-30) x US-09-978-274A-30 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368
```

```
RESULT 16
US-11-106-187-1
; Sequence 1, Application US/11106187
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  WANG, PINGER
;  TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
;  FILE REFERENCE: OCIRS 3.9-060 CONT
;  CURRENT APPLICATION NUMBER: US/11/106,187
;  CURRENT FILING DATE:  2005-04-14
;  PRIOR APPLICATION NUMBER: US/09/721,047
;  PRIOR FILING DATE: 2000-11-22
;  PRIOR APPLICATION NUMBER: PCT/US99/11301
;  PRIOR FILING DATE: 1999-05-21
;  PRIOR APPLICATION NUMBER: 60/086,374
;  PRIOR FILING DATE: 1998-05-22
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
;   LENGTH: 1379
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (225)..(1163)
US-11-106-187-1

Alignment Scores:
Pred. No.:              18.2          Length:        1379
Score:                  61.00         Matches:       12
Percent Similarity:     68.0%         Conservative:  5
Best Local Similarity:  48.0%         Mismatches:    6
Query Match:            38.1%         Indels:        2
DB:                     69            Gaps:          1

US-10-758-902-1 (1-30) x US-11-106-187-1 (1-1379)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              ||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 17
US-10-301-480-72772/c
; Sequence 72772, Application US/10301480
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72772
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-72772

Alignment Scores:
Pred. No.:              6.67          Length:        569
Score:                  60.50         Matches:       14
Percent Similarity:     40.9%         Conservative:  4
Best Local Similarity:  31.8%         Mismatches:    7
Query Match:            37.8%         Indels:        19
```

```
DB:                    44            Gaps:          1

US-10-758-902-1 (1-30) x US-10-301-480-72772 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 18
US-10-301-480-72773/c
; Sequence 72773, Application US/10301480
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72773
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-72773

Alignment Scores:
Pred. No.:              6.67          Length:        569
Score:                  60.50         Matches:       14
Percent Similarity:     40.9%         Conservative:  4
Best Local Similarity:  31.8%         Mismatches:    7
Query Match:            37.8%         Indels:        19
DB:                     44            Gaps:          1

US-10-758-902-1 (1-30) x US-10-301-480-72773 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 19
US-10-301-480-686181/c
; Sequence 686181, Application US/10301480
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 686181
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-686181

Alignment Scores:
Pred. No.:              6.67          Length:        569
Score:                  60.50         Matches:       14
Percent Similarity:     40.9%         Conservative:  4
Best Local Similarity:  31.8%         Mismatches:    7
Query Match:            37.8%         Indels:        19
DB:                     44            Gaps:          1

US-10-758-902-1 (1-30) x US-10-301-480-686181 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 20
US-10-301-480-686182/c
; Sequence 686182, Application US/10301480
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 686182
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-686182

Alignment Scores:
Pred. No.:              6.67          Length:        569
Score:                  60.50         Matches:       14
Percent Similarity:     40.9%         Conservative:  4
Best Local Similarity:  31.8%         Mismatches:    7
Query Match:            37.8%         Indels:        19
DB:                     44            Gaps:          1

US-10-758-902-1 (1-30) x US-10-301-480-686182 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
```

```
Db        434 AGAAACTCCCTA 423

RESULT 21
US-10-301-480A-448841/c
; Sequence 448841, Application US/10301480A
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827-137
;  CURRENT APPLICATION NUMBER: US/10/301,480A
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 989478
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 448841
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-301-480A-448841

Alignment Scores:
Pred. No.:              6.67          Length:         569
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     45            Gaps:           1

US-10-758-902-1 (1-30) x US-10-301-480A-448841 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||    |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 ----------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                          ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 22
US-10-301-480A-448842/c
; Sequence 448842, Application US/10301480A
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827-137
;  CURRENT APPLICATION NUMBER: US/10/301,480A
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 989478
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 448842
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-301-480A-448842

Alignment Scores:
Pred. No.:              6.67          Length:         569
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     45            Gaps:           1

US-10-758-902-1 (1-30) x US-10-301-480A-448842 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||    |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 ----------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                          ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 23
US-10-301-480B-448841/c
; Sequence 448841, Application US/10301480B
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827-137
;  CURRENT APPLICATION NUMBER: US/10/301,480B
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 989478
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 448841
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-301-480B-448841

Alignment Scores:
Pred. No.:              6.67          Length:         569
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     46            Gaps:           1

US-10-758-902-1 (1-30) x US-10-301-480B-448841 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||    |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 ----------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                          ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 24
US-10-301-480B-448842/c
; Sequence 448842, Application US/10301480B
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827-137
;  CURRENT APPLICATION NUMBER: US/10/301,480B
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
```

```
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 989478
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 448842
;    LENGTH: 569
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-301-480B-448842

Alignment Scores:
Pred. No.:              6.67          Length:         569
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     46            Gaps:           1

US-10-758-902-1 (1-30) x US-10-301-480B-448842 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 25
US-10-301-480C-448841/c
; Sequence 448841, Application US/10301480C
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827-137
;  CURRENT APPLICATION NUMBER: US/10/301,480C
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 989478
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 448841
;    LENGTH: 569
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-301-480C-448841

Alignment Scores:
Pred. No.:              6.67          Length:         569
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     47            Gaps:           1

US-10-758-902-1 (1-30) x US-10-301-480C-448841 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 26
US-10-301-480C-448842/c
; Sequence 448842, Application US/10301480C
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827-137
;  CURRENT APPLICATION NUMBER: US/10/301,480C
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 989478
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 448842
;    LENGTH: 569
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-301-480C-448842

Alignment Scores:
Pred. No.:              6.67          Length:         569
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     47            Gaps:           1

US-10-758-902-1 (1-30) x US-10-301-480C-448842 (1-569)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        554 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 495

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        494 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 435

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        434 AGAAACTCCCTA 423

RESULT 27
US-09-634-306B-230755/c
; Sequence 230755, Application US/09634306B
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/09/634,306B
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 230755
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-09-634-306B-230755

Alignment Scores:
Pred. No.:              7.11          Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     27            Gaps:           1

US-10-758-902-1 (1-30) x US-09-634-306B-230755 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 28
US-09-634-306B-230756/c
; Sequence 230756, Application US/09634306B
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/09/634,306B
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230756
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-09-634-306B-230756

Alignment Scores:
Pred. No.:              7.11          Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     27            Gaps:           1

US-10-758-902-1 (1-30) x US-09-634-306B-230756 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 29
US-09-634-306B-230757/c
; Sequence 230757, Application US/09634306B
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/09/634,306B
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230757
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-09-634-306B-230757

Alignment Scores:
Pred. No.:              7.11          Length:         596
Score:                  60.50         Matches:        14
Percent Similarity:     40.9%         Conservative:   4
Best Local Similarity:  31.8%         Mismatches:     7
Query Match:            37.8%         Indels:         19
DB:                     27            Gaps:           1

US-10-758-902-1 (1-30) x US-09-634-306B-230757 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu----------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 30
US-10-027-632-230755/c
; Sequence 230755, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
```

```
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230755
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230755

Alignment Scores:
Pred. No.:              7.11          Length:          596
Score:                  60.50         Matches:         14
Percent Similarity:     40.9%         Conservative:    4
Best Local Similarity:  31.8%         Mismatches:      7
Query Match:            37.8%         Indels:          19
DB:                     39            Gaps:            1

US-10-758-902-1 (1-30) x US-10-027-632-230755 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 31
US-10-027-632-230756/c
; Sequence 230756, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230756
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230756

Alignment Scores:
Pred. No.:              7.11          Length:          596
Score:                  60.50         Matches:         14
Percent Similarity:     40.9%         Conservative:    4
Best Local Similarity:  31.8%         Mismatches:      7
Query Match:            37.8%         Indels:          19
DB:                     39            Gaps:            1

US-10-758-902-1 (1-30) x US-10-027-632-230756 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450

RESULT 32
US-10-027-632-230757/c
; Sequence 230757, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230757
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-230757

Alignment Scores:
Pred. No.:              7.11          Length:          596
Score:                  60.50         Matches:         14
Percent Similarity:     40.9%         Conservative:    4
Best Local Similarity:  31.8%         Mismatches:      7
Query Match:            37.8%         Indels:          19
DB:                     39            Gaps:            1

US-10-758-902-1 (1-30) x US-10-027-632-230757 (1-596)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        581 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 522

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
```

```
Db        521 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 462

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        461 AGAAACTCCCTA 450
```

RESULT 33
US-10-301-480-572047/c
; Sequence 572047, Application US/10301480
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 572047
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-572047

Alignment Scores:

Pred. No.:	7.63	Length:	627
Score:	60.50	Matches:	14
Percent Similarity:	40.9%	Conservative:	4
Best Local Similarity:	31.8%	Mismatches:	7
Query Match:	37.8%	Indels:	19
DB:	44	Gaps:	1

US-10-758-902-1 (1-30) x US-10-301-480-572047 (1-627)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu------------------------------ 10
              |||:::|||||||||   |||:::
Db        531 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 472

Qy         11 ---------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        471 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 412

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        411 AGAAACTCCCTA 400
```

RESULT 34
US-10-301-480-1185456/c
; Sequence 1185456, Application US/10301480
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1185456
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1185456

Alignment Scores:

Pred. No.:	7.63	Length:	627
Score:	60.50	Matches:	14
Percent Similarity:	40.9%	Conservative:	4
Best Local Similarity:	31.8%	Mismatches:	7
Query Match:	37.8%	Indels:	19
DB:	44	Gaps:	1

US-10-758-902-1 (1-30) x US-10-301-480-1185456 (1-627)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu------------------------------ 10
              |||:::|||||||||   |||:::
Db        531 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 472

Qy         11 ---------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        471 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 412

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        411 AGAAACTCCCTA 400
```

RESULT 35
US-10-301-480A-948116/c
; Sequence 948116, Application US/10301480A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480A
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 948116
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480A-948116

Alignment Scores:

Pred. No.:	7.63	Length:	627
Score:	60.50	Matches:	14
Percent Similarity:	40.9%	Conservative:	4
Best Local Similarity:	31.8%	Mismatches:	7
Query Match:	37.8%	Indels:	19
DB:	45	Gaps:	1

US-10-758-902-1 (1-30) x US-10-301-480A-948116 (1-627)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu------------------------------ 10
              |||:::|||||||||   |||:::
Db        531 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 472

Qy         11 ---------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                         ::::::   ||||||   ||||||||||||
Db        471 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 412

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        411 AGAAACTCCCTA 400
```

RESULT 36
US-10-301-480B-948116/c
; Sequence 948116, Application US/10301480B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137

```
;  CURRENT APPLICATION NUMBER: US/10/301,480B
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 989478
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 948116
;   LENGTH: 627
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480B-948116

Alignment Scores:
Pred. No.:              7.63          Length:        627
Score:                  60.50         Matches:       14
Percent Similarity:     40.9%         Conservative:  4
Best Local Similarity:  31.8%         Mismatches:    7
Query Match:            37.8%         Indels:        19
DB:                     46            Gaps:          1

US-10-758-902-1 (1-30) x US-10-301-480B-948116 (1-627)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        531 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 472

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        471 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 412

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        411 AGAAACTCCCTA 400

RESULT 37
US-10-301-480C-948116/c
; Sequence 948116, Application US/10301480C
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827-137
;  CURRENT APPLICATION NUMBER: US/10/301,480C
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 989478
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 948116
;   LENGTH: 627
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480C-948116

Alignment Scores:
Pred. No.:              7.63          Length:        627
Score:                  60.50         Matches:       14
Percent Similarity:     40.9%         Conservative:  4
Best Local Similarity:  31.8%         Mismatches:    7
Query Match:            37.8%         Indels:        19
DB:                     47            Gaps:          1

US-10-758-902-1 (1-30) x US-10-301-480C-948116 (1-627)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGlu---------------------------- 10
              |||:::|||||||||   |||:::
Db        531 TATAGTACTGTCTCCCTAAATATTAACAACGTAAATACCAGAAATGAACATATGAAATAG 472

Qy         11 -------------------------AlaTyrGluTyrProThrPheIleGlnAspLeu 21
                                       ::::::   ||||||   ||||||||||||
Db        471 CTCCAGTCTATGACTATATAATCATTCTCTTTTCCCTATCCATTGTTTATCCAGGATTGT 412

Qy         22 ArgAsnGluLeu 25
              ||||||   |||
Db        411 AGAAACTCCCTA 400

RESULT 38
US-09-565-240-46864
; Sequence 46864, Application US/09565240
; GENERAL INFORMATION:
;  APPLICANT:       Abad, Mark S.
;  APPLICANT:  La Rosa, Thomas J.
;  TITLE OF INVENTION:       Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE:       38-21(15793)B
;  CURRENT APPLICATION NUMBER: US/09/565,240
;  CURRENT FILING DATE:  2000-05-03
;  NUMBER OF SEQ ID NOS:       54005
; SEQ ID NO 46864
;   LENGTH: 442
;   TYPE: DNA
;   ORGANISM: Glycine max
;   OTHER INFORMATION: Clone ID: LIB3139-107-P1-N1-B2
US-09-565-240-46864

Alignment Scores:
Pred. No.:              8.98          Length:        442
Score:                  59.00         Matches:       17
Percent Similarity:     48.7%         Conservative:  2
Best Local Similarity:  43.6%         Mismatches:    8
Query Match:            36.9%         Indels:        12
DB:                     26            Gaps:          2

US-10-758-902-1 (1-30) x US-09-565-240-46864 (1-442)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        311 ACTGTCAACTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 367

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||   ||||||||     |||
Db        368 CAGGCAGAACATGCAGCAGCTTGAGTGGCTCTTAACACTCTTGCAAAAAGAGGTCCC 424

RESULT 39
US-11-239-610A-46864
; Sequence 46864, Application US/11239610A
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  APPLICANT:  La Rosa, Thomas J.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 16517.341 - 38-21(15793)C/US
;  CURRENT APPLICATION NUMBER: US/11/239,610A
;  CURRENT FILING DATE:  2005-09-30
;  PRIOR APPLICATION NUMBER: US 09/565,240
;  PRIOR FILING DATE: 2000-05-08
;  NUMBER OF SEQ ID NOS: 54005
; SEQ ID NO 46864
;   LENGTH: 442
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3139-107-P1-N1-B2
US-11-239-610A-46864

Alignment Scores:
Pred. No.:              8.98          Length:        442
Score:                  59.00         Matches:       17
Percent Similarity:     48.7%         Conservative:  2
Best Local Similarity:  43.6%         Mismatches:    8
Query Match:            36.9%         Indels:        12
DB:                     71            Gaps:          2
```

US-10-758-902-1 (1-30) x US-11-239-610A-46864 (1-442)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        311 ACTGTCAACTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 367

Qy         23 ------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                            |||   |||||||||      |||
Db        368 CAGGCAGAACATGCAGCAGCTTGAGTGGCTCTTAACACTCTTGCAAAAAGAGGTCCC 424
```

RESULT 40
US-10-424-599-70917
; Sequence 70917, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 70917
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3504C.1
US-10-424-599-70917

Alignment Scores:

Pred. No.:	11.4	Length:	526
Score:	59.00	Matches:	17
Percent Similarity:	48.7%	Conservative:	2
Best Local Similarity:	43.6%	Mismatches:	8
Query Match:	36.9%	Indels:	12
DB:	50	Gaps:	2

US-10-758-902-1 (1-30) x US-10-424-599-70917 (1-526)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        311 ACTGTCAACTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 367

Qy         23 ------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                            |||   |||||||||      |||
Db        368 CAGGCAGAACATGCAGCAGCTGGAGTGGCTCTTAACACTCTTGCAAAAAGAGGTCCC 424
```

RESULT 41
US-09-654-617-12060
; Sequence 12060, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 12060
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Glycine max
US-09-654-617-12060

Alignment Scores:

Pred. No.:	11.6	Length:	532
Score:	59.00	Matches:	17
Percent Similarity:	48.7%	Conservative:	2
Best Local Similarity:	43.6%	Mismatches:	8
Query Match:	36.9%	Indels:	12
DB:	28	Gaps:	2

US-10-758-902-1 (1-30) x US-09-654-617-12060 (1-532)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        317 ACTGTCAACTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 373

Qy         23 ------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                            |||   |||||||||      |||
Db        374 CAGGCAGAACATGCAGCAGCTGGAGTGGCTCTTAACACTCTTGCAAAAAGAGGTCCC 430
```

RESULT 42
US-09-684-016-12060
; Sequence 12060, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 12060
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Glycine max
US-09-684-016-12060

Alignment Scores:

Pred. No.:	11.6	Length:	532
Score:	59.00	Matches:	17
Percent Similarity:	48.7%	Conservative:	2
Best Local Similarity:	43.6%	Mismatches:	8
Query Match:	36.9%	Indels:	12
DB:	28	Gaps:	2

US-10-758-902-1 (1-30) x US-09-684-016-12060 (1-532)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        317 ACTGTCAACTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 373

Qy         23 ------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                            |||   |||||||||      |||
Db        374 CAGGCAGAACATGCAGCAGCTGGAGTGGCTCTTAACACTCTTGCAAAAAGAGGTCCC 430
```

RESULT 43
US-09-865-439A-77772
; Sequence 77772, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 77772
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(561)
; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: LIB3606-018-Q1-N6-H4
US-09-865-439A-77772

Alignment Scores:

Pred. No.:	12.5	Length:	561
Score:	59.00	Matches:	12
Percent Similarity:	68.4%	Conservative:	1
Best Local Similarity:	63.2%	Mismatches:	6
Query Match:	36.9%	Indels:	0
DB:	33	Gaps:	0

US-10-758-902-1 (1-30) x US-09-865-439A-77772 (1-561)

```
Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::|||||||||||||   ||||||         |||||||||   |||
Db        230 GAGCAGTACCAATACCCAACATTTTGACAGGACTTCAGTTTTGAATTGGCTGCTGGG 286
```

RESULT 44
US-60-207-458-121914
; Sequence 121914, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 121914
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3606-018-Q1-N6-H4
US-60-207-458-121914

Alignment Scores:

Pred. No.:	12.5	Length:	561
Score:	59.00	Matches:	12
Percent Similarity:	68.4%	Conservative:	1
Best Local Similarity:	63.2%	Mismatches:	6
Query Match:	36.9%	Indels:	0
DB:	79	Gaps:	0

US-10-758-902-1 (1-30) x US-60-207-458-121914 (1-561)

```
Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||   |||:::|||||||||||||   ||||||         |||||||||   |||
Db        230 GAGCAGTACCAATACCCAACATTTTGACAGGACTTCAGTTTTGAATTGGCTGCTGGG 286
```

RESULT 45
US-09-474-435A-65250
; Sequence 65250, Application US/09474435A
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ARABIDOPSIS THALIANA GENOME SEQUENCE AND USES THEREOF
; FILE REFERENCE: 38-21(15473)B
; CURRENT APPLICATION NUMBER: US/09/474,435A
; CURRENT FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/089,524
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,516
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,808
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,812
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,807
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,806
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,811
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,813
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 09/333,534
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 60/111,990
; PRIOR FILING DATE: 1998-12-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 195836
; SEQ ID NO 65250
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana landsberg
US-09-474-435A-65250

Alignment Scores:

Pred. No.:	16.9	Length:	699
Score:	59.00	Matches:	13
Percent Similarity:	62.5%	Conservative:	2
Best Local Similarity:	54.2%	Mismatches:	9
Query Match:	36.9%	Indels:	0
DB:	23	Gaps:	0

US-10-758-902-1 (1-30) x US-09-474-435A-65250 (1-699)

```
Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              |||   ||||||:::|||||||||           |||:::        |||   |||
Db        243 TTCCTCCTAGGTCAAGCATATGAAAAGGCAGTTATCATCAAACCACCGGAGAATTCCTTA 302

Qy         26 AlaLysGlyThr 29
              ||||||||||
Db        303 GCGAAAGGTACA 314
```

RESULT 46
US-09-803-736-1196
; Sequence 1196, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 1196
; LENGTH: 20509
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-1196

Alignment Scores:

Pred. No.:	1.79e+03	Length:	20509
Score:	59.00	Matches:	13
Percent Similarity:	62.5%	Conservative:	2
Best Local Similarity:	54.2%	Mismatches:	9
Query Match:	36.9%	Indels:	0

```
DB:                    32          Gaps:          0

US-10-758-902-1 (1-30) x US-09-803-736-1196 (1-20509)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu 25
              |||   ||||||:::|||||||||          |||:::       |||   |||
Db       4517 TTCCTCCTAGGTCAAGCATATGAAAAGGCAGTTATCATCAAACCACCGGAGAATTCCTTA 4576

Qy         26 AlaLysGlyThr 29
              ||||||||||||
Db       4577 GCGAAAGGTACA 4588

RESULT 47
US-09-565-306-10375/c
; Sequence 10375, Application US/09565306
; GENERAL INFORMATION:
;  APPLICANT:       Andersen, Scott E.
;  APPLICANT:  Conner, Timothy W.
;  APPLICANT:  Lalgudi, Raghunath V.
;  TITLE OF INVENTION:       Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE:       38-21(15459)C
;  CURRENT APPLICATION NUMBER: US/09/565,306
;  CURRENT FILING DATE:  2000-05-04
;  NUMBER OF SEQ ID NOS:       83523
; SEQ ID NO 10375
;   LENGTH: 251
;   TYPE: DNA
;   ORGANISM: Zea mays
;   OTHER INFORMATION: Clone ID: LIB148-008-Q1-E1-F4
US-09-565-306-10375

Alignment Scores:
Pred. No.:              6.33          Length:        251
Score:                  58.00         Matches:       11
Percent Similarity:     76.5%         Conservative:  2
Best Local Similarity:  64.7%         Mismatches:    4
Query Match:            36.2%         Indels:        0
DB:                     26            Gaps:          0

US-10-758-902-1 (1-30) x US-09-565-306-10375 (1-251)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||   |||:::|||||||||||||   ||||||      :::|||||||||
Db       119 GAGCAGTACCAATACCCAACATTTTGACAGGACTTCAGTTCTGAATTGGCT 69

RESULT 48
US-11-353-150-10375/c
; Sequence 10375, Application US/11353150
; GENERAL INFORMATION:
;  APPLICANT: Andersen, Scott E.
;  APPLICANT:  Conner, Timothy W.
;  APPLICANT:  Lalgudi, Raghunath V.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 16517.365 - 38-21(15459)D/US
;  CURRENT APPLICATION NUMBER: US/11/353,150
;  CURRENT FILING DATE:  2006-02-14
;  PRIOR APPLICATION NUMBER: 09/565,386
;  PRIOR FILING DATE: 2000-05-04
;  PRIOR APPLICATION NUMBER: 60/132,860
;  PRIOR FILING DATE: 1999-05-07
;  NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 10375
;   LENGTH: 251
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB148-008-Q1-E1-F4
US-11-353-150-10375

Alignment Scores:
Pred. No.:              6.33          Length:        251
Score:                  58.00         Matches:       11
Percent Similarity:     76.5%         Conservative:  2
Best Local Similarity:  64.7%         Mismatches:    4
Query Match:            36.2%         Indels:        0
DB:                     74            Gaps:          0

US-10-758-902-1 (1-30) x US-11-353-150-10375 (1-251)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||   |||:::|||||||||||||   ||||||      :::|||||||||
Db       119 GAGCAGTACCAATACCCAACATTTTGACAGGACTTCAGTTCTGAATTGGCT 69

RESULT 49
US-09-394-745-4271/c
; Sequence 4271, Application US/09394745
; GENERAL INFORMATION:
;  APPLICANT:       Fisher, Dane K.
;  APPLICANT:  Lalgudi, Raghunath V.
;  TITLE OF INVENTION:       NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
;  TITLE OF INVENTION:  PLANTS
;  FILE REFERENCE:       38-21(15454)B
;  CURRENT APPLICATION NUMBER: US/09/394,745
;  CURRENT FILING DATE:  1999-09-15
;  NUMBER OF SEQ ID NOS:       57264
; SEQ ID NO 4271
;   LENGTH: 286
;   TYPE: DNA
;   ORGANISM: Zea mays
;   OTHER INFORMATION: Clone ID: LIB148-008-Q1-E1-F4
US-09-394-745-4271

Alignment Scores:
Pred. No.:              7.58          Length:        286
Score:                  58.00         Matches:       11
Percent Similarity:     76.5%         Conservative:  2
Best Local Similarity:  64.7%         Mismatches:    4
Query Match:            36.2%         Indels:        0
DB:                     22            Gaps:          0

US-10-758-902-1 (1-30) x US-09-394-745-4271 (1-286)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||   |||:::|||||||||||||   ||||||      :::|||||||||
Db       119 GAGCAGTACCAATACCCAACATTTTGACAGGACTTCAGTTCTGAATTGGCT 69

RESULT 50
US-60-207-458-24805
; Sequence 24805, Application US/60207458
; GENERAL INFORMATION:
;  APPLICANT:       Abad, Mark S.
;  APPLICANT:  Conner, Timothy W.
;  APPLICANT:  Deikman, Jill
;  APPLICANT:  Hardeman, Kristine J.
;  APPLICANT:  La Rosa, Thomas J.
;  APPLICANT:  Lalgudi, Raghunath V.
;  APPLICANT:  Ruan, Yijun G.
;  APPLICANT:  Ruff, Thomas G.
;  APPLICANT:  Sammons, R. Douglas
;  APPLICANT:  Shukla, Hridayabhiranjan
;  APPLICANT:  Wu, Kunsheng
;  APPLICANT:  Xu, Nanfei
;  TITLE OF INVENTION:       NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
;  TITLE OF INVENTION:  PLANTS
;  FILE REFERENCE:       38-21(51936)A
;  CURRENT APPLICATION NUMBER: US/60/207,458
;  CURRENT FILING DATE:  2000-05-30
;  NUMBER OF SEQ ID NOS:       152403
; SEQ ID NO 24805
;   LENGTH: 496
;   TYPE: DNA
;   ORGANISM: Zea mays
;   OTHER INFORMATION: Clone ID: uC-zmflLIB3205449e01a1
US-60-207-458-24805
```

```
Alignment Scores:
Pred. No.:                16.2          Length:          496
Score:                    58.00         Matches:         11
Percent Similarity:       76.5%         Conservative:    2
Best Local Similarity:    64.7%         Mismatches:      4
Query Match:              36.2%         Indels:          0
DB:                       79            Gaps:            0

US-10-758-902-1 (1-30) x US-60-207-458-24805 (1-496)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||   |||:::|||||||||||||   ||||||      :::|||||||||
Db        158 GAGCAGTACCAATACCCAACATTTTGACAGGACTTCAGTTCTGAATTGGCT 208

RESULT 51
US-08-049-075-1
; Sequence 1, Application US/08049075
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Man-Keun
;    APPLICANT:  Lee, Kwan-Ho
;    APPLICANT:  Na, Byeong-Kook
;    APPLICANT:  Jeong, Han-Seung
;    APPLICANT:  Choi, Kyu-Whan
;    APPLICANT:  Moon, Young-Ho
;    APPLICANT:  Jeon, Hong-Seob
;    TITLE OF INVENTION:  Expression Vector for Phytolacca
;    TITLE OF INVENTION:  Antiviral Protein and Process for Preparing Transgenic
;    TITLE OF INVENTION:  Plant Transformed Thereof
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby
;      STREET:  805 Third Ave.
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/049,075
;      FILING DATE:  20-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, S. Peter
;      REGISTRATION NUMBER:  25,351
;      REFERENCE/DOCKET NUMBER:  0136/07986
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)527-7700
;      TELEFAX:  (212)753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Phytolacca americana
;      TISSUE TYPE:  leaf
US-08-049-075-1

Alignment Scores:
Pred. No.:                54.5          Length:          1195
Score:                    58.00         Matches:         11
Percent Similarity:       68.0%         Conservative:    6
Best Local Similarity:    44.0%         Mismatches:      6
Query Match:              36.2%         Indels:          2
DB:                       9             Gaps:            1

US-10-758-902-1 (1-30) x US-08-049-075-1 (1-1195)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||:::
Db        102 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGAAT 161

Qy         20 AspLeuArgAsnGlu 24
              |||||||||||:::
Db        162 GATCTTCGTAATCAA 176

RESULT 52
US-10-417-884-3648
; Sequence 3648, Application US/10417884
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/417,884
;             FILING DATE: 17-Apr-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3648:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 678 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...678
;         SEQUENCE DESCRIPTION: SEQ ID NO: 3648:
US-10-417-884-3648

Alignment Scores:
Pred. No.:                30.9          Length:          678
Score:                    57.50         Matches:         11
Percent Similarity:       62.9%         Conservative:    11
Best Local Similarity:    31.4%         Mismatches:      8
Query Match:              35.9%         Indels:          5
```

```
DB:                    50            Gaps:          1

US-10-758-902-1 (1-30) x US-10-417-884-3648 (1-678)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::      |||   :::|||||||||   |||::::::      |||::::::|||
Db        112 TTCTCAAAAACTTCTATGGATTTGGGAGAAAGATATGATTTTAAGGGGTTTATGGAAGAT 171

Qy         21 LeuArgAsnGluLeuAla--------------LysGlyThrPro 30
                  :::|||::::::                :::|||||||||
Db        172 AAAATGGACGAGGTATCAAGTAGGGAAATTCCAGAAGGCACACCT 216

RESULT 53
US-10-417-884A-3648
; Sequence 3648, Application US/10417884A
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/417,884A
;             FILING DATE: 17-Apr-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532
;             FILING DATE: 30-Jun-1998
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3648:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 678 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...678
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3648:
US-10-417-884A-3648

Alignment Scores:
Pred. No.:              30.9          Length:        678
Score:                  57.50         Matches:       11
Percent Similarity:     62.9%         Conservative:  11
Best Local Similarity:  31.4%         Mismatches:    8
Query Match:            35.9%         Indels:        5
DB:                     50            Gaps:          1

US-10-758-902-1 (1-30) x US-10-417-884A-3648 (1-678)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::      |||   :::|||||||||   |||::::::      |||::::::|||
Db        112 TTCTCAAAAACTTCTATGGATTTGGGAGAAAGATATGATTTTAAGGGGTTTATGGAAGAT 171

Qy         21 LeuArgAsnGluLeuAla--------------LysGlyThrPro 30
                  :::|||::::::                :::|||||||||
Db        172 AAAATGGACGAGGTATCAAGTAGGGAAATTCCAGAAGGCACACCT 216

RESULT 54
US-60-068-217-948
; Sequence 948, Application US/60068217
;  GENERAL INFORMATION:
;    APPLICANT:  Lagace, Robert E.
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Russo, Frank D.
;    APPLICANT:  Hann, Amy L.
;    APPLICANT:  Heath, Joe D.
;    APPLICANT:  Finney, Greogry L.
;    TITLE OF INVENTION:  NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
;    TITLE OF INVENTION:  GENOME, FRAGMENTS THEREOF, AND USES THEREOF
;    NUMBER OF SEQUENCES:  1239
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/068,217
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CERRONE, MICHAEL C.
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PM-0003-5 P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  948:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14560 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  genomic DNA
;    IMMEDIATE SOURCE:
;      CLONE:  EFA1c948
US-60-068-217-948

Alignment Scores:
Pred. No.:              2.13e+03      Length:        14560
Score:                  57.50         Matches:       11
Percent Similarity:     62.9%         Conservative:  11
Best Local Similarity:  31.4%         Mismatches:    8
Query Match:            35.9%         Indels:        5
DB:                     77            Gaps:          1

US-10-758-902-1 (1-30) x US-60-068-217-948 (1-14560)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::      |||   :::|||||||||   |||::::::      |||::::::|||
Db       1270 TTCTCAAAAACTTCTATGGATTTGGGAGAAAGATATGATTTTAAGGGGTTTATGGAAGAT 1329

Qy         21 LeuArgAsnGluLeuAla--------------LysGlyThrPro 30
```

```
                    :::|||::::::              :::|||||||||
Db       1330 AAAATGGACGAGGTATCAAGTAGGGAAATTCCAGAAGGCACACCT 1374
```

RESULT 55
US-09-304-517A-250010
; Sequence 250010, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 250010
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-250010

Alignment Scores:

Pred. No.:	20.5	Length:	431
Score:	57.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.6%	Indels:	12
DB:	22	Gaps:	2

US-10-758-902-1 (1-30) x US-09-304-517A-250010 (1-431)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        216 ACTGTCAATTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 272

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||   :::||||||      |||
Db        273 CAGGCAGAACATGCAGCAACTGAAGTGGCTCTTAACACTATTGCAAAAAGAGGTCCC 329
```

RESULT 56
US-09-440-687-9039
; Sequence 9039, Application US/09440687
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15668)B
; CURRENT APPLICATION NUMBER: US/09/440,687
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 31015
; SEQ ID NO 9039
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3051-112-Q1-K1-D7
US-09-440-687-9039

Alignment Scores:

Pred. No.:	20.5	Length:	431
Score:	57.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.6%	Indels:	12
DB:	23	Gaps:	2

US-10-758-902-1 (1-30) x US-09-440-687-9039 (1-431)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        216 ACTGTCAATTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 272

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
```

```
                                                 |||   :::||||||      |||
Db        273 CAGGCAGAACATGCAGCAACTGAAGTGGCTCTTAACACTATTGCAAAAAGAGGTCCC 329
```

RESULT 57
US-09-615-606A-28851
; Sequence 28851, Application US/09615606A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Buehler, Robert E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Coombs, Brian E.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Nelson, Donald E.
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15444)C
; CURRENT APPLICATION NUMBER: US/09/615,606A
; CURRENT FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 91663
; SEQ ID NO 28851
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3051-112-Q1-K1-D7
US-09-615-606A-28851

Alignment Scores:

Pred. No.:	20.5	Length:	431
Score:	57.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.6%	Indels:	12
DB:	27	Gaps:	2

US-10-758-902-1 (1-30) x US-09-615-606A-28851 (1-431)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        216 ACTGTCAATTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 272

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                                 |||   :::||||||      |||
Db        273 CAGGCAGAACATGCAGCAACTGAAGTGGCTCTTAACACTATTGCAAAAAGAGGTCCC 329
```

RESULT 58
US-09-985-678-250010
; Sequence 250010, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 250010
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-250010

Alignment Scores:

Pred. No.:	20.5	Length:	431
Score:	57.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.6%	Indels:	12

```
DB:                    38            Gaps:          2

US-10-758-902-1 (1-30) x US-09-985-678-250010 (1-431)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||         ||||||
Db        216 ACTGTCAATTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 272

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||   :::||||||      |||
Db        273 CAGGCAGAACATGCAGCAACTGAAGTGGCTCTTAACACTATTGCAAAAAGAGGTCCC 329

RESULT 59
US-11-239-591A-9039
; Sequence 9039, Application US/11239591A
; GENERAL INFORMATION:
;  APPLICANT: BYRUM, JOSEPH R.
;  APPLICANT:  HECK, GREGORY R.
;  APPLICANT:  LA ROSA, THOMAS J.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
;  TITLE OF INVENTION:  WITH PLANTS
;  FILE REFERENCE: 16517.338
;  CURRENT APPLICATION NUMBER: US/11/239,591A
;  CURRENT FILING DATE:  2005-09-30
;  PRIOR APPLICATION NUMBER: 09/440,687
;  PRIOR FILING DATE: 1999-11-16
;  NUMBER OF SEQ ID NOS: 31015
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9039
;   LENGTH: 431
;   TYPE: DNA
;   ORGANISM: Glycine max
US-11-239-591A-9039

Alignment Scores:
Pred. No.:              20.5          Length:        431
Score:                  57.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.6%         Indels:        12
DB:                     71            Gaps:          2

US-10-758-902-1 (1-30) x US-11-239-591A-9039 (1-431)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||         ||||||
Db        216 ACTGTCAATTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 272

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||   :::||||||      |||
Db        273 CAGGCAGAACATGCAGCAACTGAAGTGGCTCTTAACACTATTGCAAAAAGAGGTCCC 329

RESULT 60
US-60-144-084-39395
; Sequence 39395, Application US/60144084
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  APPLICANT: Buehler, Robert E.
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT: Coombs, Brian E.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT: Nelson, Donald E.
;  APPLICANT: Shukla, Hridayabhiramjam
;  APPLICANT: Thompson, Michael D.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
;  TITLE OF INVENTION: PLANTS
;  FILE REFERENCE: 38-21(15444)B
;  CURRENT APPLICATION NUMBER: US/60/144,084
;  CURRENT FILING DATE: 1999-07-16
;  NUMBER OF SEQ ID NOS: 47776
; SEQ ID NO 39395
;   LENGTH: 431
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3051-112-Q1-K1-D7
US-60-144-084-39395

Alignment Scores:
Pred. No.:              20.5          Length:        431
Score:                  57.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.6%         Indels:        12
DB:                     78            Gaps:          2

US-10-758-902-1 (1-30) x US-60-144-084-39395 (1-431)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||         ||||||
Db        216 ACTGTCAATTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 272

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||   :::||||||      |||
Db        273 CAGGCAGAACATGCAGCAACTGAAGTGGCTCTTAACACTATTGCAAAAAGAGGTCCC 329

RESULT 61
US-09-654-617-415334
; Sequence 415334, Application US/09654617
; GENERAL INFORMATION:
;  APPLICANT:       Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION:       Annotated Plant Genes
;  FILE REFERENCE:       38-21(15097)D
;  CURRENT APPLICATION NUMBER: US/09/654,617
;  CURRENT FILING DATE:  2000-09-05
;  NUMBER OF SEQ ID NOS:       463173
; SEQ ID NO 415334
;   LENGTH: 526
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-09-654-617-415334

Alignment Scores:
Pred. No.:              27            Length:        526
Score:                  57.00         Matches:       16
Percent Similarity:     48.7%         Conservative:  3
Best Local Similarity:  41.0%         Mismatches:    8
Query Match:            35.6%         Indels:        12
DB:                     28            Gaps:          2

US-10-758-902-1 (1-30) x US-09-654-617-415334 (1-526)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db        396 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 452

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        453 CTGGCAAAACAAGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAAAGAGGGCCA 509

RESULT 62
US-09-669-817A-6666
; Sequence 6666, Application US/09669817A
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT:  Ruan, Yijun G.
;  APPLICANT:  Wallick, C. Kevin
;  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(51469)B
;  CURRENT APPLICATION NUMBER: US/09/669,817A
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: US 60/156,951
;  PRIOR FILING DATE: 1999-09-30
```

```
;  NUMBER OF SEQ ID NOS: 43701
; SEQ ID NO 6666
;   LENGTH: 526
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: uC-osflcyp173f11b1
US-09-669-817A-6666

Alignment Scores:
Pred. No.:              27          Length:         526
Score:                  57.00       Matches:        16
Percent Similarity:     48.7%       Conservative:   3
Best Local Similarity:  41.0%       Mismatches:     8
Query Match:            35.6%       Indels:         12
DB:                     28          Gaps:           2

US-10-758-902-1 (1-30) x US-09-669-817A-6666 (1-526)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        396 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 452

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        453 CTGGCAAAACAAGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAAAGAGGGCCA 509

RESULT 63
US-09-684-016-415334
; Sequence 415334, Application US/09684016
; GENERAL INFORMATION:
;  APPLICANT:       Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION:       Annotated Plant Genes
;  FILE REFERENCE:       38-21(15097)D
;  CURRENT APPLICATION NUMBER: US/09/684,016
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER:       US 09/654,617
;  PRIOR FILING DATE:       2000-09-05
;  NUMBER OF SEQ ID NOS:       463173
; SEQ ID NO 415334
;   LENGTH: 526
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-09-684-016-415334

Alignment Scores:
Pred. No.:              27          Length:         526
Score:                  57.00       Matches:        16
Percent Similarity:     48.7%       Conservative:   3
Best Local Similarity:  41.0%       Mismatches:     8
Query Match:            35.6%       Indels:         12
DB:                     28          Gaps:           2

US-10-758-902-1 (1-30) x US-09-684-016-415334 (1-526)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        396 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 452

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        453 CTGGCAAAACAAGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAAAGAGGGCCA 509

RESULT 64
US-09-371-146A-250010
; Sequence 250010, Application US/09371146A
; GENERAL INFORMATION:
;  APPLICANT: Cheikh, Nordine
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION: ANNOTATED PLANT GENES
;  FILE REFERENCE: 38-21(15097)C
;  CURRENT APPLICATION NUMBER: US/09/371,146A
;  CURRENT FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER: US 09/304,517
;  PRIOR FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 250010
;   LENGTH: 549
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(549)
;   OTHER INFORMATION: unsure at all n locations
US-09-371-146A-250010

Alignment Scores:
Pred. No.:              28.7        Length:         549
Score:                  57.00       Matches:        16
Percent Similarity:     48.7%       Conservative:   3
Best Local Similarity:  41.0%       Mismatches:     8
Query Match:            35.6%       Indels:         12
DB:                     22          Gaps:           2

US-10-758-902-1 (1-30) x US-09-371-146A-250010 (1-549)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||||||||          ||||||
Db        302 ACTGTCAATTTTAAT---GGAGAGACCTTTGAAAGCCCTACATTCTGCTCTACTCTTAGA 358

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                                 |||   :::||||||      |||
Db        359 CAGGCAGAACATGCAGCAACTGAAGTGGCTCTTAACACTATTGCAAAAAGAGGTCCC 415

RESULT 65
US-10-437-963-43964
; Sequence 43964, Application US/10437963
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 43964
;   LENGTH: 1452
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_47070C.1
US-10-437-963-43964

Alignment Scores:
Pred. No.:              110         Length:         1452
Score:                  57.00       Matches:        16
Percent Similarity:     48.7%       Conservative:   3
Best Local Similarity:  41.0%       Mismatches:     8
Query Match:            35.6%       Indels:         12
DB:                     50          Gaps:           2

US-10-758-902-1 (1-30) x US-10-437-963-43964 (1-1452)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        396 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 452

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
```

```
                                                     |||||||||:::|||      |||
Db        453 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 509
```

RESULT 66
US-09-815-264-3642/c
; Sequence 3642, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 3642
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-3642

Alignment Scores:

Pred. No.:	115	Length:	1501
Score:	57.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.6%	Indels:	12
DB:	32	Gaps:	2

US-10-758-902-1 (1-30) x US-09-815-264-3642 (1-1501)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db       1081 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 1025

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db       1024 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 968
```

RESULT 67
US-10-449-902-13635
; Sequence 13635, Application US/10449902
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13635
; LENGTH: 2392
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK110983
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-13635

Alignment Scores:

Pred. No.:	219	Length:	2392
Score:	57.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.6%	Indels:	12
DB:	50	Gaps:	2

US-10-758-902-1 (1-30) x US-10-449-902-13635 (1-2392)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        471 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 527

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        528 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 584
```

RESULT 68
US-09-620-392-68993/c
; Sequence 68993, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 68993
; LENGTH: 5443
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-68993

Alignment Scores:

Pred. No.:	680	Length:	5443
Score:	57.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.6%	Indels:	12
DB:	27	Gaps:	2

US-10-758-902-1 (1-30) x US-09-620-392-68993 (1-5443)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db       5326 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 5270

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db       5269 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 5213
```

RESULT 69
US-09-620-392-44492
; Sequence 44492, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 44492
; LENGTH: 15153
; TYPE: DNA

```
;   ORGANISM:. Oryza sativa
;   OTHER INFORMATION: unsure at all n locations
US-09-620-392-44492

Alignment Scores:
Pred. No.:              2.79e+03        Length:         15153
Score:                  57.00           Matches:        16
Percent Similarity:     48.7%           Conservative:   3
Best Local Similarity:  41.0%           Mismatches:     8
Query Match:            35.6%           Indels:         12
DB:                     27              Gaps:           2

US-10-758-902-1 (1-30) x US-09-620-392-44492 (1-15153)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db       5708 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 5764

Qy         23 ------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                            |||||||||:::|||      |||
Db       5765 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 5821

RESULT 70
US-09-702-134-8583
; Sequence 8583, Application US/09702134
; GENERAL INFORMATION:
;  APPLICANT:       Boukharov, Andrey A.
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  McIninch, James
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION:       Plant Genome Sequence and Uses Thereof
;  FILE REFERENCE:       38-21(51237)F
;  CURRENT APPLICATION NUMBER: US/09/702,134
;  CURRENT FILING DATE:  2000-10-31
;  NUMBER OF SEQ ID NOS:       52202
; SEQ ID NO 8583
;   LENGTH: 57600
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(57600)
;   OTHER INFORMATION: unsure at all n locations
US-09-702-134-8583

Alignment Scores:
Pred. No.:              1.76e+04        Length:         57600
Score:                  57.00           Matches:        16
Percent Similarity:     48.7%           Conservative:   3
Best Local Similarity:  41.0%           Mismatches:     8
Query Match:            35.6%           Indels:         12
DB:                     30              Gaps:           2

US-10-758-902-1 (1-30) x US-09-702-134-8583 (1-57600)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db      42540 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 42596

Qy         23 ------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                            |||||||||:::|||      |||
Db      42597 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 42653

RESULT 71
US-09-815-264-68788
; Sequence 68788, Application US/09815264
; GENERAL INFORMATION:
;  APPLICANT: Boukharov, Andrey A.
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Dotson, Stanton B.
;  APPLICANT:  Koshi, Jeffrey M.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  McIninch, James
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
;  FILE REFERENCE: 38-21(51237)G
;  CURRENT APPLICATION NUMBER: US/09/815,264
;  CURRENT FILING DATE:  2001-03-23
;  PRIOR APPLICATION NUMBER: US 09/620,392
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: US 09/702,134
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 68788
;   LENGTH: 57600
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(57600)
;   OTHER INFORMATION: unsure at all n locations
US-09-815-264-68788

Alignment Scores:
Pred. No.:              1.76e+04        Length:         57600
Score:                  57.00           Matches:        16
Percent Similarity:     48.7%           Conservative:   3
Best Local Similarity:  41.0%           Mismatches:     8
Query Match:            35.6%           Indels:         12
DB:                     32              Gaps:           2

US-10-758-902-1 (1-30) x US-09-815-264-68788 (1-57600)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db      42540 ACGGTTAATTTCAAT---GGAGAAACGTTCGAAAGCCCCGCCTTCTGTTCTACTCTGCGG 42596

Qy         23 ------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                            |||||||||:::|||      |||
Db      42597 CTGGCAGAGCATGCGGCGGCAGAGGTTGCGCTCAATGAGCTGTCGAAGAGAGGGCCA 42653

RESULT 72
PCT-US06-06593-19
; Sequence 19, Application PC/TUS0606593
; GENERAL INFORMATION:
;  APPLICANT: Mushegian, Arcady
;  APPLICANT:  Liu, Jing
;  TITLE OF INVENTION: NOVEL THERMOPHILIC PROTEINS AND THE NUCLEIC ACIDS ENCODING THEM
;  FILE REFERENCE: 047755-098512
;  CURRENT APPLICATION NUMBER: PCT/US06/06593
;  CURRENT FILING DATE:  2006-03-01
;  NUMBER OF SEQ ID NOS: 174
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 1236
;   TYPE: DNA
;   ORGANISM: YS40 BACTERIOPHAGE
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: YS40 ORF19
PCT-US06-06593-19

Alignment Scores:
Pred. No.:              109             Length:         1236
Score:                  56.50           Matches:        14
Percent Similarity:     56.7%           Conservative:   3
Best Local Similarity:  46.7%           Mismatches:     12
Query Match:            35.3%           Indels:         1
DB:                     3               Gaps:           1

US-10-758-902-1 (1-30) x PCT-US06-06593-19 (1-1236)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
```

```
Db        373 TATAGGTTAGCTTCTTTTAATACT---TTTGCCGTACCTTACGAAACCTTCTTTGAGGAT 429

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
Db        430 TTGGCTAGTGAAATAGCAGGAATGACTCCT 459
```

RESULT 73
US-11-361-092-19
; Sequence 19, Application US/11361092
; GENERAL INFORMATION:
; APPLICANT: Mushegian, Arcady
; APPLICANT: Liu, Jing
; TITLE OF INVENTION: NOVEL THERMOPHILIC PROTEINS AND THE NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 047755-098512
; CURRENT APPLICATION NUMBER: US/11/361,092
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: YS40 BACTERIOPHAGE
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: YS40 ORF19
US-11-361-092-19

Alignment Scores:

Pred. No.:	109	Length:	1236
Score:	56.50	Matches:	14
Percent Similarity:	56.7%	Conservative:	3
Best Local Similarity:	46.7%	Mismatches:	12
Query Match:	35.3%	Indels:	1
DB:	74	Gaps:	1

US-10-758-902-1 (1-30) x US-11-361-092-19 (1-1236)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
Db        373 TATAGGTTAGCTTCTTTTAATACT---TTTGCCGTACCTTACGAAACCTTCTTTGAGGAT 429

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
Db        430 TTGGCTAGTGAAATAGCAGGAATGACTCCT 459
```

RESULT 74
PCT-US06-06593-171/c
; Sequence 171, Application PC/TUS0606593
; GENERAL INFORMATION:
; APPLICANT: Mushegian, Arcady
; APPLICANT: Liu, Jing
; TITLE OF INVENTION: NOVEL THERMOPHILIC PROTEINS AND THE NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 047755-098512
; CURRENT APPLICATION NUMBER: PCT/US06/06593
; CURRENT FILING DATE: 2006-03-01
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 171
; LENGTH: 152372
; TYPE: DNA
; ORGANISM: YS40 BACTERIOPHAGE
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: The Entire YS40 Genome
PCT-US06-06593-171

Alignment Scores:

Pred. No.:	8.38e+04	Length:	152372
Score:	56.50	Matches:	14
Percent Similarity:	56.7%	Conservative:	3
Best Local Similarity:	46.7%	Mismatches:	12
Query Match:	35.3%	Indels:	1
DB:	3	Gaps:	1

US-10-758-902-1 (1-30) x PCT-US06-06593-171 (1-152372)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
Db      17971 TATAGGTTAGCTTCTTTTAATACT---TTTGCCGTACCTTACGAAACCTTCTTTGAGGAT 17915

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
Db      17914 TTGGCTAGTGAAATAGCAGGAATGACTCCT 17885
```

RESULT 75
US-11-361-092-171/c
; Sequence 171, Application US/11361092
; GENERAL INFORMATION:
; APPLICANT: Mushegian, Arcady
; APPLICANT: Liu, Jing
; TITLE OF INVENTION: NOVEL THERMOPHILIC PROTEINS AND THE NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 047755-098512
; CURRENT APPLICATION NUMBER: US/11/361,092
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 171
; LENGTH: 152372
; TYPE: DNA
; ORGANISM: YS40 BACTERIOPHAGE
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: The Entire YS40 Genome
US-11-361-092-171

Alignment Scores:

Pred. No.:	8.38e+04	Length:	152372
Score:	56.50	Matches:	14
Percent Similarity:	56.7%	Conservative:	3
Best Local Similarity:	46.7%	Mismatches:	12
Query Match:	35.3%	Indels:	1
DB:	74	Gaps:	1

US-10-758-902-1 (1-30) x US-11-361-092-171 (1-152372)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
Db      17971 TATAGGTTAGCTTCTTTTAATACT---TTTGCCGTACCTTACGAAACCTTCTTTGAGGAT 17915

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
Db      17914 TTGGCTAGTGAAATAGCAGGAATGACTCCT 17885
```

RESULT 76
US-09-304-517A-12197
; Sequence 12197, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 12197
; LENGTH: 295
; TYPE: DNA
; ORGANISM: Zea mays
US-09-304-517A-12197

Alignment Scores:

Pred. No.:	18.7	Length:	295
Score:	56.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8

```
Query Match:            35.0%       Indels:        12
DB:                     22          Gaps:          2

US-10-758-902-1 (1-30) x US-09-304-517A-12197 (1-295)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGACGGGGCCT 125

RESULT 77
US-09-371-146A-12197
; Sequence 12197, Application US/09371146A
; GENERAL INFORMATION:
;  APPLICANT: Cheikh, Nordine
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION: ANNOTATED PLANT GENES
;  FILE REFERENCE: 38-21(15097)C
;  CURRENT APPLICATION NUMBER: US/09/371,146A
;  CURRENT FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER: US 09/304,517
;  PRIOR FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 12197
;   LENGTH: 295
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-371-146A-12197

Alignment Scores:
Pred. No.:              18.7        Length:        295
Score:                  56.00       Matches:       16
Percent Similarity:     48.7%       Conservative:  3
Best Local Similarity:  41.0%       Mismatches:    8
Query Match:            35.0%       Indels:        12
DB:                     22          Gaps:          2

US-10-758-902-1 (1-30) x US-09-371-146A-12197 (1-295)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGACGGGGCCT 125

RESULT 78
US-09-985-678-12197
; Sequence 12197, Application US/09985678
; GENERAL INFORMATION:
;  APPLICANT: Cheikh, Nordine
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION: Annotated Plant Genes
;  FILE REFERENCE: 16517.255/38-21(15097)F
;  CURRENT APPLICATION NUMBER: US/09/985,678
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: US 09/304,517
;  PRIOR FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 12197
;   LENGTH: 295
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-985-678-12197

Alignment Scores:
Pred. No.:              18.7        Length:        295
Score:                  56.00       Matches:       16
Percent Similarity:     48.7%       Conservative:  3
Best Local Similarity:  41.0%       Mismatches:    8
Query Match:            35.0%       Indels:        12
DB:                     38          Gaps:          2

US-10-758-902-1 (1-30) x US-09-985-678-12197 (1-295)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGACGGGGCCT 125

RESULT 79
US-09-304-517A-9966
; Sequence 9966, Application US/09304517A
; GENERAL INFORMATION:
;  APPLICANT:       Cheikh, Nordine
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION:       Annotated Plant Genes
;  FILE REFERENCE:       38-21(15097)B
;  CURRENT APPLICATION NUMBER: US/09/304,517A
;  CURRENT FILING DATE:  1999-05-06
;  NUMBER OF SEQ ID NOS:       295529
; SEQ ID NO 9966
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-304-517A-9966

Alignment Scores:
Pred. No.:              19.3        Length:        301
Score:                  56.00       Matches:       16
Percent Similarity:     48.7%       Conservative:  3
Best Local Similarity:  41.0%       Mismatches:    8
Query Match:            35.0%       Indels:        12
DB:                     22          Gaps:          2

US-10-758-902-1 (1-30) x US-09-304-517A-9966 (1-301)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 125

RESULT 80
US-09-371-146A-9966
; Sequence 9966, Application US/09371146A
; GENERAL INFORMATION:
;  APPLICANT: Cheikh, Nordine
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION: ANNOTATED PLANT GENES
;  FILE REFERENCE: 38-21(15097)C
;  CURRENT APPLICATION NUMBER: US/09/371,146A
;  CURRENT FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER: US 09/304,517
;  PRIOR FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 9966
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-371-146A-9966

Alignment Scores:
Pred. No.:              19.3        Length:        301
Score:                  56.00       Matches:       16
Percent Similarity:     48.7%       Conservative:  3
Best Local Similarity:  41.0%       Mismatches:    8
```

```
Query Match:          35.0%       Indels:       12
DB:                   22          Gaps:         2

US-10-758-902-1 (1-30) x US-09-371-146A-9966 (1-301)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::|||||| ||||||  :::|||  |||  |||        ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||     |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 125

RESULT 81
US-09-985-678-9966
; Sequence 9966, Application US/09985678
; GENERAL INFORMATION:
;  APPLICANT: Cheikh, Nordine
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION: Annotated Plant Genes
;  FILE REFERENCE: 16517.255/38-21(15097)F
;  CURRENT APPLICATION NUMBER: US/09/985,678
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: US 09/304,517
;  PRIOR FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 9966
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-985-678-9966

Alignment Scores:
Pred. No.:            19.3        Length:       301
Score:                56.00       Matches:      16
Percent Similarity:   48.7%       Conservative: 3
Best Local Similarity: 41.0%      Mismatches:   8
Query Match:          35.0%       Indels:       12
DB:                   38          Gaps:         2

US-10-758-902-1 (1-30) x US-09-985-678-9966 (1-301)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::|||||| ||||||  :::|||  |||  |||        ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||     |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 125

RESULT 82
US-09-304-517A-12223
; Sequence 12223, Application US/09304517A
; GENERAL INFORMATION:
;  APPLICANT:       Cheikh, Nordine
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION:       Annotated Plant Genes
;  FILE REFERENCE:       38-21(15097)B
;  CURRENT APPLICATION NUMBER: US/09/304,517A
;  CURRENT FILING DATE:  1999-05-06
;  NUMBER OF SEQ ID NOS:       295529
; SEQ ID NO 12223
;   LENGTH: 308
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-304-517A-12223

Alignment Scores:
Pred. No.:            19.9        Length:       308
Score:                56.00       Matches:      16
Percent Similarity:   48.7%       Conservative: 3
Best Local Similarity: 41.0%      Mismatches:   8
Query Match:          35.0%       Indels:       12
DB:                   22          Gaps:         2

US-10-758-902-1 (1-30) x US-09-304-517A-12223 (1-308)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::|||||| ||||||  :::|||  |||  |||        ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||     |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 125

RESULT 83
US-09-371-146A-12223
; Sequence 12223, Application US/09371146A
; GENERAL INFORMATION:
;  APPLICANT: Cheikh, Nordine
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION: ANNOTATED PLANT GENES
;  FILE REFERENCE: 38-21(15097)C
;  CURRENT APPLICATION NUMBER: US/09/371,146A
;  CURRENT FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER: US 09/304,517
;  PRIOR FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 12223
;   LENGTH: 308
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-371-146A-12223

Alignment Scores:
Pred. No.:            19.9        Length:       308
Score:                56.00       Matches:      16
Percent Similarity:   48.7%       Conservative: 3
Best Local Similarity: 41.0%      Mismatches:   8
Query Match:          35.0%       Indels:       12
DB:                   22          Gaps:         2

US-10-758-902-1 (1-30) x US-09-371-146A-12223 (1-308)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::|||||| ||||||  :::|||  |||  |||        ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||     |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 125

RESULT 84
US-09-654-617-288444
; Sequence 288444, Application US/09654617
; GENERAL INFORMATION:
;  APPLICANT:       Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION:       Annotated Plant Genes
;  FILE REFERENCE:       38-21(15097)D
;  CURRENT APPLICATION NUMBER: US/09/654,617
;  CURRENT FILING DATE:  2000-09-05
;  NUMBER OF SEQ ID NOS:       463173
; SEQ ID NO 288444
;   LENGTH: 308
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-654-617-288444

Alignment Scores:
Pred. No.:            19.9        Length:       308
Score:                56.00       Matches:      16
Percent Similarity:   48.7%       Conservative: 3
Best Local Similarity: 41.0%      Mismatches:   8
Query Match:          35.0%       Indels:       12
DB:                   28          Gaps:         2
```

US-10-758-902-1 (1-30) x US-09-654-617-288444 (1-308)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 125
```

RESULT 85
US-09-684-016-288444
; Sequence 288444, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 288444
; LENGTH: 308
; TYPE: DNA
; ORGANISM: Zea mays
US-09-684-016-288444

Alignment Scores:

Pred. No.:	19.9	Length:	308
Score:	56.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.0%	Indels:	12
DB:	28	Gaps:	2

US-10-758-902-1 (1-30) x US-09-684-016-288444 (1-308)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 125
```

RESULT 86
US-09-985-678-12223
; Sequence 12223, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 12223
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Zea mays
US-09-985-678-12223

Alignment Scores:

Pred. No.:	19.9	Length:	308
Score:	56.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.0%	Indels:	12
DB:	38	Gaps:	2

US-10-758-902-1 (1-30) x US-09-985-678-12223 (1-308)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db         12 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 68

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db         69 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 125
```

RESULT 87
US-09-978-274A-5
; Sequence 5, Application US/09978274A
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-5

Alignment Scores:

Pred. No.:	35.1	Length:	465
Score:	56.00	Matches:	11
Percent Similarity:	72.0%	Conservative:	7
Best Local Similarity:	44.0%	Mismatches:	5
Query Match:	35.0%	Indels:	2
DB:	37	Gaps:	1

US-10-758-902-1 (1-30) x US-09-978-274A-5 (1-465)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                ||||||||||:::
Db         67 TCTCTTCGTAATCAA 81
```

RESULT 88
US-09-270-849B-89668
; Sequence 89668, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89668
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-89668

Alignment Scores:

Pred. No.:	36	Length:	474

```
Score:                  56.00          Matches:       10
Percent Similarity:     65.2%          Conservative:  5
Best Local Similarity:  43.5%          Mismatches:    8
Query Match:            35.0%          Indels:        0
DB:                     21             Gaps:          0

US-10-758-902-1 (1-30) x US-09-270-849B-89668 (1-474)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              :::|||||||||      :::   |||   |||  ||||||      :::   :::|||
Db         52 CATACCGTGTCCCTGCGTGTAGTCGAAGAATACTCGTATCCGAAGACAGTTTCAGAGTTG 111

Qy         22 ArgAsnGlu 24
              ||||||:::
Db        112 CGCAACCAA 120

RESULT 89
US-10-767-701-6363
; Sequence 6363, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 6363
;   LENGTH: 655
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41259_1
US-10-767-701-6363

Alignment Scores:
Pred. No.:              56.3           Length:        655
Score:                  56.00          Matches:       16
Percent Similarity:     48.7%          Conservative:  3
Best Local Similarity:  41.0%          Mismatches:    8
Query Match:            35.0%          Indels:        12
DB:                     60             Gaps:          2

US-10-758-902-1 (1-30) x US-10-767-701-6363 (1-655)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db        530 ACAGTTAATTTCAAT---GGGGAGATGTTCGAGAGCCCCGCGTTTTGTTCTACTTTGCGG 586

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        587 CAGGCGGAGCATGCGGCAGCTGAGGTAGCGCTCAATGAGTTATCGAAGAGGGGCCCT 643

RESULT 90
US-10-425-115-166418
; Sequence 166418, Application US/10425115
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166418
;   LENGTH: 791
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83354C.1
US-10-425-115-166418

Alignment Scores:
Pred. No.:              73             Length:        791
Score:                  56.00          Matches:       16
Percent Similarity:     48.7%          Conservative:  3
Best Local Similarity:  41.0%          Mismatches:    8
Query Match:            35.0%          Indels:        12
DB:                     50             Gaps:          2

US-10-758-902-1 (1-30) x US-10-425-115-166418 (1-791)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||         ||||||
Db        535 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 591

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        592 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 648

RESULT 91
US-09-978-274A-3
; Sequence 3, Application US/09978274A
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 792
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-3

Alignment Scores:
Pred. No.:              73.2           Length:        792
Score:                  56.00          Matches:       11
Percent Similarity:     72.0%          Conservative:  7
Best Local Similarity:  44.0%          Mismatches:    5
Query Match:            35.0%          Indels:        2
DB:                     37             Gaps:          1

US-10-758-902-1 (1-30) x US-09-978-274A-3 (1-792)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                ||||||||||:::
Db         67 TCTCTTCGTAATCAA 81

RESULT 92
US-08-715-074A-1
; Sequence 1, Application US/08715074A
;  GENERAL INFORMATION:
;    APPLICANT:  MOON, YOUNG-HO
;    APPLICANT:  CHOI, JIN-NAM
;    APPLICANT:  YUN, YOUNG-CHAE
;    APPLICANT:  JIN, JUNG-HUN
;    APPLICANT:  HONG, EUN-JU
;    APPLICANT:  LEE, JEONG-HO
;    APPLICANT:  CHOI, KYU-WHAN
```

```
;    APPLICANT:  LEE, JONG-SEOB
;    APPLICANT:  SONG, SANG-KEE
;    APPLICANT:  CHOI, YANG-DO ET AL.
;    TITLE OF INVENTION:  NOVEL GENES ENCODING ANTIVIRAL
;    TITLE OF INVENTION:  PROTEINS OF PHYTOLACCA...
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby, P.C.
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/715,074A
;      FILING DATE:  19-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  96-17404
;      FILING DATE:  22-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LUDWIG  S., PETER
;      REGISTRATION NUMBER:  25,351
;      REFERENCE/DOCKET NUMBER:  0136/0C430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  882 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Phytolacca insularis Nakai
;    IMMEDIATE SOURCE:
;      LIBRARY:  genomic library from Phytolacca insularis Nakai
US-08-715-074A-1

Alignment Scores:
Pred. No.:              84.9          Length:         882
Score:                  56.00         Matches:        11
Percent Similarity:     68.0%         Conservative:   6
Best Local Similarity:  44.0%         Mismatches:     6
Query Match:            35.0%         Indels:         2
DB:                     16            Gaps:           1

US-10-758-902-1 (1-30) x US-08-715-074A-1 (1-882)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||           :::|||   ||||||:::
Db          7 AATACCATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCTGGAT 66

Qy         20 AspLeuArgAsnGlu 24
              :::||||||||||||
Db         67 AATCTTCGTAATGAA 81

RESULT 93
PCT-US02-15033A-15
; Sequence 15, Application PC/TUS0215033A
; GENERAL INFORMATION:
;  APPLICANT: E. I. du Pont de Nemours & Company
;  APPLICANT:  Bramucci, Michael G
;  APPLICANT:  Brzostowicz, Patricia C.
;  APPLICANT:  Cheng, Qiong
;  APPLICANT:  Kostichka, Kristy N.
;  APPLICANT:  Nagarajan, Vasantha
;  APPLICANT:  Rouviere, Pierre E.
;  APPLICANT:  Tao, Luan
;  APPLICANT:  Thomas, Stuart M.
;  TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production
;  FILE REFERENCE: CL1788 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/15033A
;  CURRENT FILING DATE:  2002-04-24
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Rhodococcus erythropolis
PCT-US02-15033A-15

Alignment Scores:
Pred. No.:              93.4          Length:         945
Score:                  56.00         Matches:        10
Percent Similarity:     72.7%         Conservative:   6
Best Local Similarity:  45.5%         Mismatches:     6
Query Match:            35.0%         Indels:         0
DB:                     1             Gaps:           0

US-10-758-902-1 (1-30) x PCT-US02-15033A-15 (1-945)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||||||||||::::::          ||||||:::|||:::     :::|||
Db        520 AATCTCGGTGAGGCGTTTCAGCTGACCAACTTCATCCGCGACGTCGGTGAAGACCTCGAC 579

Qy         27 LysGly 28
              :::|||
Db        580 CGGGGA 585

RESULT 94
US-09-978-274A-1
; Sequence 1, Application US/09978274A
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-1

Alignment Scores:
Pred. No.:              93.4          Length:         945
Score:                  56.00         Matches:        11
Percent Similarity:     72.0%         Conservative:   7
Best Local Similarity:  44.0%         Mismatches:     5
Query Match:            35.0%         Indels:         2
DB:                     37            Gaps:           1

US-10-758-902-1 (1-30) x US-09-978-274A-1 (1-945)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||       :::|||   ||||||::::::
Db         76 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 135

Qy         20 AspLeuArgAsnGlu 24
```

```
                 |||||||||:::
Db        136 TCTCTTCGTAATCAA 150
```

RESULT 95
US-10-425-115-166417
; Sequence 166417, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166417
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1020)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_83353C.1
US-10-425-115-166417

Alignment Scores:

Pred. No.:	104	Length:	1020
Score:	56.00	Matches:	16
Percent Similarity:	48.7%	Conservative:	3
Best Local Similarity:	41.0%	Mismatches:	8
Query Match:	35.0%	Indels:	12
DB:	50	Gaps:	2

US-10-758-902-1 (1-30) x US-10-425-115-166417 (1-1020)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        572 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCTACTCTGCGG 628

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||     |||
Db        629 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 685
```

RESULT 96
US-09-978-274A-19
; Sequence 19, Application US/09978274A
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19

Alignment Scores:

Pred. No.:	114	Length:	1092
Score:	56.00	Matches:	11
Percent Similarity:	72.0%	Conservative:	7
Best Local Similarity:	44.0%	Mismatches:	5
Query Match:	35.0%	Indels:	2
DB:	37	Gaps:	1

US-10-758-902-1 (1-30) x US-09-978-274A-19 (1-1092)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||::::::|||:::   |||   |||         :::|||   ||||||::::::
Db          7 AATACGATCACCTTTGATGCTGGAAATGCCACCATTAACAAATATGCCACCTTTATGGAA 66

Qy         20 AspLeuArgAsnGlu 24
                 |||||||||:::
Db         67 TCTCTTCGTAATCAA 81
```

RESULT 97
US-09-404-520-27610
; Sequence 27610, Application US/09404520
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Ghodssi, Azita
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: McIninch, James
; APPLICANT: Timberlake, William E.
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 27610
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-09-404-520-27610

Alignment Scores:

Pred. No.:	122	Length:	1149
Score:	56.00	Matches:	11
Percent Similarity:	64.0%	Conservative:	5
Best Local Similarity:	44.0%	Mismatches:	9
Query Match:	35.0%	Indels:	0
DB:	23	Gaps:	0

US-10-758-902-1 (1-30) x US-09-404-520-27610 (1-1149)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||   |||   ::::::|||         |||      ||||||   ::::::||||||
Db        472 AACATCGTATTCTACCATCTCCTTCATCTCTACGCTAACCCGACGCTCCTGGAGGATCTT 531

Qy         22 ArgAsnGluLeuAla 26
              |||   |||:::|||
Db        532 CGAAAGGAGATCGCC 546
```

RESULT 98
US-09-404-520B-27610
; Sequence 27610, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 27610
; LENGTH: 1149
; TYPE: DNA

```
;   ORGANISM: Emericella nidulans
US-09-404-520B-27610

Alignment Scores:
Pred. No.:              122          Length:        1149
Score:                  56.00        Matches:       11
Percent Similarity:     64.0%        Conservative:  5
Best Local Similarity:  44.0%        Mismatches:    9
Query Match:            35.0%        Indels:        0
DB:                     23           Gaps:          0

US-10-758-902-1 (1-30) x US-09-404-520B-27610 (1-1149)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||   |||   ::::::|||         |||      ||||||   ::::::||||||
Db        472 AACATCGTATTCTACCATCTCCTTCATCTCTACGCTAACCCGACGCTCCTGGAGGATCTT 531

Qy         22 ArgAsnGluLeuAla 26
              |||   |||:::|||
Db        532 CGAAAGGAGATCGCC 546

RESULT 99
US-09-978-274A-31
; Sequence 31, Application US/09978274A
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 1368
;   TYPE: DNA
;   ORGANISM: Phytolacca americana
US-09-978-274A-31

Alignment Scores:
Pred. No.:              156          Length:        1368
Score:                  56.00        Matches:       12
Percent Similarity:     64.0%        Conservative:  4
Best Local Similarity:  48.0%        Mismatches:    7
Query Match:            35.0%        Indels:        2
DB:                     37           Gaps:          1

US-10-758-902-1 (1-30) x US-09-978-274A-31 (1-1368)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGln 19
              ||||||:::   :::|||:::|||              :::|||   ||||||
Db        294 AATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAAATACGCCACTTTTCGGAAT 353

Qy         20 AspLeuArgAsnGlu 24
              |||||||||||||||
Db        354 GATCTTCGTAATGAA 368

RESULT 100
US-10-219-999-29690
; Sequence 29690, Application US/10219999
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Edgerton, Michael D
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  Stein, Joshua
;  TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-10(52726)C
;  CURRENT APPLICATION NUMBER: US/10/219,999
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: US 60/324,109
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: US 60/312,544
;  PRIOR FILING DATE: 2001-08-15
;  NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 29690
;   LENGTH: 2197
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (359)..(1228)
;   OTHER INFORMATION:
US-10-219-999-29690

Alignment Scores:
Pred. No.:              299          Length:        2197
Score:                  56.00        Matches:       16
Percent Similarity:     48.7%        Conservative:  3
Best Local Similarity:  41.0%        Mismatches:    8
Query Match:            35.0%        Indels:        12
DB:                     42           Gaps:          2

US-10-758-902-1 (1-30) x US-10-219-999-29690 (1-2197)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        464 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCCACTCTGCGG 520

Qy         23 --------------------------------AsnGluLeuAlaLysGlyThrPro 30
                                              |||||||||:::|||      |||
Db        521 CAGGCGGAGCATGCGGCAGCTGAGGTAGCACTCAATGAGTTATCAAAGAGGGGGCCT 577


Search completed: September 18, 2006, 20:23:10
Job time : 1611.94 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 17:57:26 ; Search time 124.022 Seconds
(without alignments)
693.279 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2651964 seqs, 955356087 residues

Total number of hits satisfying chosen parameters: 5303928

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_18092006_162716_11719/app_query.fasta_1
-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10758902_@CGN_1_1_342_@runat_18092006_162716_11719 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pna/US11_NEW_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pna/US11_NEW_COMB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	55.5	34.7	2429	1	PCT-US06-33148-307	Sequence 307, App
	2	55	34.4	630	8	US-11-504-538-8967	Sequence 8967, Ap
	3	54	33.8	3828	7	US-11-514-704-1179	Sequence 1179, Ap
	4	52	32.5	1837	7	US-11-514-704-1178	Sequence 1178, Ap
c	5	51.5	32.2	628	8	US-11-433-832-35722	Sequence 35722, A
c	6	51.5	32.2	1398	8	US-11-371-354-62944	Sequence 62944, A
c	7	51	31.9	1764	8	US-11-433-832-44725	Sequence 44725, A
	8	51	31.9	10000	9	US-60-831-153-157	Sequence 157, App
	9	51	31.9	194534	1	PCT-US03-41389-458	Sequence 458, App
	10	50.5	31.6	1830	1	PCT-US06-33712-1119	Sequence 1119, Ap
	11	50.5	31.6	1840	1	PCT-US06-11960-230	Sequence 230, App
	12	50.5	31.6	3633	8	US-11-434-137-2491	Sequence 2491, Ap
	13	50.5	31.6	3633	8	US-11-434-184-2491	Sequence 2491, Ap
	14	50.5	31.6	3633	8	US-11-434-203-2491	Sequence 2491, Ap
	15	50.5	31.6	3633	8	US-11-434-127-2491	Sequence 2491, Ap
	16	50.5	31.6	3633	8	US-11-434-199-2491	Sequence 2491, Ap
	17	50.5	31.6	365906	8	US-11-033-056A-37346	Sequence 37346, A
c	18	50	31.2	1350	7	US-11-514-704-4673	Sequence 4673, Ap
c	19	50	31.2	1847	7	US-11-514-704-4675	Sequence 4675, Ap
c	20	50	31.2	5166	7	US-11-514-704-4674	Sequence 4674, Ap
	21	50	31.2	16669	8	US-11-033-056A-38192	Sequence 38192, A
c	22	50	31.2	24231	1	PCT-US03-41389-353	Sequence 353, App
	23	50	31.2	418550	8	US-11-214-063B-1463	Sequence 1463, Ap
c	24	50	31.2	2132949	8	US-11-033-056A-38500	Sequence 38500, A
	25	49.5	30.9	4830	6	US-10-805-394A-3166	Sequence 3166, Ap
	26	49.5	30.9	4953	8	US-11-507-094-13	Sequence 13, Appl
	27	49.5	30.9	4953	8	US-11-507-094-55	Sequence 55, Appl
c	28	49.5	30.9	3309400	6	US-10-805-394A-1	Sequence 1, Appli
	29	49	30.6	7224	9	US-60-836-986-2918	Sequence 2918, Ap
	30	49	30.6	7561	8	US-11-437-729-3157	Sequence 3157, Ap
	31	49	30.6	7561	9	US-60-836-986-2917	Sequence 2917, Ap
	32	49	30.6	8295	8	US-11-437-729-3153	Sequence 3153, Ap
	33	49	30.6	8295	8	US-11-437-729-3154	Sequence 3154, Ap
	34	49	30.6	8295	8	US-11-437-729-3155	Sequence 3155, Ap
	35	49	30.6	8295	8	US-11-437-729-3159	Sequence 3159, Ap
	36	49	30.6	8295	8	US-11-437-729-3160	Sequence 3160, Ap
	37	49	30.6	8295	8	US-11-475-062-10037	Sequence 10037, A
	38	49	30.6	8295	8	US-11-475-062-10038	Sequence 10038, A
	39	49	30.6	8295	8	US-11-475-062-10039	Sequence 10039, A
	40	49	30.6	8295	8	US-11-475-062-10041	Sequence 10041, A
	41	49	30.6	8295	8	US-11-475-062-10042	Sequence 10042, A
	42	49	30.6	8521	8	US-11-437-729-3156	Sequence 3156, Ap
	43	49	30.6	8521	8	US-11-475-062-10040	Sequence 10040, A
	44	49	30.6	9074	8	US-11-437-729-3161	Sequence 3161, Ap
	45	49	30.6	9074	8	US-11-475-062-10043	Sequence 10043, A
	46	49	30.6	30989	8	US-11-033-056A-35955	Sequence 35955, A
	47	49	30.6	156814	8	US-11-033-056A-37713	Sequence 37713, A
	48	49	30.6	246604	8	US-11-033-056A-38635	Sequence 38635, A
c	49	49	30.6	507300	8	US-11-033-056A-36751	Sequence 36751, A
	50	48.5	30.3	2135	8	US-11-490-374-2108	Sequence 2108, Ap
	51	48.5	30.3	2135	8	US-11-490-374-2110	Sequence 2110, Ap
	52	48.5	30.3	2135	8	US-11-431-708-5669	Sequence 5669, Ap
	53	48.5	30.3	2135	8	US-11-431-708-5671	Sequence 5671, Ap
	54	48.5	30.3	2135	8	US-11-437-729-5152	Sequence 5152, Ap
	55	48.5	30.3	2135	8	US-11-437-729-5154	Sequence 5154, Ap
	56	48.5	30.3	2135	8	US-11-475-062-7780	Sequence 7780, Ap
	57	48.5	30.3	2135	8	US-11-475-062-7781	Sequence 7781, Ap
	58	48.5	30.3	2135	8	US-11-475-062-7783	Sequence 7783, Ap
	59	48.5	30.3	2135	8	US-11-475-062-7784	Sequence 7784, Ap
	60	48.5	30.3	2135	8	US-11-475-062-9236	Sequence 9236, Ap
	61	48.5	30.3	2135	8	US-11-475-062-9238	Sequence 9238, Ap
	62	48.5	30.3	2393	9	US-60-836-986-5300	Sequence 5300, Ap
	63	48.5	30.3	2534	8	US-11-475-062-7782	Sequence 7782, Ap
	64	48.5	30.3	2653	8	US-11-490-374-2107	Sequence 2107, Ap
	65	48.5	30.3	2653	8	US-11-490-374-2109	Sequence 2109, Ap
	66	48.5	30.3	2653	8	US-11-431-708-5668	Sequence 5668, Ap
	67	48.5	30.3	2653	8	US-11-431-708-5670	Sequence 5670, Ap
	68	48.5	30.3	2653	8	US-11-437-729-5150	Sequence 5150, Ap
	69	48.5	30.3	2653	8	US-11-437-729-5153	Sequence 5153, Ap
	70	48.5	30.3	2653	8	US-11-475-062-9234	Sequence 9234, Ap
	71	48.5	30.3	2653	8	US-11-475-062-9237	Sequence 9237, Ap
c	72	48.5	30.3	99610	8	US-11-033-056A-36451	Sequence 36451, A
c	73	48.5	30.3	99610	8	US-11-033-056A-36452	Sequence 36452, A
	74	48.5	30.3	131999	8	US-11-033-056A-37757	Sequence 37757, A
	75	48.5	30.3	663814	1	PCT-US06-20103-1	Sequence 1, Appli
	76	48	30.0	1383	8	US-11-371-354-67580	Sequence 67580, A
c	77	48	30.0	1617	8	US-11-371-354-73254	Sequence 73254, A
	78	48	30.0	1826	8	US-11-433-832-8527	Sequence 8527, Ap
	79	48	30.0	2526	8	US-11-414-403-140	Sequence 140, App
c	80	48	30.0	3046	6	US-10-433-793A-82	Sequence 82, Appl
c	81	48	30.0	4161	7	US-11-514-704-24120	Sequence 24120, A

82	48	30.0	5640	7	US-11-514-704-18783	Sequence 18783, A
c 83	48	30.0	687411	1	PCT-US03-41389-26	Sequence 26, Appl
84	48	30.0	1130575	6	US-10-833-833-125	Sequence 125, App
85	48	30.0	2132949	8	US-11-033-056A-38500	Sequence 38500, A
c 86	47.5	29.7	177481	8	US-11-033-056A-36422	Sequence 36422, A
c 87	47.5	29.7	177492	9	US-60-819-087-10	Sequence 10, Appl
88	47.5	29.7	265847	8	US-11-033-056A-37336	Sequence 37336, A
89	47.5	29.7	1983043	6	US-10-961-644A-1	Sequence 1, Appli
c 90	47	29.4	353	8	US-11-491-371-50837	Sequence 50837, A
c 91	47	29.4	396	6	US-10-582-413-7	Sequence 7, Appli
c 92	47	29.4	721	6	US-10-363-345B-15631	Sequence 15631, A
93	47	29.4	721	6	US-10-363-345B-15632	Sequence 15632, A
c 94	47	29.4	1753	6	US-10-536-184-157	Sequence 157, App
95	47	29.4	2358	6	US-10-309-407-347	Sequence 347, App
96	47	29.4	2412	8	US-11-433-832-46627	Sequence 46627, A
97	47	29.4	2412	8	US-11-371-354-70010	Sequence 70010, A
c 98	47	29.4	3072	7	US-11-514-704-12860	Sequence 12860, A
c 99	47	29.4	4591	1	PCT-US06-11960-326	Sequence 326, App
c 100	47	29.4	4843	9	US-60-836-986-9427	Sequence 9427, Ap

ALIGNMENTS

RESULT 1
PCT-US06-33148-307
; Sequence 307, Application PC/TUS0633148
; GENERAL INFORMATION:
; APPLICANT: Genizon BioSciences
; TITLE OF INVENTION: GeneMap of the Human Genes Associated with Crohn's Disease
; FILE REFERENCE: GENI-009/00WO
; CURRENT APPLICATION NUMBER: PCT/US06/33148
; CURRENT FILING DATE: 2006-08-24
; PRIOR APPLICATION NUMBER: US 60/710,726
; PRIOR FILING DATE: 2005-08-24
; NUMBER OF SEQ ID NOS: 16984
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 307
; LENGTH: 2429
; TYPE: DNA
; ORGANISM: Homosapiens
PCT-US06-33148-307

Alignment Scores:

Pred. No.:	24.2	Length:	2429
Score:	55.50	Matches:	10
Percent Similarity:	48.7%	Conservative:	9
Best Local Similarity:	25.6%	Mismatches:	11
Query Match:	34.7%	Indels:	9
DB:	1	Gaps:	1

US-10-758-902-1 (1-30) x PCT-US06-33148-307 (1-2429)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyr---------------------- 12
              ||||||::::::   |||:::        |||
Db       1773 TATAATTCCCTACATTTCTCTCGAGCTCACAAATACTTTTTTTTCTTTTTCCTTATTCAA 1832

Qy         13 ---GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
                 ::::::|||   ::::::      :::||||||||||   :::      ||||||
Db       1833 TCAGATTTTCCAAAGTACCTTTCCACCATAAGAAATGAATTTTCTACTTCTACACCC 1889
```

RESULT 2
US-11-504-538-8967
; Sequence 8967, Application US/11504538
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C.
; TITLE OF INVENTION: Maize Polymorphisms and Methods of Genotyping
; FILE REFERENCE: 38-10(52018)B
; CURRENT APPLICATION NUMBER: US/11/504,538
; CURRENT FILING DATE: 2006-08-14
; NUMBER OF SEQ ID NOS: 10380
; SEQ ID NO 8967
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Zea mays
US-11-504-538-8967

Alignment Scores:

Pred. No.:	6.07	Length:	630
Score:	55.00	Matches:	15
Percent Similarity:	58.6%	Conservative:	2
Best Local Similarity:	51.7%	Mismatches:	10
Query Match:	34.4%	Indels:	2
DB:	8	Gaps:	2

US-10-758-902-1 (1-30) x US-11-504-538-8967 (1-630)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              ||||||:::||||||   ||||||   :::|||   |||   |||          ||||||
Db        533 ACAGTTAATTTCAAC---GGGGAGATGTTCGAGAGCCCAGTGTTTTGTTCTACTCTGCGG 589

Qy         23 Asn---GluLeuAlaLysGlyThrPro 30
                 |||   |||   |||   |||
Db        590 CAGGCGGAGCATGCGGCAGGGGTACCG 616
```

RESULT 3
US-11-514-704-1179
; Sequence 1179, Application US/11514704
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: Wu, Kunsheng
; APPLICANT: Dasgupta, Santanu
; APPLICANT: Cherian, Shoba
; APPLICANT: Jayaprakash, Targolli L
; TITLE OF INVENTION: Zea mays Ribulose Bisphosphate Carboxylase
; TITLE OF INVENTION: Activase Promoter
; FILE REFERENCE: 38-21(53660)C
; CURRENT APPLICATION NUMBER: US/11/514,704
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1179
; LENGTH: 3828
; TYPE: DNA
; ORGANISM: Zea mays
US-11-514-704-1179

Alignment Scores:

Pred. No.:	74.7	Length:	3828
Score:	54.00	Matches:	11
Percent Similarity:	66.7%	Conservative:	3
Best Local Similarity:	52.4%	Mismatches:	7
Query Match:	33.8%	Indels:	0
DB:	7	Gaps:	0

US-10-758-902-1 (1-30) x US-11-514-704-1179 (1-3828)

```
Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||||   |||   :::||||||                :::||||||||
Db       1634 GGCGAAGCGTATGAACCGCCTTGTTACATACAACCTTCTGAAAAGGGAGTGGCAAAAGGT 1693

Qy         29 Thr 29
                :::
Db       1694 TCC 1696
```

RESULT 4
US-11-514-704-1178
; Sequence 1178, Application US/11514704
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: Wu, Kunsheng
; APPLICANT: Dasgupta, Santanu
; APPLICANT: Cherian, Shoba
; APPLICANT: Jayaprakash, Targolli L
; TITLE OF INVENTION: Zea mays Ribulose Bisphosphate Carboxylase
; TITLE OF INVENTION: Activase Promoter
; FILE REFERENCE: 38-21(53660)C

```
;  CURRENT APPLICATION NUMBER: US/11/514,704
;  CURRENT FILING DATE:  2006-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1178
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-514-704-1178

Alignment Scores:
Pred. No.:              69.7          Length:         1837
Score:                  52.00         Matches:        10
Percent Similarity:     66.7%         Conservative:   4
Best Local Similarity:  47.6%         Mismatches:     7
Query Match:            32.5%         Indels:         0
DB:                     7             Gaps:           0

US-10-758-902-1 (1-30) x US-11-514-704-1178 (1-1837)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ||||||||||||||   |||   :::||||||           :::|||:::|||
Db       1385 GGCGAAGCATATGAACCGCCTTGTTACATACAACCTTTTGAAAAGGGAGTGGCAGAAGGT 1444

Qy         29 Thr 29
              :::
Db       1445 TCC 1447

RESULT 5
US-11-433-832-35722/c
; Sequence 35722, Application US/11433832
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Matthew
;  APPLICANT:  Kinch, Deborah
;  APPLICANT:  Rosenberg, Michael
;  APPLICANT:  Subramaniam, S. Sai
;  APPLICANT:  Szak, Suzanne
;  APPLICANT:  Li, Huo
;  APPLICANT:  Bandaru, Raj
;  APPLICANT:  Derbel, Maher
;  TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary t
;  TITLE OF INVENTION:  Fragments of, Cynomolgus Monkey Genes and the Use Thereof
;  FILE REFERENCE: 2159.0290002
;  CURRENT APPLICATION NUMBER: US/11/433,832
;  CURRENT FILING DATE:  2006-05-15
;  NUMBER OF SEQ ID NOS: 48714
;  SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 35722
;   LENGTH: 628
;   TYPE: DNA
;   ORGANISM: Macaca Mulatta
US-11-433-832-35722

Alignment Scores:
Pred. No.:              24.1          Length:         628
Score:                  51.50         Matches:        13
Percent Similarity:     52.6%         Conservative:   7
Best Local Similarity:  34.2%         Mismatches:     10
Query Match:            32.2%         Indels:         8
DB:                     8             Gaps:           1

US-10-758-902-1 (1-30) x US-11-433-832-35722 (1-628)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db        414 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATATGTATCCTTCCTTCCCTCCAAGA 355

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                    :::   :::||||||:::      |||
Db        354 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 303

RESULT 6
US-11-371-354-62944/c
; Sequence 62944, Application US/11371354
; GENERAL INFORMATION:
;  APPLICANT: CARRINO, JOHN
;  APPLICANT:  LIANG, FENG
;  TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFYING MATCHED REAGENTS
;  FILE REFERENCE: INV-1005-UT2
;  CURRENT APPLICATION NUMBER: US/11/371,354
;  CURRENT FILING DATE:  2006-03-07
;  PRIOR APPLICATION NUMBER: 60/673,045
;  PRIOR FILING DATE: 2005-04-19
;  PRIOR APPLICATION NUMBER: 60/665,199
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/665,200
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/659,493
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/659,492
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/953,586
;  PRIOR FILING DATE: 2005-02-15
;  PRIOR APPLICATION NUMBER: 60/651,390
;  PRIOR FILING DATE: 2005-02-08
;  NUMBER OF SEQ ID NOS: 78682
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62944
;   LENGTH: 1398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-371-354-62944

Alignment Scores:
Pred. No.:              61.6          Length:         1398
Score:                  51.50         Matches:        13
Percent Similarity:     52.6%         Conservative:   7
Best Local Similarity:  34.2%         Mismatches:     10
Query Match:            32.2%         Indels:         8
DB:                     8             Gaps:           1

US-10-758-902-1 (1-30) x US-11-371-354-62944 (1-1398)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPhe-IleGlnAs 20
              |||:::   :::      |||   |||   ||||||   ||||||:::||| :::|||||
Db       1335 TATTCTAGAATAAGAGTCAATTTTGGCAATGCGTATGTGTATCCTTCCTTCCCTCCAAGA 1276

Qy         20 p--------------------LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |                    :::   :::||||||:::      |||
Db       1275 TCCTGTTCTGCAGTCTTCAAAGCAACAGAAGAAGCTGGCACAATCTTTGCCC 1224

RESULT 7
US-11-433-832-44725/c
; Sequence 44725, Application US/11433832
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Matthew
;  APPLICANT:  Kinch, Deborah
;  APPLICANT:  Rosenberg, Michael
;  APPLICANT:  Subramaniam, S. Sai
;  APPLICANT:  Szak, Suzanne
;  APPLICANT:  Li, Huo
;  APPLICANT:  Bandaru, Raj
;  APPLICANT:  Derbel, Maher
;  TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary to
;  TITLE OF INVENTION:  Fragments of, Cynomolgus Monkey Genes and the Use Thereof
;  FILE REFERENCE: 2159.0290002
;  CURRENT APPLICATION NUMBER: US/11/433,832
;  CURRENT FILING DATE:  2006-05-15
;  NUMBER OF SEQ ID NOS: 48714
;  SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 44725
;   LENGTH: 1764
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-433-832-44725
```

```
Alignment Scores:
Pred. No.:              98.7          Length:        1764
Score:                  51.00         Matches:       8
Percent Similarity:     62.5%         Conservative:  7
Best Local Similarity:  33.3%         Mismatches:    9
Query Match:            31.9%         Indels:        0
DB:                     8             Gaps:          0

US-10-758-902-1 (1-30) x US-11-433-832-44725 (1-1764)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ::::::|||   |||::::::   |||   |||:::||||||   ::::::
Db        837 CATGTGGGCACTGCCCATCAGCAGCCCCCCTTTGTACAGGACAGAAAGCACAATCAGGTT 778

Qy         27 LysGlyThrPro 30
                 |||   |||
Db        777 TCCGGACAGCCT 766

RESULT 8
US-60-831-153-157
; Sequence 157, Application US/60831153
; GENERAL INFORMATION:
;  APPLICANT: GRUPE, Andrew
;  APPLICANT:  LI, Yonghong
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Alzheimer's Disease, Methods of Detection and Uses Thereof
;  FILE REFERENCE: CD000009PRO
;  CURRENT APPLICATION NUMBER: US/60/831,153
;  CURRENT FILING DATE:  2006-07-14
;  NUMBER OF SEQ ID NOS: 189
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 157
;   LENGTH: 10000
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(10000)
;   OTHER INFORMATION: n = A,T,C or G
US-60-831-153-157

Alignment Scores:
Pred. No.:              754           Length:        10000
Score:                  51.00         Matches:       11
Percent Similarity:     63.6%         Conservative:  3
Best Local Similarity:  50.0%         Mismatches:    2
Query Match:            31.9%         Indels:        6
DB:                     9             Gaps:          1

US-10-758-902-1 (1-30) x US-60-831-153-157 (1-10000)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||||||||:::|||   |||   |||::::::|||                  ||||||
Db       7921 GGTGAGGCCTGGGAAGCACCTTGGTTTCTAGAAGAC-----------------AAAGGC 7962

Qy         29 ThrPro 30
              ||||||
Db       7963 ACTCCA 7968

RESULT 9
PCT-US03-41389-458
; Sequence 458, Application PC/TUS0341389
; GENERAL INFORMATION:
;  APPLICANT: Sagres Discovery, Inc.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
;  FILE REFERENCE: 20366-020WO1
;  CURRENT APPLICATION NUMBER: PCT/US03/41389
;  CURRENT FILING DATE:  2003-12-22
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 458
;   LENGTH: 194534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(194534)
;   OTHER INFORMATION: n = A,T,C or G
PCT-US03-41389-458

Alignment Scores:
Pred. No.:              2.44e+04      Length:        194534
Score:                  51.00         Matches:       12
Percent Similarity:     63.6%         Conservative:  2
Best Local Similarity:  54.5%         Mismatches:    8
Query Match:            31.9%         Indels:        0
DB:                     1             Gaps:          0

US-10-758-902-1 (1-30) x PCT-US03-41389-458 (1-194534)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              |||:::   |||||||||   |||   |||   ||||||   :::       ||||||
Db      64117 GTGGCTCTCAATCTTGGCTGGGCATCAGAATCACCCACGCTGCTTTACAAACTGAGGCCT 64176

Qy         24 GluLeu 25
              ||||||
Db      64177 GAGCTA 64182

RESULT 10
PCT-US06-33712-1119
; Sequence 1119, Application PC/TUS0633712
; GENERAL INFORMATION:
;  APPLICANT: Gene Logic, Inc.
;  TITLE OF INVENTION: MOLECULAR CARDIOTOXICOLOGY MODELING
;  FILE REFERENCE: GENE-127/01WO
;  CURRENT APPLICATION NUMBER: PCT/US06/33712
;  CURRENT FILING DATE:  2006-09-08
;  PRIOR APPLICATION NUMBER: US 60/711,444
;  PRIOR FILING DATE: 2005-08-26
;  NUMBER OF SEQ ID NOS: 1263
;  SOFTWARE: PatentIn version 2.1
; SEQ ID NO 1119
;   LENGTH: 1830
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
PCT-US06-33712-1119

Alignment Scores:
Pred. No.:              126           Length:        1830
Score:                  50.50         Matches:       11
Percent Similarity:     62.5%         Conservative:  4
Best Local Similarity:  45.8%         Mismatches:    6
Query Match:            31.6%         Indels:        3
DB:                     1             Gaps:          1

US-10-758-902-1 (1-30) x PCT-US06-33712-1119 (1-1830)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::||||||||||||   :::         |||   ||||||   |||
Db        406 AACGTGGGCATGTCATACGAGTATCCAGAATACTTTTTGGAAATTCCTGACTTGGACAAC 465

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        466 ACCATCAAGAAA 477

RESULT 11
PCT-US06-11960-230
; Sequence 230, Application PC/TUS0611960
; GENERAL INFORMATION:
;  APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION,
;  TITLE OF INVENTION:  ASSESSMENT, PREVENTION, AND THERAPY OF NEUROLOGICAL
;  TITLE OF INVENTION:  DISEASES, DISORDERS AND CONDITIONS
```

```
;  FILE REFERENCE: DFS-060.25
;  CURRENT APPLICATION NUMBER: PCT/US06/11960
;  CURRENT FILING DATE:  2006-03-31
;  PRIOR APPLICATION NUMBER: 60/667,922
;  PRIOR FILING DATE: 2005-03-31
;  NUMBER OF SEQ ID NOS: 767
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 230
;   LENGTH: 1840
;   TYPE: DNA
;   ORGANISM: Mus musculus
PCT-US06-11960-230

Alignment Scores:
Pred. No.:              126          Length:        1840
Score:                  50.50        Matches:       11
Percent Similarity:     62.5%        Conservative:  4
Best Local Similarity:  45.8%        Mismatches:    6
Query Match:            31.6%        Indels:        3
DB:                     1            Gaps:          1

US-10-758-902-1 (1-30) x PCT-US06-11960-230 (1-1840)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         |||   ||||||   |||
Db        438 AACGTGGGCATGTCATACGAGTATCCGGAATACTTTCTGGAAATTCCCGACTTGGACAAC 497

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        498 ACCATCAAGAAA 509

RESULT 12
US-11-434-137-2491
; Sequence 2491, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2491
;   LENGTH: 3633
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
US-11-434-137-2491

Alignment Scores:
Pred. No.:              280          Length:        3633
Score:                  50.50        Matches:       10
Percent Similarity:     66.7%        Conservative:  6
Best Local Similarity:  41.7%        Mismatches:    7
Query Match:            31.6%        Indels:        1
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-434-137-2491 (1-3633)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              ::::::|||:::||||||         ||||||      |||:::   |||:::   |||
Db       3532 ATAAACTTTAGTTTAGGC---GGAAACGAATACGAAGCATTTGTAAGTGACATCACTAAT 3588

Qy         24 GluLeuAlaLys 27
                :::   ||||||
Db       3589 CAACAAGCAAAA 3600

RESULT 13
US-11-434-184-2491
; Sequence 2491, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2491
;   LENGTH: 3633
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
US-11-434-184-2491

Alignment Scores:
Pred. No.:              280          Length:        3633
Score:                  50.50        Matches:       10
Percent Similarity:     66.7%        Conservative:  6
Best Local Similarity:  41.7%        Mismatches:    7
Query Match:            31.6%        Indels:        1
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-434-184-2491 (1-3633)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              ::::::|||:::||||||         ||||||      |||:::   |||:::   |||
Db       3532 ATAAACTTTAGTTTAGGC---GGAAACGAATACGAAGCATTTGTAAGTGACATCACTAAT 3588

Qy         24 GluLeuAlaLys 27
                :::   ||||||
Db       3589 CAACAAGCAAAA 3600

RESULT 14
US-11-434-203-2491
; Sequence 2491, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
```

```
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2491
;   LENGTH: 3633
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
US-11-434-203-2491

Alignment Scores:
Pred. No.:                280          Length:         3633
Score:                    50.50        Matches:        10
Percent Similarity:       66.7%        Conservative:   6
Best Local Similarity:    41.7%        Mismatches:     7
Query Match:              31.6%        Indels:         1
DB:                       8            Gaps:           1

US-10-758-902-1 (1-30) x US-11-434-203-2491 (1-3633)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              ::::::|||:::||||||       ||||||      |||:::   |||:::   |||
Db       3532 ATAAACTTTAGTTTAGGC---GGAAACGAATACGAAGCATTTGTAAGTGACATCACTAAT 3588

Qy         24 GluLeuAlaLys 27
              :::   ||||||
Db       3589 CAACAAGCAAAA 3600

RESULT 15
US-11-434-127-2491
; Sequence 2491, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2491
;   LENGTH: 3633
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
US-11-434-127-2491

Alignment Scores:
Pred. No.:                280          Length:         3633
Score:                    50.50        Matches:        10
Percent Similarity:       66.7%        Conservative:   6
Best Local Similarity:    41.7%        Mismatches:     7
Query Match:              31.6%        Indels:         1
DB:                       8            Gaps:           1

US-10-758-902-1 (1-30) x US-11-434-127-2491 (1-3633)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              ::::::|||:::||||||       ||||||      |||:::   |||:::   |||
Db       3532 ATAAACTTTAGTTTAGGC---GGAAACGAATACGAAGCATTTGTAAGTGACATCACTAAT 3588

Qy         24 GluLeuAlaLys 27
              :::   ||||||
Db       3589 CAACAAGCAAAA 3600

RESULT 16
US-11-434-199-2491
; Sequence 2491, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2491
;   LENGTH: 3633
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
US-11-434-199-2491

Alignment Scores:
Pred. No.:                280          Length:         3633
Score:                    50.50        Matches:        10
Percent Similarity:       66.7%        Conservative:   6
Best Local Similarity:    41.7%        Mismatches:     7
Query Match:              31.6%        Indels:         1
DB:                       8            Gaps:           1

US-10-758-902-1 (1-30) x US-11-434-199-2491 (1-3633)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              ::::::|||:::||||||       ||||||      |||:::   |||:::   |||
Db       3532 ATAAACTTTAGTTTAGGC---GGAAACGAATACGAAGCATTTGTAAGTGACATCACTAAT 3588

Qy         24 GluLeuAlaLys 27
              :::   ||||||
Db       3589 CAACAAGCAAAA 3600

RESULT 17
US-11-033-056A-37346
; Sequence 37346, Application US/11033056A
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
```

```
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37346
;   LENGTH: 365906
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-37346

Alignment Scores:
Pred. No.:              6.21e+04        Length:         365906
Score:                  50.50           Matches:        9
Percent Similarity:     70.4%           Conservative:   10
Best Local Similarity:  33.3%           Mismatches:     5
Query Match:            31.6%           Indels:         3
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-033-056A-37346 (1-365906)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg--- 22
              :::||||||   :::|||:::   ::::::   |||:::|||:::   |||||||:::
Db     208942 ATGAGCTTCAGAATGGGGAAGCCTTTCCAGCTCCCCTCATTTCTCTATGATCTTAAAAAA 209001

Qy         23 ------AsnGluLeuAlaLys 27
                  |||::::::   |||
Db     209002 TGAATAAACCAGGTTTTCAAG 209022

RESULT 18
US-11-514-704-4673/c
; Sequence 4673, Application US/11514704
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  Wu, Kunsheng
;  APPLICANT:  Dasgupta, Santanu
;  APPLICANT:  Cherian, Shoba
;  APPLICANT:  Jayaprakash, Targolli L
;  TITLE OF INVENTION: Zea mays Ribulose Bisphosphate Carboxylase
;  TITLE OF INVENTION:  Activase Promoter
;  FILE REFERENCE: 38-21(53660)C
;  CURRENT APPLICATION NUMBER: US/11/514,704
;  CURRENT FILING DATE:  2006-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4673
;   LENGTH: 1350
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-514-704-4673

Alignment Scores:
Pred. No.:              107             Length:         1350
Score:                  50.00           Matches:        10
Percent Similarity:     70.6%           Conservative:   2
Best Local Similarity:  58.8%           Mismatches:     5
Query Match:            31.2%           Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-1 (1-30) x US-11-514-704-4673 (1-1350)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||   |||:::|||||||||      ||||||      :::|||||||||
Db       1194 GAGCAGTACCAATACCCAACATCTTGACAGGACTTCAGTTCTGAATTGGCT 1144

RESULT 19
US-11-514-704-4675/c
; Sequence 4675, Application US/11514704
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  Wu, Kunsheng
;  APPLICANT:  Dasgupta, Santanu
;  APPLICANT:  Cherian, Shoba
;  APPLICANT:  Jayaprakash, Targolli L
;  TITLE OF INVENTION: Zea mays Ribulose Bisphosphate Carboxylase
;  TITLE OF INVENTION:  Activase Promoter
;  FILE REFERENCE: 38-21(53660)C
;  CURRENT APPLICATION NUMBER: US/11/514,704
;  CURRENT FILING DATE:  2006-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4675
;   LENGTH: 1847
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-514-704-4675

Alignment Scores:
Pred. No.:              155             Length:         1847
Score:                  50.00           Matches:        10
Percent Similarity:     70.6%           Conservative:   2
Best Local Similarity:  58.8%           Mismatches:     5
Query Match:            31.2%           Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-1 (1-30) x US-11-514-704-4675 (1-1847)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||   |||:::|||||||||      ||||||      :::|||||||||
Db       1691 GAGCAGTACCAATACCCAACATCTTGACAGGACTTCAGTTCTGAATTGGCT 1641

RESULT 20
US-11-514-704-4674/c
; Sequence 4674, Application US/11514704
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  Wu, Kunsheng
;  APPLICANT:  Dasgupta, Santanu
;  APPLICANT:  Cherian, Shoba
;  APPLICANT:  Jayaprakash, Targolli L
;  TITLE OF INVENTION: Zea mays Ribulose Bisphosphate Carboxylase
;  TITLE OF INVENTION:  Activase Promoter
;  FILE REFERENCE: 38-21(53660)C
;  CURRENT APPLICATION NUMBER: US/11/514,704
;  CURRENT FILING DATE:  2006-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4674
;   LENGTH: 5166
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-514-704-4674

Alignment Scores:
Pred. No.:              516             Length:         5166
Score:                  50.00           Matches:        10
Percent Similarity:     70.6%           Conservative:   2
Best Local Similarity:  58.8%           Mismatches:     5
Query Match:            31.2%           Indels:         0
DB:                     7               Gaps:           0

US-10-758-902-1 (1-30) x US-11-514-704-4674 (1-5166)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||   |||:::|||||||||      ||||||      :::|||||||||
Db       1069 GAGCAGTACCAATACCCAACATCTTGACAGGACTTCAGTTCTGAATTGGCT 1019

RESULT 21
US-11-033-056A-38192
; Sequence 38192, Application US/11033056A
; GENERAL INFORMATION:
```

```
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38192
;   LENGTH: 16669
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-38192

Alignment Scores:
Pred. No.:              2.04e+03        Length:         16669
Score:                  50.00           Matches:        9
Percent Similarity:     68.2%           Conservative:   6
Best Local Similarity:  40.9%           Mismatches:     7
Query Match:            31.2%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-033-056A-38192 (1-16669)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
              |||:::      ||||||||||||   |||:::|||      ::::::   :::|||
Db      10604 ACGTTGTGTCAGAACTTGGGTGAACCTTATAAATATACCCGTTATGTGGCAAACTTATCA 10663

Qy         23 AsnGlu 24
              :::|||
Db      10664 CACGAG 10669

RESULT 22
PCT-US03-41389-353/c
; Sequence 353, Application PC/TUS0341389
; GENERAL INFORMATION:
;  APPLICANT: Sagres Discovery, Inc.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
;  FILE REFERENCE: 20366-020WO1
;  CURRENT APPLICATION NUMBER: PCT/US03/41389
;  CURRENT FILING DATE:  2003-12-22
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 353
;   LENGTH: 24231
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(24231)
;   OTHER INFORMATION: n = A,T,C or G
PCT-US03-41389-353

Alignment Scores:
Pred. No.:              3.16e+03        Length:         24231
Score:                  50.00           Matches:        13
Percent Similarity:     50.0%           Conservative:   0
Best Local Similarity:  50.0%           Mismatches:     3
Query Match:            31.2%           Indels:         10
DB:                     1               Gaps:           1

US-10-758-902-1 (1-30) x PCT-US03-41389-353 (1-24231)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              ||||||   ||||||||||||                                  ||||||
Db       6466 TCCTTTGGCCTTGGCGAGGCT----------------------------AGGAATCGC 6437

Qy         25 LeuAlaLysGlyThrPro 30
              ||||||   |||||||||
Db       6436 CTTGCGCCAGGAACCCCA 6419

RESULT 23
US-11-214-063B-1463
; Sequence 1463, Application US/11214063B
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 084335/166
;  CURRENT APPLICATION NUMBER: US/11/214,063B
;  CURRENT FILING DATE:  2005-08-30
;  PRIOR APPLICATION NUMBER: 10/017,161
;  PRIOR FILING DATE: 2001-12-18
;  PRIOR APPLICATION NUMBER: JP 2001-246789
;  PRIOR FILING DATE: 2001-06-18
;  NUMBER OF SEQ ID NOS: 2070
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1463
;   LENGTH: 418550
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   LOCATION: source
;   FEATURE:
;   LOCATION: (1)..(418550)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (201)..(521)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (130865)..(131002)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (166894)..(167064)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (212423)..(212524)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (227940)..(228005)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (235591)..(235791)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (254720)..(254956)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (302793)..(302853)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (314679)..(314759)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (319930)..(320080)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (323162)..(323294)
```

```
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (337363)..(337470)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (346097)..(346219)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (397729)..(397839)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (402589)..(402813)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (405511)..(405693)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (409581)..(409710)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (415032)..(415149)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (418185)..(418350)
US-11-214-063B-1463

Alignment Scores:
Pred. No.:              8.83e+04        Length:         418550
Score:                  50.00           Matches:        12
Percent Similarity:     46.9%           Conservative:   3
Best Local Similarity:  37.5%           Mismatches:     7
Query Match:            31.2%           Indels:         10
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-214-063B-1463 (1-418550)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu--------- 21
              |||   :::      :::   |||   ||||||||||||:::   ||||||
Db     220164 AGCCTCTCAACATTCCAAGGTTACTCATACCCAACATTTTTAAATGACCTGTCTCCCCCC 220223

Qy         22 --------------------ArgAsnGluLeuAla 26
                                  |||||||||   |||
Db     220224 ATTTCTTCTTAGTAACAAAACAGGAATGAAAGGGCT 220259

RESULT 24
US-11-033-056A-38500/c
; Sequence 38500, Application US/11033056A
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38500
;   LENGTH: 2132949
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-38500

Alignment Scores:
Pred. No.:              5.68e+05        Length:         2132949
Score:                  50.00           Matches:        12
Percent Similarity:     53.6%           Conservative:   3
Best Local Similarity:  42.9%           Mismatches:     13
Query Match:            31.2%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-033-056A-38500 (1-2132949)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||                    |||:::|||      |||||||||:::
Db     173489 TATAATACAGTATTACACTGAAATAGCATAAAATATGATTATGTAAAGTTCATTCAAGAA 173430

Qy         21 LeuArgAsnGluLeuAlaLysGly 28
                :::|||   |||      |||
Db     173429 TGCAAAAATGTTTTACTATTAGGA 173406

RESULT 25
US-10-805-394A-3166
; Sequence 3166, Application US/10805394A
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/10/805,394A
;  CURRENT FILING DATE:  2004-03-22
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3166
;   LENGTH: 4830
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-10-805-394A-3166

Alignment Scores:
Pred. No.:              581             Length:         4830
Score:                  49.50           Matches:        11
Percent Similarity:     65.0%           Conservative:   2
Best Local Similarity:  55.0%           Mismatches:     6
Query Match:            30.9%           Indels:         1
DB:                     6               Gaps:           1

US-10-758-902-1 (1-30) x US-10-805-394A-3166 (1-4830)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||   |||:::   |||         |||   :::|||   |||
Db        211 GCTTATGAGTACCCAACG---ATCCGTAGTTTGGCGCAGCGCCTTGTTGAGGGCGAGCCT 267

RESULT 26
US-11-507-094-13
; Sequence 13, Application US/11507094
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr?ger, Burkhard
```

; APPLICANT: Sch?der, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/11/507,094
; CURRENT FILING DATE: 2006-08-18
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 13
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(4930)
; OTHER INFORMATION: RXA02582
US-11-507-094-13

Alignment Scores:

Pred. No.:	599	Length:	4953
Score:	49.50	Matches:	11
Percent Similarity:	65.0%	Conservative:	2
Best Local Similarity:	55.0%	Mismatches:	6
Query Match:	30.9%	Indels:	1
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-507-094-13 (1-4953)

```
Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||   |||:::   |||          |||   :::|||   |||
Db        311 GCTTATGAGTACCCAACG---ATCCGTAGTTTGGCGCAGCGCCTTGTTGAGGGCGAGCCT 367
```

RESULT 27
US-11-507-094-55
; Sequence 55, Application US/11507094
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kr?ger, Burkhard
; APPLICANT: Sch?der, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/11/507,094
; CURRENT FILING DATE: 2006-08-18
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 55
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(4930)
; OTHER INFORMATION: RXA02582
US-11-507-094-55

Alignment Scores:

Pred. No.:	599	Length:	4953
Score:	49.50	Matches:	11
Percent Similarity:	65.0%	Conservative:	2
Best Local Similarity:	55.0%	Mismatches:	6
Query Match:	30.9%	Indels:	1
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-507-094-55 (1-4953)

```
Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||   |||:::   |||          |||   :::|||   |||
Db        311 GCTTATGAGTACCCAACG---ATCCGTAGTTTGGCGCAGCGCCTTGTTGAGGGCGAGCCT 367
```

RESULT 28
US-10-805-394A-1/c
; Sequence 1, Application US/10805394A
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/10/805,394A
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum

US-10-805-394A-1

Alignment Scores:

Pred. No.:	1.09e+06	Length:	3309400
Score:	49.50	Matches:	11
Percent Similarity:	65.0%	Conservative:	2
Best Local Similarity:	55.0%	Mismatches:	6
Query Match:	30.9%	Indels:	1
DB:	6	Gaps:	1

US-10-758-902-1 (1-30) x US-10-805-394A-1 (1-3309400)

```
Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              ||||||||||||||||||   |||:::   |||         |||   :::|||   |||
Db    3067570 GCTTATGAGTACCCAACG---ATCCGTAGTTTGGCGCAGCGCCTTGTTGAGGGCGAGCCT 3067514
```

RESULT 29
US-60-836-986-2918
; Sequence 2918, Application US/60836986
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Johnson, Richard
; APPLICANT: Marelli, Marcello
; APPLICANT: Li, Xiaojun
; TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 460092.405P1
; CURRENT APPLICATION NUMBER: US/60/836,986
; CURRENT FILING DATE: 2006-08-09
; NUMBER OF SEQ ID NOS: 32934
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2918
; LENGTH: 7224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-836-986-2918

Alignment Scores:

Pred. No.:	1.14e+03	Length:	7224
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	9	Gaps:	0

US-10-758-902-1 (1-30) x US-60-836-986-2918 (1-7224)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   |||||||:::   |||   :::|||:::         |||
Db       5513 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5572

Qy         25 LeuAlaLysGlyThr 29
                 |||:::   |||
Db       5573 TTTGCCCGAGACACC 5587
```

RESULT 30
US-11-437-729-3157
; Sequence 3157, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3157
; LENGTH: 7561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-437-729-3157

Alignment Scores:

Pred. No.:	1.2e+03	Length:	7561
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-437-729-3157 (1-7561)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   |||||||:::   |||   :::|||:::         |||
Db       5477 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5536

Qy         25 LeuAlaLysGlyThr 29
                 |||:::   |||
Db       5537 TTTGCCCGAGACACC 5551
```

RESULT 31
US-60-836-986-2917
; Sequence 2917, Application US/60836986
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Johnson, Richard
; APPLICANT: Marelli, Marcello
; APPLICANT: Li, Xiaojun
; TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 460092.405P1
; CURRENT APPLICATION NUMBER: US/60/836,986
; CURRENT FILING DATE: 2006-08-09
; NUMBER OF SEQ ID NOS: 32934
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2917
; LENGTH: 7561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-836-986-2917

Alignment Scores:

Pred. No.:	1.2e+03	Length:	7561
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	9	Gaps:	0

US-10-758-902-1 (1-30) x US-60-836-986-2917 (1-7561)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   |||||||:::   |||   :::|||:::         |||
Db       5477 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5536

Qy         25 LeuAlaLysGlyThr 29
                 |||:::   |||
Db       5537 TTTGCCCGAGACACC 5551
```

RESULT 32
US-11-437-729-3153
; Sequence 3153, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3153
; LENGTH: 8295
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-437-729-3153

Alignment Scores:

Pred. No.:	1.34e+03	Length:	8295
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-437-729-3153 (1-8295)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::  ||||||:::  |||  :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                |||:::  |||
Db       5321 TTTGCCCGAGACACC 5335
```

RESULT 33
US-11-437-729-3154
; Sequence 3154, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3154
; LENGTH: 8295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-437-729-3154

Alignment Scores:

Pred. No.:	1.34e+03	Length:	8295
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-437-729-3154 (1-8295)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::  ||||||:::  |||  :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                |||:::  |||
Db       5321 TTTGCCCGAGACACC 5335
```

RESULT 34
US-11-437-729-3155
; Sequence 3155, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3155
; LENGTH: 8295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-437-729-3155

Alignment Scores:

Pred. No.:	1.34e+03	Length:	8295
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-437-729-3155 (1-8295)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::  ||||||:::  |||  :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                |||:::  |||
Db       5321 TTTGCCCGAGACACC 5335
```

RESULT 35
US-11-437-729-3159
; Sequence 3159, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3159
; LENGTH: 8295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-437-729-3159

Alignment Scores:

Pred. No.:	1.34e+03	Length:	8295
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-437-729-3159 (1-8295)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::  ||||||:::  |||  :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                |||:::  |||
Db       5321 TTTGCCCGAGACACC 5335
```

RESULT 36
US-11-437-729-3160
; Sequence 3160, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3160
; LENGTH: 8295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-437-729-3160

Alignment Scores:

Pred. No.:	1.34e+03	Length:	8295
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5

```
Best Local Similarity:  40.0%          Mismatches:    10
Query Match:            30.6%          Indels:        0
DB:                     8              Gaps:          0

US-10-758-902-1 (1-30) x US-11-437-729-3160 (1-8295)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                |||:::   |||
Db       5321 TTTGCCCGAGACACC 5335

RESULT 37
US-11-475-062-10037
; Sequence 10037, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10037
;   LENGTH: 8295
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-10037

Alignment Scores:
Pred. No.:              1.34e+03       Length:        8295
Score:                  49.00          Matches:       10
Percent Similarity:     60.0%          Conservative:  5
Best Local Similarity:  40.0%          Mismatches:    10
Query Match:            30.6%          Indels:        0
DB:                     8              Gaps:          0

US-10-758-902-1 (1-30) x US-11-475-062-10037 (1-8295)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                |||:::   |||
Db       5321 TTTGCCCGAGACACC 5335

RESULT 38
US-11-475-062-10038
; Sequence 10038, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10038
;   LENGTH: 8295
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-10038

Alignment Scores:
Pred. No.:              1.34e+03       Length:        8295
Score:                  49.00          Matches:       10
Percent Similarity:     60.0%          Conservative:  5
Best Local Similarity:  40.0%          Mismatches:    10
Query Match:            30.6%          Indels:        0
DB:                     8              Gaps:          0

US-10-758-902-1 (1-30) x US-11-475-062-10038 (1-8295)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                |||:::   |||
Db       5321 TTTGCCCGAGACACC 5335

RESULT 39
US-11-475-062-10039
; Sequence 10039, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10039
;   LENGTH: 8295
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-10039

Alignment Scores:
Pred. No.:              1.34e+03       Length:        8295
Score:                  49.00          Matches:       10
Percent Similarity:     60.0%          Conservative:  5
Best Local Similarity:  40.0%          Mismatches:    10
Query Match:            30.6%          Indels:        0
DB:                     8              Gaps:          0

US-10-758-902-1 (1-30) x US-11-475-062-10039 (1-8295)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                |||:::   |||
Db       5321 TTTGCCCGAGACACC 5335

RESULT 40
US-11-475-062-10041
; Sequence 10041, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10041
;   LENGTH: 8295
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-10041

Alignment Scores:
Pred. No.:              1.34e+03       Length:        8295
Score:                  49.00          Matches:       10
Percent Similarity:     60.0%          Conservative:  5
Best Local Similarity:  40.0%          Mismatches:    10
Query Match:            30.6%          Indels:        0
DB:                     8              Gaps:          0

US-10-758-902-1 (1-30) x US-11-475-062-10041 (1-8295)
```

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                ||:::   |||
Db       5321 TTTGCCCGAGACACC 5335
```

RESULT 41
US-11-475-062-10042
; Sequence 10042, Application US/11475062
; GENERAL INFORMATION:
; APPLICANT: BIRSE, Charles et al.
; TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
; FILE REFERENCE: CL001706
; CURRENT APPLICATION NUMBER: US/11/475,062
; CURRENT FILING DATE: 2006-06-27
; NUMBER OF SEQ ID NOS: 16099
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10042
; LENGTH: 8295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-475-062-10042

Alignment Scores:

Pred. No.:	1.34e+03	Length:	8295
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-475-062-10042 (1-8295)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5261 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5320

Qy         25 LeuAlaLysGlyThr 29
                ||:::   |||
Db       5321 TTTGCCCGAGACACC 5335
```

RESULT 42
US-11-437-729-3156
; Sequence 3156, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3156
; LENGTH: 8521
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-437-729-3156

Alignment Scores:

Pred. No.:	1.38e+03	Length:	8521
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-437-729-3156 (1-8521)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5400 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5459

Qy         25 LeuAlaLysGlyThr 29
                ||:::   |||
Db       5460 TTTGCCCGAGACACC 5474
```

RESULT 43
US-11-475-062-10040
; Sequence 10040, Application US/11475062
; GENERAL INFORMATION:
; APPLICANT: BIRSE, Charles et al.
; TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
; FILE REFERENCE: CL001706
; CURRENT APPLICATION NUMBER: US/11/475,062
; CURRENT FILING DATE: 2006-06-27
; NUMBER OF SEQ ID NOS: 16099
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10040
; LENGTH: 8521
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-475-062-10040

Alignment Scores:

Pred. No.:	1.38e+03	Length:	8521
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-475-062-10040 (1-8521)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5400 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5459

Qy         25 LeuAlaLysGlyThr 29
                ||:::   |||
Db       5460 TTTGCCCGAGACACC 5474
```

RESULT 44
US-11-437-729-3161
; Sequence 3161, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3161
; LENGTH: 9074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-437-729-3161

Alignment Scores:

Pred. No.:	1.48e+03	Length:	9074
Score:	49.00	Matches:	10
Percent Similarity:	60.0%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	10
Query Match:	30.6%	Indels:	0
DB:	8	Gaps:	0

US-10-758-902-1 (1-30) x US-11-437-729-3161 (1-9074)

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      ||||||:::   ||||||:::   |||   :::|||:::         |||
Db       5513 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5572

Qy         25 LeuAlaLysGlyThr 29
                ||:::   |||
```

```
Db       5573 TTTGCCCGAGACACC 5587

RESULT 45
US-11-475-062-10043
; Sequence 10043, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10043
;   LENGTH: 9074
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-10043

Alignment Scores:
Pred. No.:              1.48e+03        Length:         9074
Score:                  49.00           Matches:        10
Percent Similarity:     60.0%           Conservative:   5
Best Local Similarity:  40.0%           Mismatches:     10
Query Match:            30.6%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-475-062-10043 (1-9074)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||       ||||||:::   ||||||:::   |||   :::|||:::        |||
Db       5513 TCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAG 5572

Qy         25 LeuAlaLysGlyThr 29
              |||:::   |||
Db       5573 TTTGCCCGAGACACC 5587

RESULT 46
US-11-033-056A-35955
; Sequence 35955, Application US/11033056A
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35955
;   LENGTH: 30989
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-35955

Alignment Scores:
Pred. No.:              6.26e+03        Length:         30989
Score:                  49.00           Matches:        8
Percent Similarity:     68.4%           Conservative:   5
Best Local Similarity:  42.1%           Mismatches:     6
Query Match:            30.6%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-033-056A-35955 (1-30989)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              :::   ||||||   |||:::||||||:::   :::       |||   |||:::|||
Db       7952 TTTAAGACAGTCATTTTTAGTCTTGGTCAAGTACATCCAGTGCCTGCATTTCTTCAG 8008

RESULT 47
US-11-033-056A-37713
; Sequence 37713, Application US/11033056A
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37713
;   LENGTH: 156814
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-37713

Alignment Scores:
Pred. No.:              4.19e+04        Length:         156814
Score:                  49.00           Matches:        11
Percent Similarity:     60.9%           Conservative:   3
Best Local Similarity:  47.8%           Mismatches:     7
Query Match:            30.6%           Indels:         2
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-033-056A-37713 (1-156814)

Qy          9 GlyGluAlaTyrGlu------TyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||   |||          ||||||::::::   ||||||   |||       |||
Db      29114 GGGGAGGAGTATGTGCGTTTCATACCAACATACCTGAGTGATCTGACAAATGCTTGTGCT 29173

Qy         27 LysGlyThr 29
              :::||||||
Db      29174 GAGGGGACT 29182

RESULT 48
US-11-033-056A-38635
; Sequence 38635, Application US/11033056A
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
```

```
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38635
;   LENGTH: 246604
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-38635

Alignment Scores:
Pred. No.:              7.07e+04        Length:         246604
Score:                  49.00           Matches:        9
Percent Similarity:     73.7%           Conservative:   5
Best Local Similarity:  47.4%           Mismatches:     5
Query Match:            30.6%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-033-056A-38635 (1-246604)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              :::::::||||||:::|||||||||||||      |||:::         ||||||:::
Db     111205 CATTCAACAGTAAACTTTAACCTTGGATCACATTATCAGTGTTCCTTATTCATTAAA 111261

RESULT 49
US-11-033-056A-36751/c
; Sequence 36751, Application US/11033056A
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36751
;   LENGTH: 507300
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-36751

Alignment Scores:
Pred. No.:              1.63e+05        Length:         507300
Score:                  49.00           Matches:        10
Percent Similarity:     57.7%           Conservative:   5
Best Local Similarity:  38.5%           Mismatches:     11
Query Match:            30.6%           Indels:         0
DB:                     8               Gaps:           0

US-10-758-902-1 (1-30) x US-11-033-056A-36751 (1-507300)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||       |||       |||:::||||||   :::   :::|||:::      :::
Db     356763 AACGTAAGGTCCAGCAGGGCAGGTGATGCCTATGTGTTCACCAGTTTCCTTCCCAGTGTT 356704

Qy         22 ArgAsnGluLeuAlaLys 27
                |||||||||   |||
Db     356703 TCAAATGAACTCCACAAA 356686

RESULT 50
US-11-490-374-2108
; Sequence 2108, Application US/11490374
; GENERAL INFORMATION:
;  APPLICANT: KIM, Yeounjin
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001615ORD
;  CURRENT APPLICATION NUMBER: US/11/490,374
;  CURRENT FILING DATE:  2006-07-21
;  NUMBER OF SEQ ID NOS: 2638
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2108
;   LENGTH: 2135
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-490-374-2108

Alignment Scores:
Pred. No.:              332             Length:         2135
Score:                  48.50           Matches:        10
Percent Similarity:     62.5%           Conservative:   5
Best Local Similarity:  41.7%           Mismatches:     6
Query Match:            30.3%           Indels:         3
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-490-374-2108 (1-2135)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        695 GTGATCAAGAAA 706

RESULT 51
US-11-490-374-2110
; Sequence 2110, Application US/11490374
; GENERAL INFORMATION:
;  APPLICANT: KIM, Yeounjin
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001615ORD
;  CURRENT APPLICATION NUMBER: US/11/490,374
;  CURRENT FILING DATE:  2006-07-21
;  NUMBER OF SEQ ID NOS: 2638
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2110
;   LENGTH: 2135
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-490-374-2110

Alignment Scores:
Pred. No.:              332             Length:         2135
Score:                  48.50           Matches:        10
Percent Similarity:     62.5%           Conservative:   5
Best Local Similarity:  41.7%           Mismatches:     6
Query Match:            30.3%           Indels:         3
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-490-374-2110 (1-2135)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
```

```
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        695 GTGATCAAGAAA 706
```

RESULT 52
US-11-431-708-5669
; Sequence 5669, Application US/11431708
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001599-ORD
; CURRENT APPLICATION NUMBER: US/11/431,708
; CURRENT FILING DATE: 2006-05-11
; NUMBER OF SEQ ID NOS: 8544
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5669
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-431-708-5669

Alignment Scores:

Pred. No.:	332	Length:	2135
Score:	48.50	Matches:	10
Percent Similarity:	62.5%	Conservative:	5
Best Local Similarity:	41.7%	Mismatches:	6
Query Match:	30.3%	Indels:	3
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-431-708-5669 (1-2135)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        695 GTGATCAAGAAA 706
```

RESULT 53
US-11-431-708-5671
; Sequence 5671, Application US/11431708
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001599-ORD
; CURRENT APPLICATION NUMBER: US/11/431,708
; CURRENT FILING DATE: 2006-05-11
; NUMBER OF SEQ ID NOS: 8544
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5671
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-431-708-5671

Alignment Scores:

Pred. No.:	332	Length:	2135
Score:	48.50	Matches:	10
Percent Similarity:	62.5%	Conservative:	5
Best Local Similarity:	41.7%	Mismatches:	6
Query Match:	30.3%	Indels:	3
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-431-708-5671 (1-2135)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        695 GTGATCAAGAAA 706
```

RESULT 54
US-11-437-729-5152
; Sequence 5152, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5152
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-437-729-5152

Alignment Scores:

Pred. No.:	332	Length:	2135
Score:	48.50	Matches:	10
Percent Similarity:	62.5%	Conservative:	5
Best Local Similarity:	41.7%	Mismatches:	6
Query Match:	30.3%	Indels:	3
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-437-729-5152 (1-2135)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        695 GTGATCAAGAAA 706
```

RESULT 55
US-11-437-729-5154
; Sequence 5154, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22
; NUMBER OF SEQ ID NOS: 6151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5154
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-437-729-5154

Alignment Scores:

Pred. No.:	332	Length:	2135
Score:	48.50	Matches:	10
Percent Similarity:	62.5%	Conservative:	5
Best Local Similarity:	41.7%	Mismatches:	6
Query Match:	30.3%	Indels:	3
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-437-729-5154 (1-2135)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        695 GTGATCAAGAAA 706
```

```
RESULT 56
US-11-475-062-7780
; Sequence 7780, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7780
;   LENGTH: 2135
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-7780

Alignment Scores:
Pred. No.:                332             Length:         2135
Score:                    48.50           Matches:        10
Percent Similarity:       62.5%           Conservative:   5
Best Local Similarity:    41.7%           Mismatches:     6
Query Match:              30.3%           Indels:         3
DB:                       8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-475-062-7780 (1-2135)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        695 GTGATCAAGAAA 706

RESULT 57
US-11-475-062-7781
; Sequence 7781, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7781
;   LENGTH: 2135
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-7781

Alignment Scores:
Pred. No.:                332             Length:         2135
Score:                    48.50           Matches:        10
Percent Similarity:       62.5%           Conservative:   5
Best Local Similarity:    41.7%           Mismatches:     6
Query Match:              30.3%           Indels:         3
DB:                       8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-475-062-7781 (1-2135)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        695 GTGATCAAGAAA 706

RESULT 58
US-11-475-062-7783
; Sequence 7783, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7783
;   LENGTH: 2135
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-7783

Alignment Scores:
Pred. No.:                332             Length:         2135
Score:                    48.50           Matches:        10
Percent Similarity:       62.5%           Conservative:   5
Best Local Similarity:    41.7%           Mismatches:     6
Query Match:              30.3%           Indels:         3
DB:                       8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-475-062-7783 (1-2135)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        695 GTGATCAAGAAA 706

RESULT 59
US-11-475-062-7784
; Sequence 7784, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7784
;   LENGTH: 2135
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-7784

Alignment Scores:
Pred. No.:                332             Length:         2135
Score:                    48.50           Matches:        10
Percent Similarity:       62.5%           Conservative:   5
Best Local Similarity:    41.7%           Mismatches:     6
Query Match:              30.3%           Indels:         3
DB:                       8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-475-062-7784 (1-2135)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        695 GTGATCAAGAAA 706

RESULT 60
US-11-475-062-9236
; Sequence 9236, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
```

```
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9236
;   LENGTH: 2135
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-9236

Alignment Scores:
Pred. No.:              332          Length:          2135
Score:                  48.50        Matches:         10
Percent Similarity:     62.5%        Conservative:    5
Best Local Similarity:  41.7%        Mismatches:      6
Query Match:            30.3%        Indels:          3
DB:                     8            Gaps:            1

US-10-758-902-1 (1-30) x US-11-475-062-9236 (1-2135)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        695 GTGATCAAGAAA 706

RESULT 61
US-11-475-062-9238
; Sequence 9238, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9238
;   LENGTH: 2135
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-9238

Alignment Scores:
Pred. No.:              332          Length:          2135
Score:                  48.50        Matches:         10
Percent Similarity:     62.5%        Conservative:    5
Best Local Similarity:  41.7%        Mismatches:      6
Query Match:            30.3%        Indels:          3
DB:                     8            Gaps:            1

US-10-758-902-1 (1-30) x US-11-475-062-9238 (1-2135)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        635 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 694

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        695 GTGATCAAGAAA 706

RESULT 62
US-60-836-986-5300
; Sequence 5300, Application US/60836986
; GENERAL INFORMATION:
;  APPLICANT: Hood, Leroy
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Johnson, Richard
;  APPLICANT:  Marelli, Marcello
;  APPLICANT:  Li, Xiaojun
;  TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 460092.405P1
;  CURRENT APPLICATION NUMBER: US/60/836,986
;  CURRENT FILING DATE:  2006-08-09
;  NUMBER OF SEQ ID NOS: 32934
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5300
;   LENGTH: 2393
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-836-986-5300

Alignment Scores:
Pred. No.:              379          Length:          2393
Score:                  48.50        Matches:         10
Percent Similarity:     62.5%        Conservative:    5
Best Local Similarity:  41.7%        Mismatches:      6
Query Match:            30.3%        Indels:          3
DB:                     9            Gaps:            1

US-10-758-902-1 (1-30) x US-60-836-986-5300 (1-2393)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        470 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 529

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        530 GTGATCAAGAAA 541

RESULT 63
US-11-475-062-7782
; Sequence 7782, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7782
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-7782

Alignment Scores:
Pred. No.:              405          Length:          2534
Score:                  48.50        Matches:         10
Percent Similarity:     62.5%        Conservative:    5
Best Local Similarity:  41.7%        Mismatches:      6
Query Match:            30.3%        Indels:          3
DB:                     8            Gaps:            1

US-10-758-902-1 (1-30) x US-11-475-062-7782 (1-2534)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        636 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 695

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        696 GTGATCAAGAAA 707

RESULT 64
US-11-490-374-2107
; Sequence 2107, Application US/11490374
; GENERAL INFORMATION:
;  APPLICANT: KIM, Yeounjin
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
```

```
;  FILE REFERENCE: CL001615ORD
;  CURRENT APPLICATION NUMBER: US/11/490,374
;  CURRENT FILING DATE:  2006-07-21
;  NUMBER OF SEQ ID NOS: 2638
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2107
;   LENGTH: 2653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-490-374-2107

Alignment Scores:
Pred. No.:              428          Length:        2653
Score:                  48.50        Matches:       10
Percent Similarity:     62.5%        Conservative:  5
Best Local Similarity:  41.7%        Mismatches:    6
Query Match:            30.3%        Indels:        3
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-490-374-2107 (1-2653)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        755 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 814

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        815 GTGATCAAGAAA 826

RESULT 65
US-11-490-374-2109
; Sequence 2109, Application US/11490374
; GENERAL INFORMATION:
;  APPLICANT: KIM, Yeounjin
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001615ORD
;  CURRENT APPLICATION NUMBER: US/11/490,374
;  CURRENT FILING DATE:  2006-07-21
;  NUMBER OF SEQ ID NOS: 2638
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2109
;   LENGTH: 2653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-490-374-2109

Alignment Scores:
Pred. No.:              428          Length:        2653
Score:                  48.50        Matches:       10
Percent Similarity:     62.5%        Conservative:  5
Best Local Similarity:  41.7%        Mismatches:    6
Query Match:            30.3%        Indels:        3
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-490-374-2109 (1-2653)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        755 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 814

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        815 GTGATCAAGAAA 826

RESULT 66
US-11-431-708-5668
; Sequence 5668, Application US/11431708
; GENERAL INFORMATION:
;  APPLICANT: RUBEN, Steven
;  TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001599-ORD
;  CURRENT APPLICATION NUMBER: US/11/431,708
;  CURRENT FILING DATE:  2006-05-11
;  NUMBER OF SEQ ID NOS: 8544
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5668
;   LENGTH: 2653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-431-708-5668

Alignment Scores:
Pred. No.:              428          Length:        2653
Score:                  48.50        Matches:       10
Percent Similarity:     62.5%        Conservative:  5
Best Local Similarity:  41.7%        Mismatches:    6
Query Match:            30.3%        Indels:        3
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-431-708-5668 (1-2653)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        755 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 814

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        815 GTGATCAAGAAA 826

RESULT 67
US-11-431-708-5670
; Sequence 5670, Application US/11431708
; GENERAL INFORMATION:
;  APPLICANT: RUBEN, Steven
;  TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001599-ORD
;  CURRENT APPLICATION NUMBER: US/11/431,708
;  CURRENT FILING DATE:  2006-05-11
;  NUMBER OF SEQ ID NOS: 8544
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5670
;   LENGTH: 2653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-431-708-5670

Alignment Scores:
Pred. No.:              428          Length:        2653
Score:                  48.50        Matches:       10
Percent Similarity:     62.5%        Conservative:  5
Best Local Similarity:  41.7%        Mismatches:    6
Query Match:            30.3%        Indels:        3
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-431-708-5670 (1-2653)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        755 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 814

Qy         24 GluLeuAlaLys 27
                 :::   |||
Db        815 GTGATCAAGAAA 826

RESULT 68
US-11-437-729-5150
; Sequence 5150, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5150
```

```
;   LENGTH: 2653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-437-729-5150

Alignment Scores:
Pred. No.:              428          Length:        2653
Score:                  48.50        Matches:       10
Percent Similarity:     62.5%        Conservative:  5
Best Local Similarity:  41.7%        Mismatches:    6
Query Match:            30.3%        Indels:        3
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-437-729-5150 (1-2653)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        755 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 814

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        815 GTGATCAAGAAA 826

RESULT 69
US-11-437-729-5153
; Sequence 5153, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5153
;   LENGTH: 2653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-437-729-5153

Alignment Scores:
Pred. No.:              428          Length:        2653
Score:                  48.50        Matches:       10
Percent Similarity:     62.5%        Conservative:  5
Best Local Similarity:  41.7%        Mismatches:    6
Query Match:            30.3%        Indels:        3
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-437-729-5153 (1-2653)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        755 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 814

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        815 GTGATCAAGAAA 826

RESULT 70
US-11-475-062-9234
; Sequence 9234, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9234
;   LENGTH: 2653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-9234

Alignment Scores:
Pred. No.:              428          Length:        2653
Score:                  48.50        Matches:       10
Percent Similarity:     62.5%        Conservative:  5
Best Local Similarity:  41.7%        Mismatches:    6
Query Match:            30.3%        Indels:        3
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-475-062-9234 (1-2653)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        755 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 814

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        815 GTGATCAAGAAA 826

RESULT 71
US-11-475-062-9237
; Sequence 9237, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9237
;   LENGTH: 2653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-475-062-9237

Alignment Scores:
Pred. No.:              428          Length:        2653
Score:                  48.50        Matches:       10
Percent Similarity:     62.5%        Conservative:  5
Best Local Similarity:  41.7%        Mismatches:    6
Query Match:            30.3%        Indels:        3
DB:                     8            Gaps:          1

US-10-758-902-1 (1-30) x US-11-475-062-9237 (1-2653)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPhe---------IleGlnAspLeuArgAsn 23
              |||:::|||   :::|||||||||||||   :::         :::   ||||||   |||
Db        755 AACGTGGGAATGTCGTATGAGTATCCTGAATACTTTTTGGATGTTCCTGACTTGGACAAT 814

Qy         24 GluLeuAlaLys 27
                :::   |||
Db        815 GTGATCAAGAAA 826

RESULT 72
US-11-033-056A-36451/c
; Sequence 36451, Application US/11033056A
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
```

; CURRENT APPLICATION NUMBER: US/11/033,056A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,382
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: 60/536,163
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 38888
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36451
; LENGTH: 99610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-033-056A-36451

Alignment Scores:

Pred. No.:	3e+04	Length:	99610
Score:	48.50	Matches:	11
Percent Similarity:	66.7%	Conservative:	1
Best Local Similarity:	61.1%	Mismatches:	5
Query Match:	30.3%	Indels:	1
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-033-056A-36451 (1-99610)

```
Qy          3 ThrValSerPheAsnLeu---GlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||   ||||||||||||   |||      |||   ||||||   ||||||:::
Db      21954 ACTTTCTCATTTAACCTGTGAGGTAGGTATTACCATTATCCCCATTTTATAGAG 21901
```

RESULT 73
US-11-033-056A-36452/c
; Sequence 36452, Application US/11033056A
; GENERAL INFORMATION:
; APPLICANT: STUART, ROBERT O.
; APPLICANT: STUART, ELIZABETH DUFF
; APPLICANT: WACHSMAN, WILLIAM
; APPLICANT: MERCOLA, DANIEL
; APPLICANT: MCCLELLAND, MICHAEL
; APPLICANT: WANG-RODRIGUEZ, JESSICA
; APPLICANT: TARIN, DAVID
; APPLICANT: BERRY, CHARLES C.
; APPLICANT: ARDEN, KAREN
; APPLICANT: WASSERMAN, LINDA
; APPLICANT: GOODISON, STEVEN
; APPLICANT: KLACANSKY, IGOR
; TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
; FILE REFERENCE: 15670-073001
; CURRENT APPLICATION NUMBER: US/11/033,056A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,382
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: 60/536,163
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 38888
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36452
; LENGTH: 99610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-033-056A-36452

Alignment Scores:

Pred. No.:	3e+04	Length:	99610
Score:	48.50	Matches:	11
Percent Similarity:	66.7%	Conservative:	1
Best Local Similarity:	61.1%	Mismatches:	5
Query Match:	30.3%	Indels:	1
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-033-056A-36452 (1-99610)

```
Qy          3 ThrValSerPheAsnLeu---GlyGluAlaTyrGluTyrProThrPheIleGln 19
              |||   ||||||||||||   |||      |||   ||||||   ||||||:::
Db      21954 ACTTTCTCATTTAACCTGTGAGGTAGGTATTACCATTATCCCCATTTTATAGAG 21901
```

RESULT 74
US-11-033-056A-37757
; Sequence 37757, Application US/11033056A
; GENERAL INFORMATION:
; APPLICANT: STUART, ROBERT O.
; APPLICANT: STUART, ELIZABETH DUFF
; APPLICANT: WACHSMAN, WILLIAM
; APPLICANT: MERCOLA, DANIEL
; APPLICANT: MCCLELLAND, MICHAEL
; APPLICANT: WANG-RODRIGUEZ, JESSICA
; APPLICANT: TARIN, DAVID
; APPLICANT: BERRY, CHARLES C.
; APPLICANT: ARDEN, KAREN
; APPLICANT: WASSERMAN, LINDA
; APPLICANT: GOODISON, STEVEN
; APPLICANT: KLACANSKY, IGOR
; TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
; FILE REFERENCE: 15670-073001
; CURRENT APPLICATION NUMBER: US/11/033,056A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,382
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: 60/536,163
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 38888
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37757
; LENGTH: 131999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-033-056A-37757

Alignment Scores:

Pred. No.:	4.17e+04	Length:	131999
Score:	48.50	Matches:	12
Percent Similarity:	65.4%	Conservative:	5
Best Local Similarity:	46.2%	Mismatches:	8
Query Match:	30.3%	Indels:	1
DB:	8	Gaps:	1

US-10-758-902-1 (1-30) x US-11-033-056A-37757 (1-131999)

```
Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu--- 21
              :::   |||:::||||||   ||||||:::   |||   |||:::   |||   |||
Db      50535 TCTACCTCATACAATTTGGTGGAAGCTTTTATGTATAATACTTACAGTCAGCATTTGGGG 50594

Qy         22 ArgAsnGluLeuAlaLys 27
              |||   ||||||   :::
Db      50595 AGGGAGGAATTGGGGGAA 50612
```

RESULT 75
PCT-US06-20103-1
; Sequence 1, Application PC/TUS0620103
; GENERAL INFORMATION:
; APPLICANT: University of Maryland Biotechnology Institute
; APPLICANT: Belas, Robert M.
; APPLICANT: Todd, Miller R.
; APPLICANT: Bruhn, Jesper B.
; TITLE OF INVENTION: SILICIBACTER SP. STRAIN USEFUL FOR GENETIC TRANSFORMATION OF
; TITLE OF INVENTION: MARINE ALGAE AND PRODUCTION OF ANTIBIOTIC AGENTS
; FILE REFERENCE: 4115-225 PCT
; CURRENT APPLICATION NUMBER: PCT/US06/20103
; CURRENT FILING DATE: 2006-06-05
; PRIOR APPLICATION NUMBER: US 60/683,763
; PRIOR FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: US 60/718,542
; PRIOR FILING DATE: 2005-09-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 663814
; TYPE: DNA

; ORGANISM: Silicibacter sp.
PCT-US06-20103-1

Alignment Scores:
Pred. No.: 2.7e+05 Length: 663814
Score: 48.50 Matches: 12
Percent Similarity: 66.7% Conservative: 4
Best Local Similarity: 50.0% Mismatches: 7
Query Match: 30.3% Indels: 1
DB: 1 Gaps: 1

US-10-758-902-1 (1-30) x PCT-US06-20103-1 (1-663814)

Qy 6 PheAsnLeuGlyGluAlaTyr---GluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
Db 164852 TTTACTCTTGGTCAGGCATTCGGCGAGTTTGAAACGGGTATTCTGGAACTGCGTGAGCGG 164911

Qy 25 LeuAlaLysGly 28
Db 164912 CCCGCCAAAGGC 164923

RESULT 76
US-11-371-354-67580
; Sequence 67580, Application US/11371354
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67580
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-371-354-67580

Alignment Scores:
Pred. No.: 243 Length: 1383
Score: 48.00 Matches: 9
Percent Similarity: 68.4% Conservative: 4
Best Local Similarity: 47.4% Mismatches: 6
Query Match: 30.0% Indels: 0
DB: 8 Gaps: 0

US-10-758-902-1 (1-30) x US-11-371-354-67580 (1-1383)

Qy 10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
Db 594 CAAGCCCCACAAGTGCCCACATTGCTCCAAGACCTTCGCCAACAGCTCCTACCTGGC 650

RESULT 77
US-11-371-354-73254/c
; Sequence 73254, Application US/11371354
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73254
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-371-354-73254

Alignment Scores:
Pred. No.: 292 Length: 1617
Score: 48.00 Matches: 11
Percent Similarity: 48.1% Conservative: 2
Best Local Similarity: 40.7% Mismatches: 4
Query Match: 30.0% Indels: 10
DB: 8 Gaps: 1

US-10-758-902-1 (1-30) x US-11-371-354-73254 (1-1617)

Qy 14 TyrProThrPheIleGlnAspLeuArgAsnGlu---------- 24
Db 595 TACCCCCTATTTGTGCAAGACTGTGCAAATCAGTGTCAAGTGTGTGCAGCTGGCCTGGAG 536

Qy 25 ---LeuAlaLysGlyThrPro 30
Db 535 GGGCTGGCCCTGGGGACTCCC 515

RESULT 78
US-11-433-832-8527
; Sequence 8527, Application US/11433832
; GENERAL INFORMATION:
; APPLICANT: Cooper, Matthew
; APPLICANT: Kinch, Deborah
; APPLICANT: Rosenberg, Michael
; APPLICANT: Subramaniam, S. Sai
; APPLICANT: Szak, Suzanne
; APPLICANT: Li, Huo
; APPLICANT: Bandaru, Raj
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary to
; TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
; FILE REFERENCE: 2159.0290002
; CURRENT APPLICATION NUMBER: US/11/433,832
; CURRENT FILING DATE: 2006-05-15
; NUMBER OF SEQ ID NOS: 48714
; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 8527
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Macaca Fascicularis
US-11-433-832-8527

Alignment Scores:
Pred. No.: 336 Length: 1826

```
Score:                  48.00          Matches:        7
Percent Similarity:     71.4%          Conservative:   8
Best Local Similarity:  33.3%          Mismatches:     6
Query Match:            30.0%          Indels:         0
DB:                     8              Gaps:           0

US-10-758-902-1 (1-30) x US-11-433-832-8527 (1-1826)

Qy          4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
              :::||||||   :::|||:::   ::::::||||||      ::::::      ||||||
Db        732 ATATCTTTTTAGATTGGTAAGATTTTTCAGTACCCAATGCTGGTGAGAAAGTGGAGAAAT 791

Qy         24 Glu 24
              :::
Db        792 AAA 794

RESULT 79
US-11-414-403-140
; Sequence 140, Application US/11414403
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
;  FILE REFERENCE: P025035WO
;  CURRENT APPLICATION NUMBER: US/11/414,403
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US/10/312,273
;  PRIOR FILING DATE: 2003-05-05
;  PRIOR APPLICATION NUMBER: 0016363.4
;  PRIOR FILING DATE: 2000-07-03
;  PRIOR APPLICATION NUMBER: 0017047.2
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 0017983.8
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 0019368.0
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: 0020440.4
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: 0022583.9
;  PRIOR FILING DATE: 2000-09-14
;  PRIOR APPLICATION NUMBER: 0027549.5
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: 0031706.5
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 664
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 140
;   LENGTH: 2526
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-11-414-403-140

Alignment Scores:
Pred. No.:              492            Length:         2526
Score:                  48.00          Matches:        10
Percent Similarity:     68.2%          Conservative:   5
Best Local Similarity:  45.5%          Mismatches:     3
Query Match:            30.0%          Indels:         4
DB:                     8              Gaps:           1

US-10-758-902-1 (1-30) x US-11-414-403-140 (1-2526)

Qy         10 GluAlaTyrGluTyrProThrPhe----------IleGlnAspLeuArgAsnGluLeu 25
              :::   |||:::||||||||||||          ::::::|||   |||   ||||||
Db       2325 CAAATGTACGACTACCCTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAACTT 2384

Qy         26 AlaLys 27
              :::|||
Db       2385 AGCAAG 2390

RESULT 80
US-10-433-793A-82/c
; Sequence 82, Application US/10433793A
; GENERAL INFORMATION:
;  APPLICANT: Schacht, Oliver
;  TITLE OF INVENTION: DIAGNOSIS OF DISEASES ASSOCIATED WITH ANGIOGENESIS
;  FILE REFERENCE: 47675-185
;  CURRENT APPLICATION NUMBER: US/10/433,793A
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: PCT/EP01/14320
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: DE 10061338.1
;  PRIOR FILING DATE: 2000-12-06
;  NUMBER OF SEQ ID NOS: 212
; SEQ ID NO 82
;   LENGTH: 3046
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-433-793A-82

Alignment Scores:
Pred. No.:              613            Length:         3046
Score:                  48.00          Matches:        7
Percent Similarity:     70.0%          Conservative:   7
Best Local Similarity:  35.0%          Mismatches:     6
Query Match:            30.0%          Indels:         0
DB:                     6              Gaps:           0

US-10-758-902-1 (1-30) x US-10-433-793A-82 (1-3046)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              :::   |||   ||||||   |||:::::::::::||||||::::::         |||
Db       450 CAACGTTATACATACCCCGTATTTCTACGAAATATTCGAAACGACGTAAAAACTAAAACC 391

RESULT 81
US-11-514-704-24120/c
; Sequence 24120, Application US/11514704
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  Wu, Kunsheng
;  APPLICANT:  Dasgupta, Santanu
;  APPLICANT:  Cherian, Shoba
;  APPLICANT:  Jayaprakash, Targolli L
;  TITLE OF INVENTION: Zea mays Ribulose Bisphosphate Carboxylase
;  TITLE OF INVENTION:  Activase Promoter
;  FILE REFERENCE: 38-21(53660)C
;  CURRENT APPLICATION NUMBER: US/11/514,704
;  CURRENT FILING DATE:  2006-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24120
;   LENGTH: 4161
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-514-704-24120

Alignment Scores:
Pred. No.:              883            Length:         4161
Score:                  48.00          Matches:        7
Percent Similarity:     70.6%          Conservative:   5
Best Local Similarity:  41.2%          Mismatches:     5
Query Match:            30.0%          Indels:         0
DB:                     7              Gaps:           0

US-10-758-902-1 (1-30) x US-11-514-704-24120 (1-4161)

Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||:::||||||   |||:::   ||||||      ::::::   :::|||
Db       1424 TACGACTACCCGGAGTTCGTCGCCGACCTGGCCAAGCAGGTGAAGCAGGGG 1374

RESULT 82
US-11-514-704-18783
; Sequence 18783, Application US/11514704
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
```

```
;  APPLICANT:  Wu, Kunsheng
;  APPLICANT:  Dasgupta, Santanu
;  APPLICANT:  Cherian, Shoba
;  APPLICANT:  Jayaprakash, Targolli L
;  TITLE OF INVENTION: Zea mays Ribulose Bisphosphate Carboxylase
;  TITLE OF INVENTION:  Activase Promoter
;  FILE REFERENCE: 38-21(53660)C
;  CURRENT APPLICATION NUMBER: US/11/514,704
;  CURRENT FILING DATE:  2006-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18783
;   LENGTH: 5640
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (79)..(79)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (88)..(88)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (104)..(104)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (149)..(149)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (185)..(185)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (213)..(213)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (223)..(223)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (275)..(275)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-514-704-18783

Alignment Scores:
Pred. No.:                1.26e+03        Length:         5640
Score:                    48.00           Matches:        7
Percent Similarity:       81.2%           Conservative:   6
Best Local Similarity:    43.8%           Mismatches:     3
Query Match:              30.0%           Indels:         0
DB:                       7               Gaps:           0

US-10-758-902-1 (1-30) x US-11-514-704-18783 (1-5640)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              ::::::|||   |||:::   :::||||||::::::   |||||||||
Db       1380 CAGTGGCCTGCCTTTGTTGATGAGCTCCGCCATGACGCAGCCAAGGGA 1427

RESULT 83
PCT-US03-41389-26/c
; Sequence 26, Application PC/TUS0341389
; GENERAL INFORMATION:
;  APPLICANT: Sagres Discovery, Inc.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
;  FILE REFERENCE: 20366-020WO1
;  CURRENT APPLICATION NUMBER: PCT/US03/41389
;  CURRENT FILING DATE:  2003-12-22
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 687411
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(687411)
;   OTHER INFORMATION: n = A,T,C or G
PCT-US03-41389-26

Alignment Scores:
Pred. No.:                3.4e+05         Length:         687411
Score:                    48.00           Matches:        8
Percent Similarity:       73.7%           Conservative:   6
Best Local Similarity:    42.1%           Mismatches:     5
Query Match:              30.0%           Indels:         0
DB:                       1               Gaps:           0

US-10-758-902-1 (1-30) x PCT-US03-41389-26 (1-687411)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGln 19
              :::|||   |||:::|||:::      |||:::|||   :::|||:::|||   |||
Db     618175 TTCAACAAAGTCAATTTTCATTTTTTGAAAGCTACATTTTTCCTTCCTTTTATCAA 618119

RESULT 84
US-10-833-833-125
; Sequence 125, Application US/10833833
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  APPLICANT:  Lai, Albert
;  APPLICANT:  Tse, Christin
;  APPLICANT:  Fattaey, Ali
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-038001
;  CURRENT APPLICATION NUMBER: US/10/833,833
;  CURRENT FILING DATE:  2004-04-27
;  NUMBER OF SEQ ID NOS: 175
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125
;   LENGTH: 1130575
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1130575)
;   OTHER INFORMATION: n = A, C, G, or T/U
US-10-833-833-125

Alignment Scores:
Pred. No.:                5.94e+05        Length:         1130575
Score:                    48.00           Matches:        11
Percent Similarity:       61.9%           Conservative:   2
Best Local Similarity:    52.4%           Mismatches:     8
Query Match:              30.0%           Indels:         0
DB:                       6               Gaps:           0

US-10-758-902-1 (1-30) x US-10-833-833-125 (1-1130575)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              |||   ||||||         |||||||||:::|||||||||      |||      :::
Db      89387 CTGTGTGAAGCAATATACCTACCCACCTTCTTACAGGACCTGAGCCTGGAGCAAGGAAGG 89446

Qy         28 Gly 28
              |||
Db      89447 GGT 89449

RESULT 85
US-11-033-056A-38500
; Sequence 38500, Application US/11033056A
```

```
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38500
;   LENGTH: 2132949
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-38500

Alignment Scores:
Pred. No.:              1.17e+06      Length:          2132949
Score:                  48.00         Matches:         8
Percent Similarity:     70.0%         Conservative:    6
Best Local Similarity:  40.0%         Mismatches:      6
Query Match:            30.0%         Indels:          0
DB:                     8             Gaps:            0

US-10-758-902-1 (1-30) x US-11-033-056A-38500 (1-2132949)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||      :::|||   ||||||:::      :::|||||||:::   ::::::|||
Db    1992056 TATAATAATTGAAACTTTGCCCTTGGAAAACTAGTTCAATATCCATCAGTCCTCAGGGAC 1992115

RESULT 86
US-11-033-056A-36422/c
; Sequence 36422, Application US/11033056A
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36422
;   LENGTH: 177481
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-36422

Alignment Scores:
Pred. No.:              8.69e+04      Length:          177481
Score:                  47.50         Matches:         11
Percent Similarity:     52.0%         Conservative:    2
Best Local Similarity:  44.0%         Mismatches:      9
Query Match:            29.7%         Indels:          3
DB:                     8             Gaps:            1

US-10-758-902-1 (1-30) x US-11-033-056A-36422 (1-177481)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGln---------AspLeuArgAsnGluLeu 25
              |||      ||||||   |||  ||||||            |||   |||   :::|||
Db       7394 GGTTCACCCTATGAATAGCCAGCCTTCATTGACTAAGTGACTGACAGAAGGAGGCAACTG 7335

Qy         26 AlaLysGlyThrPro 30
                ::::|||   |||
Db       7334 TGCAGAGGCATGCCC 7320

RESULT 87
US-60-819-087-10/c
; Sequence 10, Application US/60819087
; GENERAL INFORMATION:
;  APPLICANT: Chelsky, Daniel
;  APPLICANT:  Kearney, Paul E
;  APPLICANT:  Paramithiotis, Eustache
;  APPLICANT:  Hamaidi, Lyes
;  APPLICANT:  Kondejewski, Leslie H
;  APPLICANT:  Lanoix, Joel
;  APPLICANT:  Hugo, Patrice
;  TITLE OF INVENTION: TAT-052 AND METHODS OF ASSESSING AND TREATING CANCER
;  FILE REFERENCE: 50111-109001
;  CURRENT APPLICATION NUMBER: US/60/819,087
;  CURRENT FILING DATE:  2006-07-07
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
;   LENGTH: 177492
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-819-087-10

Alignment Scores:
Pred. No.:              8.69e+04      Length:          177492
Score:                  47.50         Matches:         11
Percent Similarity:     52.0%         Conservative:    2
Best Local Similarity:  44.0%         Mismatches:      9
Query Match:            29.7%         Indels:          3
DB:                     9             Gaps:            1

US-10-758-902-1 (1-30) x US-60-819-087-10 (1-177492)

Qy          9 GlyGluAlaTyrGluTyrProThrPheIleGln----------AspLeuArgAsnGluLeu 25
              |||      ||||||   |||  ||||||            |||   |||   :::|||
Db       7394 GGTTCACCCTATGAATAGCCAGCCTTCATTGACTAAGTGACTGACAGAAGGAGGCAACTG 7335

Qy         26 AlaLysGlyThrPro 30
                ::::|||   |||
Db       7334 TGCAGAGGCATGCCC 7320

RESULT 88
US-11-033-056A-37336
; Sequence 37336, Application US/11033056A
; GENERAL INFORMATION:
;  APPLICANT: STUART, ROBERT O.
;  APPLICANT:  STUART, ELIZABETH DUFF
;  APPLICANT:  WACHSMAN, WILLIAM
;  APPLICANT:  MERCOLA, DANIEL
;  APPLICANT:  MCCLELLAND, MICHAEL
;  APPLICANT:  WANG-RODRIGUEZ, JESSICA
;  APPLICANT:  TARIN, DAVID
;  APPLICANT:  BERRY, CHARLES C.
```

```
;  APPLICANT:  ARDEN, KAREN
;  APPLICANT:  WASSERMAN, LINDA
;  APPLICANT:  GOODISON, STEVEN
;  APPLICANT:  KLACANSKY, IGOR
;  TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
;  FILE REFERENCE: 15670-073001
;  CURRENT APPLICATION NUMBER: US/11/033,056A
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 60/535,382
;  PRIOR FILING DATE: 2004-01-09
;  PRIOR APPLICATION NUMBER: 60/536,163
;  PRIOR FILING DATE: 2004-01-12
;  NUMBER OF SEQ ID NOS: 38888
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37336
;   LENGTH: 265847
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-033-056A-37336

Alignment Scores:
Pred. No.:              1.39e+05        Length:         265847
Score:                  47.50           Matches:        8
Percent Similarity:     59.3%           Conservative:   8
Best Local Similarity:  29.6%           Mismatches:     6
Query Match:            29.7%           Indels:         5
DB:                     8               Gaps:           1

US-10-758-902-1 (1-30) x US-11-033-056A-37336 (1-265847)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyr----------GluTyrProThr 16
              |||   |||::::::      ||||||   |||              ||||||
Db      87457 AACAATGTAGCCTATACTTTTGGAGAGGGGTATATTTAACAGAAATAAGAATATAAAGAA 87516

Qy         17 PheIleGlnAspLeuArgAsn 23
              ::::::::::::::::::|||
Db      87517 TATGTGAAGAACATAAAGAAT 87537

RESULT 89
US-10-961-644A-1
; Sequence 1, Application US/10961644A
; GENERAL INFORMATION:
;  APPLICANT: PRIDMORE, Raymond
;  APPLICANT:  MOLLET, Beat
;  APPLICANT:  ARIGONI, Fabrizio
;  APPLICANT:  HERMANNS, Josef
;  TITLE OF INVENTION: LA1-THE GENOME OF A LACTOBACILLUS STRAIN
;  FILE REFERENCE: 112701-523
;  CURRENT APPLICATION NUMBER: US/10/961,644A
;  CURRENT FILING DATE:  2004-10-08
;  PRIOR APPLICATION NUMBER: PCT/EP03/02885
;  PRIOR FILING DATE: 2003-03-19
;  PRIOR APPLICATION NUMBER: EP 02007932.3
;  PRIOR FILING DATE: 2002-04-09
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1983043
;   TYPE: DNA
;   ORGANISM: Lactobacillus johnsonii
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1788207)..(1788207)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1788238)..(1788238)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1788240)..(1788240)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1788252)..(1788252)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1788269)..(1788269)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1788279)..(1788279)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1788282)..(1788282)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1788284)..(1788284)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1790068)..(1790068)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1980697)..(1980697)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1980698)..(1980698)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1980699)..(1980699)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1980700)..(1980700)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1980701)..(1980706)
;   OTHER INFORMATION: n may be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1982537)..(1982546)
;   OTHER INFORMATION: n may be a, c, g or t
US-10-961-644A-1

Alignment Scores:
Pred. No.:              1.29e+06        Length:         1983043
Score:                  47.50           Matches:        11
Percent Similarity:     51.7%           Conservative:   4
Best Local Similarity:  37.9%           Mismatches:     11
Query Match:            29.7%           Indels:         3
DB:                     6               Gaps:           1

US-10-758-902-1 (1-30) x US-10-961-644A-1 (1-1983043)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              ||||||      |||   ||||||:::   |||         :::|||:::   |||
Db    1292156 AACACTTCTGAATTCCCATTGGGCGACCGCTATTCAAATGGATCTTTTGTACTAGAC--- 1292212

Qy         22 ArgAsnGluLeuAlaLysGlyThrPro 30
                    :::      |||||||||
Db    1292213 ------CCAATGACAGATGGGACTCCT 1292233

RESULT 90
US-11-491-371-50837/c
; Sequence 50837, Application US/11491371
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules  Associated With
```

```
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: P02252US03/15877C
;  CURRENT APPLICATION NUMBER: US/11/491,371
;  CURRENT FILING DATE:  2006-07-24
;  PRIOR APPLICATION NUMBER: US 09/606,977
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: US 60/141,233
;  PRIOR FILING DATE: 1999-06-29
;  NUMBER OF SEQ ID NOS: 82359
; SEQ ID NO 50837
;   LENGTH: 353
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(353)
;   OTHER INFORMATION: unsure at all n locations
US-11-491-371-50837

Alignment Scores:
Pred. No.:              72.8          Length:          353
Score:                  47.00         Matches:         9
Percent Similarity:     62.5%         Conservative:    1
Best Local Similarity:  56.2%         Mismatches:      6
Query Match:            29.4%         Indels:          0
DB:                     8             Gaps:            0

US-10-758-902-1 (1-30) x US-11-491-371-50837 (1-353)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThr 16
              |||:::                |||   ||||||||||||||||||||
Db        111 TATGATGCAACACATATAACGCTGTAGGAAGCATATGAATACCCCACT 64

RESULT 91
US-10-582-413-7/c
; Sequence 7, Application US/10582413
; GENERAL INFORMATION:
;  APPLICANT: Ohtomo, Toshihiko
;  APPLICANT:  Yabuta, Naohiro
;  APPLICANT:  Tsunoda, Hiroyuki
;  APPLICANT:  Tsuchiya, Masayuki
;  TITLE OF INVENTION: Methods for enhancing antibody activity
;  FILE REFERENCE: 14875-164US1
;  CURRENT APPLICATION NUMBER: US/10/582,413
;  CURRENT FILING DATE:  2006-06-09
;  PRIOR APPLICATION NUMBER: PCT/JP2004/018493
;  PRIOR FILING DATE: 2004-12-10
;  PRIOR APPLICATION NUMBER: JP 2003-415760
;  PRIOR FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 396
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(396)
;   OTHER INFORMATION:
US-10-582-413-7

Alignment Scores:
Pred. No.:              83.3          Length:          396
Score:                  47.00         Matches:         8
Percent Similarity:     70.0%         Conservative:    6
Best Local Similarity:  40.0%         Mismatches:      6
Query Match:            29.4%         Indels:          0
DB:                     6             Gaps:            0

US-10-758-902-1 (1-30) x US-10-582-413-7 (1-396)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              |||:::   :::|||||||   ::::::|||:::   |||   :::   |||   ||||||
```

```
Db         76 GAGTCATCACAATATCCCCAATGGCTCCAGGAATCCAGAACACAAGCAGCCCCAGGAACT 17

RESULT 92
US-10-363-345B-15631/c
; Sequence 15631, Application US/10363345B
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: 82010
;  CURRENT APPLICATION NUMBER: US/10/363,345B
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 15631
;   LENGTH: 721
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 15631
US-10-363-345B-15631

Alignment Scores:
Pred. No.:              168           Length:          721
Score:                  47.00         Matches:         10
Percent Similarity:     53.3%         Conservative:    6
Best Local Similarity:  33.3%         Mismatches:      14
Query Match:            29.4%         Indels:          0
DB:                     6             Gaps:            0

US-10-758-902-1 (1-30) x US-10-363-345B-15631 (1-721)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||:::      ::::::|||      :::      |||   |||      ::::::
Db        338 TACGACCGAAACGCTTACAACTACCCGAAACGAAACGAACGACCCCAAACCCTCGAACAT 279

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||||||||      ||||||      |||
Db        278 CTTCGAAACACCCGCGCCAAATCTAATCCC 249

RESULT 93
US-10-363-345B-15632
; Sequence 15632, Application US/10363345B
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: 82010
;  CURRENT APPLICATION NUMBER: US/10/363,345B
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40723
; SEQ ID NO 15632
;   LENGTH: 721
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 15632
US-10-363-345B-15632

Alignment Scores:
Pred. No.:              168           Length:          721
Score:                  47.00         Matches:         10
Percent Similarity:     53.3%         Conservative:    6
Best Local Similarity:  33.3%         Mismatches:      14
Query Match:            29.4%         Indels:          0
DB:                     6             Gaps:            0

US-10-758-902-1 (1-30) x US-10-363-345B-15632 (1-721)
```

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||:::     ::::::|||     :::    |||   |||     ::::::
Db        384 TACGACCGAAACGCTTACAACTACCCGAAACGAAACGAACGACCCCAAACCCTCGAACAT 443

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||||||||     ||||||     |||
Db        444 CTTCGAAACACCCGCGCCAAATCTAATCCC 473

RESULT 94
US-10-536-184-157/c
; Sequence 157, Application US/10536184
; GENERAL INFORMATION:
;  APPLICANT: JORGENSEN, CLAUS BOTTCHER
;  APPLICANT:  CIRERA, SUSANNA
;  APPLICANT:  ARCHIBALD, ALAN
;  APPLICANT:  ANDERSSON, LEIF
;  APPLICANT:  FREDHOLM, MERETE
;  APPLICANT:  EDFORS-LILJA, INGER
;  TITLE OF INVENTION: PORCINE POLYMORPHISMS AND METHODS FOR
;  TITLE OF INVENTION:  DETECTING THEM
;  FILE REFERENCE: 030307-0261
;  CURRENT APPLICATION NUMBER: US/10/536,184
;  CURRENT FILING DATE:  2005-05-24
;  PRIOR APPLICATION NUMBER: PCT/DK03/000807
;  PRIOR FILING DATE: 2003-11-25
;  PRIOR APPLICATION NUMBER: 60/428,738
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: DK PA 2002 01819
;  PRIOR FILING DATE: 2002-11-25
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: Patentin Version 3.3
; SEQ ID NO 157
;   LENGTH: 1753
;   TYPE: DNA
;   ORGANISM: Sus scrofa
US-10-536-184-157

Alignment Scores:
Pred. No.:              476          Length:          1753
Score:                  47.00        Matches:         10
Percent Similarity:     73.3%        Conservative:    1
Best Local Similarity:  66.7%        Mismatches:      4
Query Match:            29.4%        Indels:          0
DB:                     6            Gaps:            0

US-10-758-902-1 (1-30) x US-10-536-184-157 (1-1753)

Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              |||   ||||||   :::||||||   |||   ||||||||||
Db       1649 CCTGACTTCATCTGGGAGCTGAGGAGAGAAGAGGCAAAGGGTACA 1605

RESULT 95
US-10-309-407-347
; Sequence 347, Application US/10309407
; GENERAL INFORMATION:
;  APPLICANT: Busby, Robert
;  APPLICANT:  Cali, Brian
;  APPLICANT:  Hecht, Peter
;  APPLICANT:  Holtzman, Douglas
;  APPLICANT:  Madden, Kevin T.
;  APPLICANT:  Maxon, Mary
;  APPLICANT:  Milne,  Todd  G.
;  APPLICANT:  Norman, Thea
;  APPLICANT:  Royer, John C.
;  APPLICANT:  Silva, Jeff
;  APPLICANT:  Summers, Eric F.
;  APPLICANT:  Zhang, Lixin
;  APPLICANT:  Mayorga, Maria
;  APPLICANT:  Feibelman, Toby
;  APPLICANT:  Doten, Reed
;  TITLE OF INVENTION: METHODS FOR IMPROVING SECONDARY
;  TITLE OF INVENTION:  METABOLITE PRODUCTION OF FUNGI
;  FILE REFERENCE: 14184-023001
;  CURRENT APPLICATION NUMBER: US/10/309,407
;  CURRENT FILING DATE:  2002-12-03
;  PRIOR APPLICATION NUMBER: US 09/691,499
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: US 09/487,558
;  PRIOR FILING DATE: 2000-01-19
;  PRIOR APPLICATION NUMBER: US 60/160,587
;  PRIOR FILING DATE: 1999-10-20
;  NUMBER OF SEQ ID NOS: 496
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 347
;   LENGTH: 2358
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
US-10-309-407-347

Alignment Scores:
Pred. No.:              674          Length:          2358
Score:                  47.00        Matches:         8
Percent Similarity:     68.4%        Conservative:    5
Best Local Similarity:  42.1%        Mismatches:      6
Query Match:            29.4%        Indels:          0
DB:                     6            Gaps:            0

US-10-758-902-1 (1-30) x US-10-309-407-347 (1-2358)

Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro 30
              |||   ||||||   ||||||:::|||:::::::::   |||   :::      |||
Db       1510 TATCTTTATCCCTTGTTCATCAGGGATATTCAGAGCGTATTGAAACAAAATAATCCA 1566

RESULT 96
US-11-433-832-46627
; Sequence 46627, Application US/11433832
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Matthew
;  APPLICANT:  Kinch, Deborah
;  APPLICANT:  Rosenberg, Michael
;  APPLICANT:  Subramaniam, S. Sai
;  APPLICANT:  Szak, Suzanne
;  APPLICANT:  Li, Huo
;  APPLICANT:  Bandaru, Raj
;  APPLICANT:  Derbel, Maher
;  TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary to
;  TITLE OF INVENTION:  Fragments of, Cynomolgus Monkey Genes and the Use Thereof
;  FILE REFERENCE: 2159.0290002
;  CURRENT APPLICATION NUMBER: US/11/433,832
;  CURRENT FILING DATE:  2006-05-15
;  NUMBER OF SEQ ID NOS: 48714
;  SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 46627
;   LENGTH: 2412
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-433-832-46627

Alignment Scores:
Pred. No.:              692          Length:          2412
Score:                  47.00        Matches:         11
Percent Similarity:     57.1%        Conservative:    5
Best Local Similarity:  39.3%        Mismatches:      4
Query Match:            29.4%        Indels:          8
DB:                     8            Gaps:            1

US-10-758-902-1 (1-30) x US-11-433-832-46627 (1-2412)

Qy          2 AsnThrValSerPheAsnLeu----------GlyGluAlaTyrGlu 13
              ||||||:::||||||:::|||          ||||||:::   |||
Db        727 AACACGATCTCCTTCAGCCTGGAAGAGGAAGAGGAACTGGAGGGTGGAGAGTCAGCAGAA 786

Qy         14 TyrProThrPheIleGlnAspLeu 21
              :::      |||   :::|||||||
Db        787 TTCACGTGCTTCTCAGAAGATCTC 810
```

```
RESULT 97
US-11-371-354-70010
; Sequence 70010, Application US/11371354
; GENERAL INFORMATION:
;  APPLICANT: CARRINO, JOHN
;  APPLICANT:  LIANG, FENG
;  TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFYING MATCHED REAGENTS
;  FILE REFERENCE: INV-1005-UT2
;  CURRENT APPLICATION NUMBER: US/11/371,354
;  CURRENT FILING DATE:  2006-03-07
;  PRIOR APPLICATION NUMBER: 60/673,045
;  PRIOR FILING DATE: 2005-04-19
;  PRIOR APPLICATION NUMBER: 60/665,199
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/665,200
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/659,493
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/659,492
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/953,586
;  PRIOR FILING DATE: 2005-02-15
;  PRIOR APPLICATION NUMBER: 60/651,390
;  PRIOR FILING DATE: 2005-02-08
;  NUMBER OF SEQ ID NOS: 78682
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70010
;   LENGTH: 2412
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-371-354-70010

Alignment Scores:
Pred. No.:              692          Length:         2412
Score:                  47.00        Matches:        11
Percent Similarity:     57.1%        Conservative:   5
Best Local Similarity:  39.3%        Mismatches:     4
Query Match:            29.4%        Indels:         8
DB:                     8            Gaps:           1

US-10-758-902-1 (1-30) x US-11-371-354-70010 (1-2412)

Qy          2 AsnThrValSerPheAsnLeu----------------------GlyGluAlaTyrGlu 13
              ||||||:::|||||||:::|||                      ||||||:::   |||
Db        727 AACACGATCTCCTTCAGCCTGGAAGAGGAAGAGGAACTGGAGGGTGGAGAGTCAGCAGAA 786

Qy         14 TyrProThrPheIleGlnAspLeu 21
              :::      |||   :::||||||
Db        787 TTCACGTGCTTCTCAGAAGATCTC 810

RESULT 98
US-11-514-704-12860/c
; Sequence 12860, Application US/11514704
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  Wu, Kunsheng
;  APPLICANT:  Dasgupta, Santanu
;  APPLICANT:  Cherian, Shoba
;  APPLICANT:  Jayaprakash, Targolli L
;  TITLE OF INVENTION: Zea mays Ribulose Bisphosphate Carboxylase
;  TITLE OF INVENTION:  Activase Promoter
;  FILE REFERENCE: 38-21(53660)C
;  CURRENT APPLICATION NUMBER: US/11/514,704
;  CURRENT FILING DATE:  2006-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12860
;   LENGTH: 3072
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-514-704-12860

Alignment Scores:
Pred. No.:              919          Length:         3072
Score:                  47.00        Matches:        10
Percent Similarity:     56.2%        Conservative:   8
Best Local Similarity:  31.2%        Mismatches:     10
Query Match:            29.4%        Indels:         4
DB:                     7            Gaps:           1

US-10-758-902-1 (1-30) x US-11-514-704-12860 (1-3072)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyr-----------ProThr 16
              :::   ::::::||||||:::   |||:::      :::              |||
Db        325 TTTAGGTCGATTAGCTTCCATTTTGGACAAGGCGCACTGTTTTGCTGTGTGTGCCCTGAA 266

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGly 28
              |||:::|||:::   |||   ||||||      |||
Db        265 TTTGTCCAGAATCCCCGTGAAGAATTAATGCTTGGT 230

RESULT 99
PCT-US06-11960-326/c
; Sequence 326, Application PC/TUS0611960
; GENERAL INFORMATION:
;  APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION,
;  TITLE OF INVENTION:  ASSESSMENT, PREVENTION, AND THERAPY OF NEUROLOGICAL
;  TITLE OF INVENTION:  DISEASES, DISORDERS AND CONDITIONS
;  FILE REFERENCE: DFS-060.25
;  CURRENT APPLICATION NUMBER: PCT/US06/11960
;  CURRENT FILING DATE:  2006-03-31
;  PRIOR APPLICATION NUMBER: 60/667,922
;  PRIOR FILING DATE: 2005-03-31
;  NUMBER OF SEQ ID NOS: 767
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 326
;   LENGTH: 4591
;   TYPE: DNA
;   ORGANISM: Mus musculus
PCT-US06-11960-326

Alignment Scores:
Pred. No.:              1.47e+03     Length:         4591
Score:                  47.00        Matches:        9
Percent Similarity:     66.7%        Conservative:   5
Best Local Similarity:  42.9%        Mismatches:     7
Query Match:            29.4%        Indels:         0
DB:                     1            Gaps:           0

US-10-758-902-1 (1-30) x PCT-US06-11960-326 (1-4591)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ::::::|||:::   :::|||:::      |||||||||   ||||||   |||
Db       3035 TTCTCTACCATTGATTACAACATTGAAGTGGCTTACGAATCACCCACACAAATATTCAGC 2976

Qy         21 Leu 21
              |||
Db       2975 TTG 2973

RESULT 100
US-60-836-986-9427/c
; Sequence 9427, Application US/60836986
; GENERAL INFORMATION:
;  APPLICANT: Hood, Leroy
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Johnson, Richard
;  APPLICANT:  Marelli, Marcello
;  APPLICANT:  Li, Xiaojun
;  TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 460092.405P1
;  CURRENT APPLICATION NUMBER: US/60/836,986
;  CURRENT FILING DATE:  2006-08-09
;  NUMBER OF SEQ ID NOS: 32934
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9427
;   LENGTH: 4843
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-836-986-9427

Alignment Scores:
Pred. No.:              1.57e+03       Length:          4843
Score:                  47.00          Matches:         9
Percent Similarity:     57.7%          Conservative:    6
Best Local Similarity:  34.6%          Mismatches:      9
Query Match:            29.4%          Indels:          2
DB:                     9              Gaps:            1

US-10-758-902-1 (1-30) x US-60-836-986-9427 (1-4843)

Qy          6 PheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp------LeuArgAsn 23
              :::|||           ::::::||||||||||||      :::         |||
Db        546 TATAATTATAGTAGGATATTTCAATACCCCACTTTCTGTAATAATAATAAAACAAGACAG 487

Qy         24 GluLeuAlaLysGlyThr 29
                ::::::|||||||||
Db        486 TATATTAGTAAGGGAACA 469


Search completed: September 18, 2006, 20:45:44
Job time : 763.022 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:14:17 ; Search time 7.5419 Seconds
(without alignments)
348.177 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	100.0	30	2	US-09-445-160B-1	Sequence 1, Appli
2	160	100.0	149	2	US-09-445-160B-9	Sequence 9, Appli
3	61	38.1	313	1	US-08-373-858-2	Sequence 2, Appli
4	61	38.1	313	1	US-08-500-611-2	Sequence 2, Appli
5	61	38.1	313	1	US-08-500-694-2	Sequence 2, Appli
6	61	38.1	313	2	US-09-005-273-2	Sequence 2, Appli
7	61	38.1	313	2	US-08-501-253A-2	Sequence 2, Appli
8	61	38.1	313	3	US-09-721-047A-2	Sequence 2, Appli
9	61	38.1	313	5	PCT-US96-11546-2	Sequence 2, Appli
10	59	36.9	261	1	US-07-901-707-9	Sequence 9, Appli
11	59	36.9	261	1	US-07-988-430-9	Sequence 9, Appli
12	59	36.9	261	1	US-08-425-336-9	Sequence 9, Appli
13	59	36.9	261	1	US-08-378-761A-79	Sequence 79, Appl
14	59	36.9	261	1	US-08-485-286-79	Sequence 79, Appl
15	59	36.9	261	1	US-08-488-113B-9	Sequence 9, Appli
16	59	36.9	261	1	US-08-477-484B-9	Sequence 9, Appli
17	59	36.9	261	1	US-08-646-360-9	Sequence 9, Appli
18	59	36.9	261	2	US-08-839-765-9	Sequence 9, Appli
19	59	36.9	261	2	US-09-136-389-9	Sequence 9, Appli
20	59	36.9	261	2	US-09-610-838-9	Sequence 9, Appli
21	59	36.9	261	2	US-09-711-485-9	Sequence 9, Appli
22	59	36.9	261	5	PCT-US92-09487-9	Sequence 9, Appli
23	57.5	35.9	225	2	US-09-107-532A-7302	Sequence 7302, Ap
24	56	35.0	313	2	US-09-005-273-4	Sequence 4, Appli
25	56	35.0	314	3	US-10-128-713A-16	Sequence 16, Appl
26	54	33.8	29	1	US-08-378-761A-28	Sequence 28, Appl
27	54	33.8	29	1	US-08-485-286-28	Sequence 28, Appl
28	53	33.1	282	1	US-08-324-301-15	Sequence 15, Appl
29	52	32.5	332	2	US-09-428-034-4	Sequence 4, Appli
30	52	32.5	376	2	US-09-428-034-2	Sequence 2, Appli
31	52	32.5	459	2	US-09-902-540-10583	Sequence 10583, A
32	51.5	32.2	238	2	US-09-902-540-16037	Sequence 16037, A
33	51	31.9	32	1	US-08-324-301-1	Sequence 1, Appli
34	51	31.9	1233	2	US-09-134-000C-4971	Sequence 4971, Ap
35	51	31.9	1416	2	US-09-071-035-404	Sequence 404, App
36	51	31.9	1416	2	US-10-206-576-404	Sequence 404, App
37	51	31.9	1448	2	US-09-071-035-402	Sequence 402, App
38	51	31.9	1448	2	US-10-206-576-402	Sequence 402, App
39	50	31.2	54	2	US-09-306-446C-13	Sequence 13, Appl
40	50	31.2	210	2	US-09-306-446C-9	Sequence 9, Appli
41	50	31.2	210	2	US-09-306-446C-16	Sequence 16, Appl
42	49.5	30.9	1610	2	US-09-602-787A-14	Sequence 14, Appl
43	49.5	30.9	1610	2	US-09-602-787A-56	Sequence 56, Appl
44	49.5	30.9	2188	2	US-09-328-352-7763	Sequence 7763, Ap
45	49	30.6	1850	2	US-09-620-093A-5	Sequence 5, Appli
46	49	30.6	2154	1	US-08-841-349-4	Sequence 4, Appli
47	49	30.6	2154	2	US-09-431-184A-4	Sequence 4, Appli
48	49	30.6	2364	2	US-09-538-092-1243	Sequence 1243, Ap
49	48.5	30.3	28	7	5248606-12	Patent No. 5248606
50	48	30.0	174	2	US-09-949-016-11600	Sequence 11600, A
51	48	30.0	174	2	US-09-949-016-11601	Sequence 11601, A
52	48	30.0	174	2	US-09-949-016-11602	Sequence 11602, A
53	48	30.0	210	2	US-09-549-831-10	Sequence 10, Appl
54	48	30.0	373	2	US-08-911-321-9	Sequence 9, Appli
55	48	30.0	373	5	PCT-US95-13975-73	Sequence 73, Appl
56	48	30.0	374	1	US-08-220-151-21	Sequence 21, Appl
57	48	30.0	374	1	US-08-413-118-21	Sequence 21, Appl
58	48	30.0	374	2	US-08-473-446-21	Sequence 21, Appl
59	48	30.0	409	2	US-09-902-540-10657	Sequence 10657, A
60	47	29.4	185	2	US-09-248-796A-18715	Sequence 18715, A
61	47	29.4	203	2	US-09-186-276B-36	Sequence 36, Appl
62	47	29.4	203	2	US-08-842-445-36	Sequence 36, Appl
63	47	29.4	203	2	US-09-186-188B-36	Sequence 36, Appl
64	47	29.4	252	2	US-09-270-767-34529	Sequence 34529, A
65	47	29.4	252	2	US-09-270-767-49746	Sequence 49746, A
66	47	29.4	310	2	US-09-265-585C-36	Sequence 36, Appl
67	47	29.4	398	2	US-09-328-352-6865	Sequence 6865, Ap
68	47	29.4	420	2	US-09-270-767-42980	Sequence 42980, A
69	47	29.4	725	2	US-10-118-328-5	Sequence 5, Appli
70	47	29.4	785	2	US-09-487-558B-348	Sequence 348, App
71	47	29.4	883	2	US-09-489-039A-12755	Sequence 12755, A
72	46.5	29.1	39	7	5248606-6	Patent No. 5248606
73	46.5	29.1	222	2	US-09-710-279-128	Sequence 128, App
74	46.5	29.1	280	1	US-07-901-707-3	Sequence 3, Appli
75	46.5	29.1	280	1	US-07-988-430-3	Sequence 3, Appli
76	46.5	29.1	280	1	US-08-425-336-3	Sequence 3, Appli
77	46.5	29.1	280	1	US-08-425-336-127	Sequence 127, App
78	46.5	29.1	280	1	US-08-425-336-128	Sequence 128, App
79	46.5	29.1	280	1	US-08-425-336-129	Sequence 129, App
80	46.5	29.1	280	1	US-08-378-761A-26	Sequence 26, Appl
81	46.5	29.1	280	1	US-08-485-286-26	Sequence 26, Appl
82	46.5	29.1	280	1	US-08-488-113B-3	Sequence 3, Appli
83	46.5	29.1	280	1	US-08-488-113B-127	Sequence 127, App
84	46.5	29.1	280	1	US-08-488-113B-128	Sequence 128, App
85	46.5	29.1	280	1	US-08-488-113B-129	Sequence 129, App
86	46.5	29.1	280	1	US-08-477-484B-3	Sequence 3, Appli
87	46.5	29.1	280	1	US-08-477-484B-127	Sequence 127, App
88	46.5	29.1	280	1	US-08-477-484B-128	Sequence 128, App
89	46.5	29.1	280	1	US-08-477-484B-129	Sequence 129, App
90	46.5	29.1	280	1	US-08-646-360-3	Sequence 3, Appli
91	46.5	29.1	280	1	US-08-646-360-127	Sequence 127, App
92	46.5	29.1	280	1	US-08-646-360-128	Sequence 128, App
93	46.5	29.1	280	1	US-08-646-360-129	Sequence 129, App
94	46.5	29.1	280	2	US-08-839-765-3	Sequence 3, Appli
95	46.5	29.1	280	2	US-08-839-765-127	Sequence 127, App
96	46.5	29.1	280	2	US-08-839-765-128	Sequence 128, App
97	46.5	29.1	280	2	US-08-839-765-129	Sequence 129, App
98	46.5	29.1	280	2	US-09-136-389-3	Sequence 3, Appli
99	46.5	29.1	280	2	US-09-136-389-127	Sequence 127, App

100 46.5 29.1 280 2 US-09-136-389-128 Sequence 128, App

ALIGNMENTS

RESULT 1
US-09-445-160B-1
; Sequence 1, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenza
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
; FILE REFERENCE: Stirpe
; CURRENT APPLICATION NUMBER: US/09/445,160B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/NL98/00336
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Bougainvillea spectrabilis
; PUBLICATION INFORMATION:
US-09-445-160B-1

Query Match 100.0%; Score 160; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
||||||||||||||||||||||||||||||
Db 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

RESULT 2
US-09-445-160B-9
; Sequence 9, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenza
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
; FILE REFERENCE: Stirpe
; CURRENT APPLICATION NUMBER: US/09/445,160B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/NL98/00336
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 9
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Bougainvillea spectrabilis
; NAME/KEY:
; LOCATION: 143
; OTHER INFORMATION: Trp uncertain
; PUBLICATION INFORMATION:
US-09-445-160B-9

Query Match 100.0%; Score 160; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 4.1e-17;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
||||||||||||||||||||||||||||||
Db 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

RESULT 3
US-08-373-858-2
; Sequence 2, Application US/08373858
; Patent No. 5633155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byeong-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytolacca
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; TITLE OF INVENTION: Plant Transformed Thereof.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/17986-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7770
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Phytolacca americana
; TISSUE TYPE: Leaf
US-08-373-858-2

Query Match 38.1%; Score 61; DB 1; Length 313;
Best Local Similarity 48.0%; Pred. No. 0.28;
Matches 12; Conservative 5; Mismatches 6; Indels 2; Gaps 1;

Qy 2 NTVSFNLGEA--YEYPTFIQDLRNE 24
|| : :|:| :| ||: |||||
Db 24 NTIIYNVGSTTISKYATFLNDLRNE 48

RESULT 4

```
US-08-500-611-2
; Sequence 2, Application US/08500611
; Patent No. 5756322
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  Pokeweed Antiviral Protein Mutants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/500,611
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.0-034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;      TELEX:  139-125
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  313 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-500-611-2

  Query Match             38.1%;  Score 61;  DB 1;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 0.28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 5
US-08-500-694-2
; Sequence 2, Application US/08500694
; Patent No. 5880329
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  DNAs Encoding Pokeweed Antiviral Protein
;    TITLE OF INVENTION:  Mutants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/500,694
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.0-039
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;      TELEX:  139-125
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  313 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-500-694-2

  Query Match             38.1%;  Score 61;  DB 1;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 0.28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 6
US-09-005-273-2
; Sequence 2, Application US/09005273
; Patent No. 6137030
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
;    TITLE OF INVENTION:  AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ &
;      ADDRESSEE:  MENTILIK
;      STREET:  600 South, Avenue West
;      CITY:  Westfield
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07090
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/005,273
;      FILING DATE:  09-JAN-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,611
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,694
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11546
;      FILING DATE:  11-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REGISTRATION NUMBER:  33,071
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.3-034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  313 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-005-273-2
```

```
  Query Match             38.1%;  Score 61;  DB 2;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 0.28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 7
US-08-501-253A-2
; Sequence 2, Application US/08501253A
; Patent No. 6146628
;  GENERAL INFORMATION:
;    APPLICANT:  Uckun, Fatih
;    APPLICANT:  Tumer, Nilgun
;    TITLE OF INVENTION:  Biotherapeutic Agents Comprising
;    TITLE OF INVENTION:  Recombinant PAp and PAP Mutants
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  90 South 7th Street, 3100 No. 6146628west Center
;      CITY:  Minneapolis
;      STATE:  MM
;      COUNTRY:  US
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/501,253A
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M.
;      REGISTRATION NUMBER:  33,924
;      REFERENCE/DOCKET NUMBER:  600.323US01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  313 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-501-253A-2

  Query Match             38.1%;  Score 61;  DB 2;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 0.28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 8
US-09-721-047A-2
; Sequence 2, Application US/09721047A
; Patent No. 7019126
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  WANG, PINGER
;  TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
;  FILE REFERENCE: OCIRS 3.9-060 CONT
;  CURRENT APPLICATION NUMBER: US/09/721,047A
;  CURRENT FILING DATE:  2000-11-22
;  PRIOR APPLICATION NUMBER: PCT/US99/11301
;  PRIOR FILING DATE: 1999-05-21
;  PRIOR APPLICATION NUMBER: 60/086,374
;  PRIOR FILING DATE: 1998-05-22
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
;    LENGTH: 313
;    TYPE: PRT
;    ORGANISM: Phytolacca americana
US-09-721-047A-2

  Query Match             38.1%;  Score 61;  DB 3;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 0.28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 9
PCT-US96-11546-2
; Sequence 2, Application PC/TUS9611546
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  DNAs Encoding Pokeweed Antiviral Protein
;    TITLE OF INVENTION:  Mutants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lerner, David, Littenberg, Krumholz & Mentlik
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07090-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11546
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,694
;      FILING DATE:  11-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.0-039
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;      TELEX:  139-125
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  313 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US96-11546-2

  Query Match             38.1%;  Score 61;  DB 5;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 0.28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 10
US-07-901-707-9
; Sequence 9, Application US/07901707
; Patent No. 5376546
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Composition and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/901,707
;      FILING DATE:  19920619
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5376546and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27129/30910
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-5750
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-901-707-9

  Query Match             36.9%;  Score 59;  DB 1;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSPNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |    :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 11
US-07-988-430-9
; Sequence 9, Application US/07988430
; Patent No. 5416202
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,430
;      FILING DATE:  19921209
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5416202and, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-988-430-9

  Query Match             36.9%;  Score 59;  DB 1;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSPNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |    :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 12
US-08-425-336-9
; Sequence 9, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
```

```
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-425-336-9

  Query Match             36.9%;  Score 59;  DB 1;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 13
US-08-378-761A-79
; Sequence 79, Application US/08378761A
; Patent No. 5635384
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761A
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-761A-79

  Query Match             36.9%;  Score 59;  DB 1;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 14
US-08-485-286-79
; Sequence 79, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,286
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/378761
;      FILING DATE:  26-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-485-286-79

  Query Match             36.9%;  Score 59;  DB 1;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 15
US-08-488-113B-9
; Sequence 9, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
```

```
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-9

  Query Match             36.9%;  Score 59;  DB 1;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |    :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 16
US-08-477-484B-9
; Sequence 9, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-9

  Query Match             36.9%;  Score 59;  DB 1;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |    :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 17
US-08-646-360-9
; Sequence 9, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/646,360
;       FILING DATE:  13-MAY-1996
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/05348
;       FILING DATE:  12-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  200-70.P4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  261 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-646-360-9

  Query Match             36.9%;  Score 59;  DB 1;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 18
US-08-839-765-9
; Sequence 9, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-9

  Query Match             36.9%;  Score 59;  DB 2;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 19
US-09-136-389-9
; Sequence 9, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-9

  Query Match             36.9%;  Score 59;  DB 2;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 20
US-09-610-838-9
; Sequence 9, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/610,838
;      FILING DATE:  06-JUL-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:  18-AUG-1998
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-610-838-9

  Query Match             36.9%;  Score 59;  DB 2;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 21
US-09-711-485-9
; Sequence 9, Application US/09711485
; Patent No. 6649742
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/711,485
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/839,765
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
```

```
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-711-485-9

  Query Match             36.9%;  Score 59;  DB 2;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |    :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 22
PCT-US92-09487-9
; Sequence 9, Application PC/TUS9209487
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/09487
;      FILING DATE:  19921104
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US92-09487-9

  Query Match             36.9%;  Score 59;  DB 5;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |    :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 23
US-09-107-532A-7302
; Sequence 7302, Application US/09107532A
; Patent No. 6583275
;  GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;  INFORMATION FOR SEQ ID NO: 7302:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 225 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: YES
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...225
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7302:
US-09-107-532A-7302

  Query Match             35.9%;  Score 57.5;  DB 2;  Length 225;
  Best Local Similarity   31.4%;  Pred. No. 0.66;
  Matches   11;  Conservative   11;  Mismatches    8;  Indels    5;  Gaps    1;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA-----KGTP 30
```

```
              ::  | :||| |::  |::|  :|::     :|||
Db         38 FSKTSMDLGERYDFKGFMEDKMDEVSSREIPEGTP 72


RESULT 24
US-09-005-273-4
; Sequence 4, Application US/09005273
; Patent No. 6137030
;  GENERAL INFORMATION:
;    APPLICANT:  Tumer, Nilgun E.
;    TITLE OF INVENTION:  PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
;    TITLE OF INVENTION:  AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ &
;      ADDRESSEE:  MENTILIK
;      STREET:  600 South, Avenue West
;      CITY:  Westfield
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07090
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/005,273
;      FILING DATE:  09-JAN-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,611
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/500,694
;      FILING DATE:  11-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11546
;      FILING DATE:  11-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REGISTRATION NUMBER:  33,071
;      REFERENCE/DOCKET NUMBER:  OCIRS 3.3-034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  313 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-005-273-4

  Query Match             35.0%;  Score 56;  DB 2;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 1.7;
  Matches   12;  Conservative    4;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||  |||||
Db         24 NTIIYNVGSTTISKYATFRNDLRNE 48


RESULT 25
US-10-128-713A-16
; Sequence 16, Application US/10128713A
; Patent No. 7034140
; GENERAL INFORMATION:
;  APPLICANT: Bramucci, Michael G
;  TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production
;  FILE REFERENCE: CL-1788
;  CURRENT APPLICATION NUMBER: US/10/128,713A
;  CURRENT FILING DATE:  2002-04-22
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Rhodococcus erythropolis
US-10-128-713A-16

  Query Match             35.0%;  Score 56;  DB 3;  Length 314;
  Best Local Similarity   45.5%;  Pred. No. 1.7;
  Matches   10;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKG 28
              |||||::   ||:|:  :| :|
Db        174 NLGEAFQLTNFIRDVGEDLDRG 195


RESULT 26
US-08-378-761A-28
; Sequence 28, Application US/08378761A
; Patent No. 5635384
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761A
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-761A-28

  Query Match             33.8%;  Score 54;  DB 1;  Length 29;
  Best Local Similarity   44.0%;  Pred. No. 0.2;
  Matches   11;  Conservative    5;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|      | ||: :||||
Db          2 NTIIYNVGSTTISNYATFMDNLRNE 26


RESULT 27
US-08-485-286-28
; Sequence 28, Application US/08485286
; Patent No. 5646026
```

```
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
;   APPLICANT:  WALSH, TERENCE A
;   APPLICANT:  HEY, TIMOTHY D
;   APPLICANT:  MORGAN, ALICE ER
;   TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;   TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;   TITLE OF INVENTION:  USING
;   NUMBER OF SEQUENCES:  81
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  ANDREA T. BORUCKI
;     STREET:  9330 ZIONSVILLE ROAD
;     CITY:  INDIANAPOLIS
;     STATE:  IN
;     COUNTRY:  US
;     ZIP:  46268
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/485,286
;     FILING DATE:
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/378761
;     FILING DATE:  26-JAN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  BORUCKI, ANDREA T
;     REGISTRATION NUMBER:  33651
;     REFERENCE/DOCKET NUMBER:  38272B
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (317) 337-4846
; INFORMATION FOR SEQ ID NO:  28:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  29 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-485-286-28

  Query Match             33.8%;  Score 54;  DB 1;  Length 29;
  Best Local Similarity   44.0%;  Pred. No. 0.2;
  Matches   11;  Conservative    5;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|      | ||: :|||| 
Db          2 NTIIYNVGSTTISNYATFMDNLRNE 26


RESULT 28
US-08-324-301-15
; Sequence 15, Application US/08324301
; Patent No. 5597569
; GENERAL INFORMATION:
;   APPLICANT:  Siegall, Clay B.
;   APPLICANT:  Gawlak, Susan L.
;   APPLICANT:  Marquardt, Hans
;   TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;   TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONICA DIOICA
;   NUMBER OF SEQUENCES:  27
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Bristol-Myers Squibb Company
;     STREET:  3005 First Avenue
;     CITY:  Seattle
;     STATE:  Washington
;     COUNTRY:  USA
;     ZIP:  98121
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/324,301
;     FILING DATE:
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/141,891
;     FILING DATE:  25-OCT-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Poor, Brian W.
;     REGISTRATION NUMBER:  32,928
;     REFERENCE/DOCKET NUMBER:  ON0109A
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  206-728-4800
;     TELEFAX:  206-727-3601
; INFORMATION FOR SEQ ID NO:  15:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  282 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
;   FRAGMENT TYPE:  N-terminal
;   ORIGINAL SOURCE:
;     ORGANISM:  Bryonia dioica
;     TISSUE TYPE:  leaf
US-08-324-301-15

  Query Match             33.1%;  Score 53;  DB 1;  Length 282;
  Best Local Similarity   58.8%;  Pred. No. 4.3;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         14 YPTFIQDLRNELAKGTP 30
              | |||::|| :|  |||
Db         36 YKTFIRNLRTKLTVGTP 52


RESULT 29
US-09-428-034-4
; Sequence 4, Application US/09428034
; Patent No. 6428996
; GENERAL INFORMATION:
;  APPLICANT:  Cheng, Kuo-Joan
;  APPLICANT:  Liu, Jin-Hao
;  APPLICANT:  Tsai, Cheng-Fang
;  APPLICANT:  Hsu, Yih-Chin
;  TITLE OF INVENTION:  CELLULASE ENZYMES
;  FILE REFERENCE:  08919/036001
;  CURRENT APPLICATION NUMBER: US/09/428,034
;  CURRENT FILING DATE:  1999-10-27
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 332
;   TYPE: PRT
;   ORGANISM: Piromyces rhizinflata
US-09-428-034-4

  Query Match             32.5%;  Score 52;  DB 2;  Length 332;
  Best Local Similarity   38.5%;  Pred. No. 7.5;
  Matches   10;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :| | | |  | ||::: : : | ||
Db          7 NFFLNEIYANPKFIEEVEDSIEKLTP 32


RESULT 30
US-09-428-034-2
; Sequence 2, Application US/09428034
; Patent No. 6428996
; GENERAL INFORMATION:
;  APPLICANT:  Cheng, Kuo-Joan
```

```
;  APPLICANT:  Liu, Jin-Hao
;  APPLICANT:  Tsai, Cheng-Fang
;  APPLICANT:  Hsu, Yih-Chin
;  TITLE OF INVENTION:  CELLULASE ENZYMES
;  FILE REFERENCE:  08919/036001
;  CURRENT APPLICATION NUMBER: US/09/428,034
;  CURRENT FILING DATE:  1999-10-27
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 376
;   TYPE: PRT
;   ORGANISM: Piromyces rhizinflata
US-09-428-034-2

  Query Match           32.5%;  Score 52;  DB 2;  Length 376;
  Best Local Similarity  38.5%;  Pred. No. 8.7;
  Matches   10;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :| | | |  | ||::: : : | ||
Db         50 NFFLNEIYANPKFIEEVEDSIEKLTP 75


RESULT 31
US-09-902-540-10583
; Sequence 10583, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10583
;   LENGTH: 459
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-10583

  Query Match           32.5%;  Score 52;  DB 2;  Length 459;
  Best Local Similarity  47.6%;  Pred. No. 11;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          8 LGEAYEYPTFIQDLRNELAKG 28
              | | ||:|  :::||| | :|
Db        336 LFEGYEWPGNVRELRNVLERG 356


RESULT 32
US-09-902-540-16037
; Sequence 16037, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16037
;   LENGTH: 238
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-16037

  Query Match           32.2%;  Score 51.5;  DB 2;  Length 238;
  Best Local Similarity  43.8%;  Pred. No. 6.1;
  Matches   14;  Conservative    4;  Mismatches   11;  Indels    3;  Gaps    2;

Qy          1 YNTV--SFNLGEAYEYPTFIQDLRNELAKGTP 30
              | |:  ||  ||    || ::|:|  || | |
Db         60 YKTLGGSFT-GELVVDPTHLRDMRRRLAAGEP 90


RESULT 33
US-08-324-301-1
; Sequence 1, Application US/08324301
; Patent No. 5597569
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    APPLICANT:  Gawlak, Susan L.
;    APPLICANT:  Marquardt, Hans
;    TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;    TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONICA DIOICA
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,301
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/141,891
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0109A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-728-4800
;      TELEFAX:  206-727-3601
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonica dioica
;      TISSUE TYPE:  Root
US-08-324-301-1

  Query Match           31.9%;  Score 51;  DB 1;  Length 32;
  Best Local Similarity  58.8%;  Pred. No. 0.66;
  Matches   10;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         14 YPTFIQDLRNELAKGTP 30
              | |||::||  |  |||
Db         15 YKTFIRNLRTTLTVGTP 31


RESULT 34
US-09-134-000C-4971
```

; Sequence 4971, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4971
; LENGTH: 1233
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4971

Query Match 31.9%; Score 51; DB 2; Length 1233;
Best Local Similarity 38.5%; Pred. No. 52;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
||||| | |: | | : |:::
Db 904 YNTVSANAGQIYTETTIDSETLNQMS 929

RESULT 35
US-09-071-035-404
; Sequence 404, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-404

Query Match 31.9%; Score 51; DB 2; Length 1416;
Best Local Similarity 38.5%; Pred. No. 61;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
||||| | |: | | : |:::
Db 873 YNTVSANAGQIYTETTIDSETLNQMS 898

RESULT 36
US-10-206-576-404
; Sequence 404, Application US/10206576
; Patent No. 6913907
; GENERAL INFORMATION:
; APPLICANT: Choi et al.
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: Dell Latitude
; OPERATING SYSTEM: Windows 98
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,576
; FILING DATE: 29-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/071,035
; FILING DATE: 1998-05-04
; APPLICATION NUMBER: US 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: US 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: US 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Mark J.
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB369P1D1
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 404:
US-10-206-576-404

Query Match 31.9%; Score 51; DB 2; Length 1416;
Best Local Similarity 38.5%; Pred. No. 61;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
||||| | |: | | : |:::
Db 873 YNTVSANAGQIYTETTIDSETLNQMS 898

RESULT 37
US-09-071-035-402
; Sequence 402, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.

```
;       STREET:  9410 Key West Avenue
;       CITY:  Rockville
;       STATE:  Maryland
;       COUNTRY:  USA
;       ZIP:  20850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;       COMPUTER:  HP Vectra 486/33
;       OPERATING SYSTEM:  MSDOS version 6.2
;       SOFTWARE:  ASCII Text
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/071,035
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  A. Anders Brookes
;       REGISTRATION NUMBER:  36,373
;       REFERENCE/DOCKET NUMBER:  PB369P2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (301) 309-8504
;       TELEFAX:  (301) 309-8512
;   INFORMATION FOR SEQ ID NO:  402:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1448 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-035-402

  Query Match             31.9%;  Score 51;  DB 2;  Length 1448;
  Best Local Similarity   38.5%;  Pred. No. 63;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |    |    :  |:::
Db        900 YNTVSANAGQIYTETTIDSETLNQMS 925


RESULT 38
US-10-206-576-402
; Sequence 402, Application US/10206576
; Patent No. 6913907
;   GENERAL INFORMATION:
;       APPLICANT: Choi et al.
;       TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;       NUMBER OF SEQUENCES: 497
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Human Genome Sciences, Inc.
;            STREET: 9410 Key West Avenue
;            CITY: Rockville
;            STATE: Maryland
;            COUNTRY: USA
;            ZIP: 20850
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: Dell Latitude
;            OPERATING SYSTEM: Windows 98
;            SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/206,576
;            FILING DATE: 29-Jul-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 09/071,035
;            FILING DATE: 1998-05-04
;            APPLICATION NUMBER: US 60/046,655
;            FILING DATE: 1997-05-16
;            APPLICATION NUMBER: US 60/044,031
;            FILING DATE: 1997-05-06
;            APPLICATION NUMBER: US 60/066,009
;            FILING DATE: 1997-11-14
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hyman, Mark J.
;            REGISTRATION NUMBER: 46,789
;            REFERENCE/DOCKET NUMBER: PB369P1D1
;   INFORMATION FOR SEQ ID NO: 402:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1448 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 402:
US-10-206-576-402

  Query Match             31.9%;  Score 51;  DB 2;  Length 1448;
  Best Local Similarity   38.5%;  Pred. No. 63;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |    |    :  |:::
Db        900 YNTVSANAGQIYTETTIDSETLNQMS 925


RESULT 39
US-09-306-446C-13
; Sequence 13, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
;  APPLICANT: KIM, Dong Soo
;  APPLICANT:  KIM, Chul Geun
;  APPLICANT:  NAM, Yoon Kwon
;  APPLICANT:  NOH, Jae Koo
;  APPLICANT:  CHO, Kyou Nam
;  TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
;  FILE REFERENCE: P06344US0/BAS
;  CURRENT APPLICATION NUMBER: US/09/306,446C
;  CURRENT FILING DATE:  1999-05-06
;  PRIOR APPLICATION NUMBER: KR 98/20255
;  PRIOR FILING DATE: 1998-06-01
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 54
;   TYPE: PRT
;   ORGANISM: Misgurnus mizolepus
US-09-306-446C-13

  Query Match             31.2%;  Score 50;  DB 2;  Length 54;
  Best Local Similarity   41.4%;  Pred. No. 1.8;
  Matches   12;  Conservative    4;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          4 VSFNLGEAYEYP--TFIQDLRNELAKGTP 30
              :|| | |::|||  |    : | |  | |
Db          7 ISFRLIESWEYPSQTLSGTISNSLTIGNP 35


RESULT 40
US-09-306-446C-9
; Sequence 9, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
;  APPLICANT: KIM, Dong Soo
;  APPLICANT:  KIM, Chul Geun
;  APPLICANT:  NAM, Yoon Kwon
;  APPLICANT:  NOH, Jae Koo
;  APPLICANT:  CHO, Kyou Nam
;  TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
;  FILE REFERENCE: P06344US0/BAS
;  CURRENT APPLICATION NUMBER: US/09/306,446C
;  CURRENT FILING DATE:  1999-05-06
;  PRIOR APPLICATION NUMBER: KR 98/20255
```

```
;  PRIOR FILING DATE: 1998-06-01
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Misgurnus mizolepus
US-09-306-446C-9

  Query Match            31.2%;  Score 50;  DB 2;  Length 210;
  Best Local Similarity  41.4%;  Pred. No. 8.9;
  Matches   12;  Conservative    4;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          4 VSFNLGEAYEYP--TFIQDLRNELAKGTP 30
              :|| | |::|||  |    : | |  | |
Db         96 ISFRLIESWEYPSQTLSGTISNSLTIGNP 124


RESULT 41
US-09-306-446C-16
; Sequence 16, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
;  APPLICANT: KIM, Dong Soo
;  APPLICANT:  KIM, Chul Geun
;  APPLICANT:  NAM, Yoon Kwon
;  APPLICANT:  NOH, Jae Koo
;  APPLICANT:  CHO, Kyou Nam
;  TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
;  FILE REFERENCE: P06344US0/BAS
;  CURRENT APPLICATION NUMBER: US/09/306,446C
;  CURRENT FILING DATE:  1999-05-06
;  PRIOR APPLICATION NUMBER: KR 98/20255
;  PRIOR FILING DATE: 1998-06-01
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Misgurnus mizolepus
US-09-306-446C-16

  Query Match            31.2%;  Score 50;  DB 2;  Length 210;
  Best Local Similarity  41.4%;  Pred. No. 8.9;
  Matches   12;  Conservative    4;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          4 VSFNLGEAYEYP--TFIQDLRNELAKGTP 30
              :|| | |::|||  |    : | |  | |
Db         96 ISFRLIESWEYPSQTLSGTISNSLTIGNP 124


RESULT 42
US-09-602-787A-14
; Sequence 14, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr"ger, Burkhard
;  APPLICANT:  Sch"der, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CP
;  CURRENT APPLICATION NUMBER: US/09/602,787A
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932182.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932190.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932191.4
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932209.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932212.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932227.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932228.7
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932229.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932230.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932927.3
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933005.0
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933006.9
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19940764.9
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940765.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940766.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940830.0
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940831.9
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940832.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940833.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19941378.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941379.7
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941395.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19942077.7
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942078.5
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942079.3
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942088.2
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 14
;   LENGTH: 1610
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-602-787A-14

  Query Match            30.9%;  Score 49.5;  DB 2;  Length 1610;
  Best Local Similarity  55.0%;  Pred. No. 1.2e+02;
```

```
  Matches   11;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         11 AYEYPTFIQDLRNELAKGTP 30
              |||||| |: |    | :| |
Db         71 AYEYPT-IRSLAQRLVEGEP 89


RESULT 43
US-09-602-787A-56
; Sequence 56, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr"ger, Burkhard
;  APPLICANT:  Sch"der, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CP
;  CURRENT APPLICATION NUMBER: US/09/602,787A
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932182.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932190.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932191.4
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932209.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932212.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932227.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932228.7
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932229.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932230.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932927.3
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933005.0
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933006.9
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19940764.9
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940765.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940766.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940830.0
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940831.9
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940832.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940833.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19941378.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941379.7
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941395.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19942077.7
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942078.5
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942079.3
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942088.2
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 56
;   LENGTH: 1610
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-602-787A-56

  Query Match             30.9%;  Score 49.5;  DB 2;  Length 1610;
  Best Local Similarity   55.0%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         11 AYEYPTFIQDLRNELAKGTP 30
              |||||| |: |    | :| |
Db         71 AYEYPT-IRSLAQRLVEGEP 89


RESULT 44
US-09-328-352-7763
; Sequence 7763, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7763
;   LENGTH: 2188
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-7763

  Query Match             30.9%;  Score 49.5;  DB 2;  Length 2188;
  Best Local Similarity   47.8%;  Pred. No. 1.8e+02;
  Matches   11;  Conservative    5;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          7 NLGEAYEYPTFIQDLRNELAKGT 29
              :| : || |   ||::| |:|||
Db        124 SLNKPYE-PVSYQDIQNVLSKGT 145


RESULT 45
US-09-620-093A-5
; Sequence 5, Application US/09620093A
; Patent No. 6420337
; GENERAL INFORMATION:
;  APPLICANT:  Iyer, Subramanian
;  APPLICANT:  Nguyen, Tay N.
;  APPLICANT:  Wu, Dauh-Rurng
;  APPLICANT:  Xing, Ruye
;  TITLE OF INVENTION:  HIGHLY PURIFIED CYTOKINE ACTIVATING FACTOR AND METHODS
```

```
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE:  3812-7
;  CURRENT APPLICATION NUMBER: US/09/620,093A
;  CURRENT FILING DATE:  2000-07-20
;  PRIOR APPLICATION NUMBER:  60/145,317
;  PRIOR FILING DATE:  1999-07-23
;  PRIOR APPLICATION NUMBER:  60/197,619
;  PRIOR FILING DATE:  2000-04-14
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1850
;   TYPE: PRT
;   ORGANISM: Gallus gallus
US-09-620-093A-5

  Query Match             30.6%;  Score 49;  DB 2;  Length 1850;
  Best Local Similarity   38.5%;  Pred. No. 1.7e+02;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ::| || ||  :  ::  | |||
Db        192 VQKSIGMAYIYPCPVDVMKERLTKGT 217


RESULT 46
US-08-841-349-4
; Sequence 4, Application US/08841349B
; Patent No. 5955594
; GENERAL INFORMATION:
;  APPLICANT: MISHRA, LOPA
;  TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .
;  FILE REFERENCE: XX/PO4470US0
;  CURRENT APPLICATION NUMBER: US/08/841,349B
;  CURRENT FILING DATE: 1997-04-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 2154
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-08-841-349-4

  Query Match             30.6%;  Score 49;  DB 1;  Length 2154;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1710 SHELGQDYEHVTMLQERFREFARDT 1734


RESULT 47
US-09-431-184A-4
; Sequence 4, Application US/09431184A
; Patent No. 6642362
; GENERAL INFORMATION:
;  APPLICANT: MISHRA, LOPA
;  TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
;  FILE REFERENCE: P04470US1/BAS
;  CURRENT APPLICATION NUMBER: US/09/431,184A
;  CURRENT FILING DATE:  1999-11-01
;  PRIOR APPLICATION NUMBER: PCT/US98/08656
;  PRIOR FILING DATE: 1998-04-30
;  PRIOR APPLICATION NUMBER: US 08/841,349
;  PRIOR FILING DATE: 1997-04-30
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 2154
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-431-184A-4

  Query Match             30.6%;  Score 49;  DB 2;  Length 2154;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1710 SHELGQDYEHVTMLQERFREFARDT 1734


RESULT 48
US-09-538-092-1243
; Sequence 1243, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1243
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number Q01082
US-09-538-092-1243

  Query Match             30.6%;  Score 49;  DB 2;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 49
5248606-12
;Patent No. 5248606
;    APPLICANT: WALSH, TERENCE A.;HEY, TIMOTHY D.;MORGAN,
;ALICE E.R.
;    TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
;ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
;    NUMBER OF SEQUENCES: 49
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/535,636
;      FILING DATE: 11-JUN-1990
;SEQ ID NO:12:
;      LENGTH: 28
5248606-12

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 28;
  Best Local Similarity   48.0%;  Pred. No. 1.4;
  Matches   12;  Conservative    4;  Mismatches    6;  Indels    3;  Gaps    2;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|       | ||: |||||
Db          2 NTIIYNVGSTTISNYATFM-DLRNE 25


RESULT 50
US-09-949-016-11600
; Sequence 11600, Application US/09949016
```

```
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11600
;   LENGTH: 174
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11600

  Query Match             30.0%;  Score 48;  DB 2;  Length 174;
  Best Local Similarity   34.6%;  Pred. No. 15;
  Matches    9;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 TVSFNLGEAYEYPTFIQDLRNELAKG 28
              | | :||| |:: : :   ||  ::|
Db         70 TSSQSLGETYDFDSIMHYARNTFSRG 95


RESULT 51
US-09-949-016-11601
; Sequence 11601, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11601
;   LENGTH: 174
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11601

  Query Match             30.0%;  Score 48;  DB 2;  Length 174;
  Best Local Similarity   34.6%;  Pred. No. 15;
  Matches    9;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 TVSFNLGEAYEYPTFIQDLRNELAKG 28
              | | :||| |:: : :   ||  ::|
Db         70 TSSQSLGETYDFDSIMHYARNTFSRG 95


RESULT 52
US-09-949-016-11602
; Sequence 11602, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11602
;   LENGTH: 174
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11602

  Query Match             30.0%;  Score 48;  DB 2;  Length 174;
  Best Local Similarity   34.6%;  Pred. No. 15;
  Matches    9;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 TVSFNLGEAYEYPTFIQDLRNELAKG 28
              | | :||| |:: : :   ||  ::|
Db         70 TSSQSLGETYDFDSIMHYARNTFSRG 95


RESULT 53
US-09-549-831-10
; Sequence 10, Application US/09549831
; Patent No. 6429305
; GENERAL INFORMATION:
;  APPLICANT:  Chang, Chi-Yao
;  APPLICANT:  Chang, Chia-Ching
;  APPLICANT:  Leu, Kuen-Lin
;  APPLICANT:  Tsai, Chih-Tung
;  APPLICANT:  Ting, Jing-Wen
;  APPLICANT:  Lin, Chih-Hung
;  TITLE OF INVENTION:  FISH GROWTH HORMONES
;  FILE REFERENCE:  08191-039001
;  CURRENT APPLICATION NUMBER: US/09/549,831
;  CURRENT FILING DATE:  2000-04-14
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Danio rerio
US-09-549-831-10

  Query Match             30.0%;  Score 48;  DB 2;  Length 210;
  Best Local Similarity   37.9%;  Pred. No. 18;
  Matches   11;  Conservative    5;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          4 VSFNLGEAYEYP--TFIQDLRNELAKGTP 30
              :|| | |::|:|  |    : | |  | |
Db         96 ISFRLIESWEFPSQTLSSTISNSLTIGNP 124


RESULT 54
US-08-911-321-9
; Sequence 9, Application US/08911321
; Patent No. 6010703
;  GENERAL INFORMATION:
;     APPLICANT:  Roger K. Maes and Stephen J. Spatz
;     TITLE OF INVENTION:  Recombinant Poxvirus
;     TITLE OF INVENTION:  Vaccine Against
;     TITLE OF INVENTION:  Feline Rhinotracheitis
;     NUMBER OF SEQUENCES:  11
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Ian C. McLeod
;       STREET:  2190  Commons Parkway
;       CITY:  Okemos
;       STATE:  Michigan
```

; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/096,183
; FILING DATE: July 26, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 6010703e
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Polypeptide
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Feline herpesvirus-1
; STRAIN: 1
; INDIVIDUAL ISOLATE: C-27
; CELL TYPE: N/A
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD: Deduced Sequence
; OTHER INFORMATION: gD
US-08-911-321-9

Query Match 30.0%; Score 48; DB 2; Length 373;
Best Local Similarity 45.8%; Pred. No. 36;
Matches 11; Conservative 5; Mismatches 6; Indels 2; Gaps 2;

Qy 1 YN-TVS-FNLGEAYEYPTFIQDLR 22
|| |:| | : : ||| |: |:|
Db 103 YNATISWFKVTQGCEYPMFLMDMR 126

RESULT 55
PCT-US95-13975-73
; Sequence 73, Application PC/TUS9513975
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: McDonell, Michael W.
; TITLE OF INVENTION: Recombinant Feline Herpes virus
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM 330 466 DX2
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13975
; FILING DATE: 26-OCT-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/329,883
; FILING DATE: 26-OCT-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39118-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0525
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13975-73

Query Match 30.0%; Score 48; DB 5; Length 373;
Best Local Similarity 45.8%; Pred. No. 36;
Matches 11; Conservative 5; Mismatches 6; Indels 2; Gaps 2;

Qy 1 YN-TVS-FNLGEAYEYPTFIQDLR 22
|| |:| | : : ||| |: |:|
Db 103 YNATISWFKVTQGCEYPMFLMDMR 126

RESULT 56
US-08-220-151-21
; Sequence 21, Application US/08220151
; Patent No. 5529780
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Limbach, Keith J.
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
; TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC AND gD AND USES THEREFOR
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,151
; FILING DATE: 30-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2540
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066 CURTMS
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  N-terminal
US-08-220-151-21

  Query Match             30.0%;  Score 48;  DB 1;  Length 374;
  Best Local Similarity   45.8%;  Pred. No. 37;
  Matches   11;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    2;

Qy          1 YN-TVS-FNLGEAYEYPTFIQDLR 22
              || |:| | : :  ||| |: |:|
Db        104 YNATISWFKVTQGCEYPMFLMDMR 127


RESULT 57
US-08-413-118-21
; Sequence 21, Application US/08413118
; Patent No. 5688920
;  GENERAL INFORMATION:
;    APPLICANT:  PAOLETTI, ENZO
;    APPLICANT:  LIMBACH, KEITH J.
;    TITLE OF INVENTION:  NUCLEOTIDE AND AMINO ACID SEQUENCES OF
;    TITLE OF INVENTION:  CANINE HERPESVIRUS gB, gC, AND gD AND USES THEREFOR
;    NUMBER OF SEQUENCES:  128
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CURTIS, MORRIS & SAFFORD, P.C.
;      STREET:  530 FIFTH AVENUE, 25TH FLOOR
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/413,118
;      FILING DATE:  29-MAR-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/220,151
;      FILING DATE:  30-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROMMER, WILLIAM S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2670
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  374 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  N-terminal
US-08-413-118-21

  Query Match             30.0%;  Score 48;  DB 1;  Length 374;
  Best Local Similarity   45.8%;  Pred. No. 37;
  Matches   11;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    2;

Qy          1 YN-TVS-FNLGEAYEYPTFIQDLR 22
              || |:| | : :  ||| |: |:|
Db        104 YNATISWFKVTQGCEYPMFLMDMR 127


RESULT 58
US-08-473-446-21
; Sequence 21, Application US/08473446
; Patent No. 6017542
;  GENERAL INFORMATION:
;    APPLICANT:  PAOLETTI, ENZO
;    APPLICANT:  LIMBACH, KEITH J.
;    TITLE OF INVENTION:  NUCLEOTIDE AND AMINO ACID SEQUENCES OF
;    TITLE OF INVENTION:  CANINE HERPESVIRUS gB, gC, AND gD AND USES THEREFOR
;    NUMBER OF SEQUENCES:  128
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CURTIS, MORRIS & SAFFORD, P.C.
;      STREET:  530 FIFTH AVENUE, 25TH FLOOR
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,446
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/413,118
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROMMER, WILLIAM S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2670
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  374 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  N-terminal
US-08-473-446-21

  Query Match             30.0%;  Score 48;  DB 2;  Length 374;
  Best Local Similarity   45.8%;  Pred. No. 37;
  Matches   11;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    2;

Qy          1 YN-TVS-FNLGEAYEYPTFIQDLR 22
              || |:| | : :  ||| |: |:|
Db        104 YNATISWFKVTQGCEYPMFLMDMR 127


RESULT 59
US-09-902-540-10657
; Sequence 10657, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10657
;   LENGTH: 409
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-10657

  Query Match             30.0%;  Score 48;  DB 2;  Length 409;
```

Best Local Similarity 45.0%; Pred. No. 41;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```
Qy         10 EAYEYPTFIQDLRNELAKGT 29
              ||||:|  :::| | | : |
Db        289 EAYEWPGNLRELANALERAT 308
```

RESULT 60
US-09-248-796A-18715
; Sequence 18715, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18715
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18715

Query Match 29.4%; Score 47; DB 2; Length 185;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

```
Qy         13 EYPTFIQDLRNELAKGTP 30
              | |:  ||:: ||  |||
Db         88 ETPSVSQDIKTELVFGTP 105
```

RESULT 61
US-09-186-276B-36
; Sequence 36, Application US/09186276B
; Patent No. 6388173
; GENERAL INFORMATION:
; APPLICANT: Benfey, Philip
; APPLICANT: DiLaurenzio, Laura
; APPLICANT: Wysocka-Diller, Joanna
; APPLICANT: Malamy, Jocelyn E.
; APPLICANT: Pysh, Leonard
; APPLICANT: Helariutta, Yrjo
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof
; FILE REFERENCE: 5914-075-999
; CURRENT APPLICATION NUMBER: US/09/186,276B
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 08/842,445
; PRIOR FILING DATE: 1997-04-24
; PRIOR APPLICATION NUMBER: 08/638,617
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Oryza sp.
US-09-186-276B-36

Query Match 29.4%; Score 47; DB 2; Length 203;
Best Local Similarity 29.6%; Pred. No. 25;
Matches 8; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKG 28
              : : ||||   :: :|:|:| :    |
Db         78 HVIDFNLGVGGQWASFLQELAHRRGAG 104
```

RESULT 62
US-08-842-445-36
; Sequence 36, Application US/08842445A
; Patent No. 6441270
; GENERAL INFORMATION:
; APPLICANT: Benfey et al.
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5914-056-999
; CURRENT APPLICATION NUMBER: US/08/842,445A
; CURRENT FILING DATE: 1997-04-24
; EARLIER APPLICATION NUMBER: 08/638,617
; EARLIER FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Plant
US-08-842-445-36

Query Match 29.4%; Score 47; DB 2; Length 203;
Best Local Similarity 29.6%; Pred. No. 25;
Matches 8; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKG 28
              : : ||||   :: :|:|:| :    |
Db         78 HVIDFNLGVGGQWASFLQELAHRRGAG 104
```

RESULT 63
US-09-186-188B-36
; Sequence 36, Application US/09186188B
; Patent No. 6455672
; GENERAL INFORMATION:
; APPLICANT: Benfey et al.
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5914-074-999
; CURRENT APPLICATION NUMBER: US/09/186,188B
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 08/842,445
; PRIOR FILING DATE: 1997-04-24
; PRIOR APPLICATION NUMBER: 08/638,617
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Plant
US-09-186-188B-36

Query Match 29.4%; Score 47; DB 2; Length 203;
Best Local Similarity 29.6%; Pred. No. 25;
Matches 8; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKG 28
              : : ||||   :: :|:|:| :    |
Db         78 HVIDFNLGVGGQWASFLQELAHRRGAG 104
```

RESULT 64
US-09-270-767-34529
; Sequence 34529, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

```
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34529
;    LENGTH: 252
;    TYPE: PRT
;    ORGANISM: Drosophila melanogaster
;    FEATURE:
;    OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34529

  Query Match             29.4%;  Score 47;  DB 2;  Length 252;
  Best Local Similarity   50.0%;  Pred. No. 33;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         15 PTFIQDLRNELAKGTP 30
              ||::| | ||:  | |
Db         36 PTYLQQLYNEMNNGDP 51


RESULT 65
US-09-270-767-49746
; Sequence 49746, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49746
;    LENGTH: 252
;    TYPE: PRT
;    ORGANISM: Drosophila melanogaster
;    FEATURE:
;    OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49746

  Query Match             29.4%;  Score 47;  DB 2;  Length 252;
  Best Local Similarity   50.0%;  Pred. No. 33;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         15 PTFIQDLRNELAKGTP 30
              ||::| | ||:  | |
Db         36 PTYLQQLYNEMNNGDP 51


RESULT 66
US-09-265-585C-36
; Sequence 36, Application US/09265585C
; Patent No. 6809234
; GENERAL INFORMATION:
;  APPLICANT: Benfey, Phillip N.
;  APPLICANT:  Di Laurenzio, Laura
;  APPLICANT:  Wysocka-Diller, Joanna
;  APPLICANT:  Malamy, Jocelyn E.
;  APPLICANT:  Pysh, Leonard
;  APPLICANT:  Helariutta, Yrjo
;  APPLICANT:  Bruce, Wesley
;  APPLICANT:  Lim, Jun
;  TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof
;  FILE REFERENCE: 5914-066
;  CURRENT APPLICATION NUMBER: US/09/265,585C
;  CURRENT FILING DATE:  1999-03-10
;  PRIOR APPLICATION NUMBER: 08/842,445
;  PRIOR FILING DATE: 1997-04-24
;  PRIOR APPLICATION NUMBER: 08/638,617
;  PRIOR FILING DATE: 1996-04-26
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;    LENGTH: 310
;    TYPE: PRT
;    ORGANISM: Oryza sativa
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: 310
;    OTHER INFORMATION: Xaa = STOP
US-09-265-585C-36

  Query Match             29.4%;  Score 47;  DB 2;  Length 310;
  Best Local Similarity   29.6%;  Pred. No. 42;
  Matches    8;  Conservative    8;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKG 28
              : : ||||   :: :|:|:| :    |
Db         78 HVIDFNLGVGGQWASFLQELAHRRGAG 104


RESULT 67
US-09-328-352-6865
; Sequence 6865, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6865
;    LENGTH: 398
;    TYPE: PRT
;    ORGANISM: Acinetobacter baumannii
US-09-328-352-6865

  Query Match             29.4%;  Score 47;  DB 2;  Length 398;
  Best Local Similarity   53.3%;  Pred. No. 56;
  Matches    8;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         13 EYPTFIQDLRNELAK 27
              || : :||:|| | |
Db         59 EYNSLVQDIRNRLVK 73


RESULT 68
US-09-270-767-42980
; Sequence 42980, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42980
;    LENGTH: 420
;    TYPE: PRT
;    ORGANISM: Drosophila melanogaster
US-09-270-767-42980

  Query Match             29.4%;  Score 47;  DB 2;  Length 420;
  Best Local Similarity   31.0%;  Pred. No. 60;
  Matches   13;  Conservative    9;  Mismatches    6;  Indels   14;  Gaps    2;

Qy          2 NTVS-FNLGEAYEYPTFIQ----------DLRNELAKGT 29
              :||| |   |  :||||::           :||::: ||:
Db        234 DTVSTFTSYELMDYPTFVRYTVYVAMIALPRNELRDKVIKGS 275


RESULT 69
```

```
US-10-118-328-5
; Sequence 5, Application US/10118328
; Patent No. 6773904
; GENERAL INFORMATION:
;  APPLICANT: YAN, Chunhua et al.
;  TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001220
;  CURRENT APPLICATION NUMBER: US/10/118,328
;  CURRENT FILING DATE:  2002-04-09
;  PRIOR APPLICATION NUMBER: 60/282,460
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 725
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-118-328-5

  Query Match             29.4%;  Score 47;  DB 2;  Length 725;
  Best Local Similarity   39.3%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    5;  Mismatches    4;  Indels    8;  Gaps    1;

Qy          2 NTVSFNL--------GEAYEYPTFIQDL 21
              ||:||:|        ||: |:  | :||
Db        200 NTISFSLEEEEELEGGESAEFTCFSEDL 227


RESULT 70
US-09-487-558B-348
; Sequence 348, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
;  APPLICANT: Busby, Robert
;  APPLICANT:  Cali, Brian
;  APPLICANT:  Hecht, Peter
;  APPLICANT:  Holtzman, Doug
;  APPLICANT:  Madden, Kevin
;  APPLICANT:  Maxon, Mary
;  APPLICANT:  Milne, Todd
;  APPLICANT:  No. 6949356man, Thea
;  APPLICANT:  Royer, John
;  APPLICANT:  Salama, Sofie
;  APPLICANT:  Sherman, Amir
;  APPLICANT:  Silva, Jeff
;  APPLICANT:  Summers, Eric
;  TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
;  FILE REFERENCE: 109272.130
;  CURRENT APPLICATION NUMBER: US/09/487,558B
;  CURRENT FILING DATE:  2000-01-19
;  PRIOR APPLICATION NUMBER: US 60/487,558
;  PRIOR FILING DATE: 1999-10-20
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 348
;   LENGTH: 785
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-348

  Query Match             29.4%;  Score 47;  DB 2;  Length 785;
  Best Local Similarity   42.1%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 YEYPTFIQDLRNELAKGTP 30
              | || ||:|::: | :  |
Db        504 YLYPLFIRDIQSVLKQNNP 522


RESULT 71
US-09-489-039A-12755
; Sequence 12755, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 12755
;   LENGTH: 883
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12755

  Query Match             29.4%;  Score 47;  DB 2;  Length 883;
  Best Local Similarity   41.9%;  Pred. No. 1.5e+02;
  Matches   13;  Conservative    3;  Mismatches    9;  Indels    6;  Gaps    2;

Qy          1 YNTVSFNLGEAYEYPTFI---QDLRNELAKG 28
              ||    |:|::   |  |   ||| |||  |
Db        296 YNN---NVGDSSRMPKLIKLQQDLNNELKDG 323


RESULT 72
5248606-6
;Patent No. 5248606
;     APPLICANT: WALSH, TERENCE A.;HEY, TIMOTHY D.;MORGAN,
;ALICE E.R.
;     TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
;ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
;     NUMBER OF SEQUENCES: 49
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/535,636
;       FILING DATE: 11-JUN-1990
;SEQ ID NO:6:
;       LENGTH: 39
5248606-6

  Query Match             29.1%;  Score 46.5;  DB 7;  Length 39;
  Best Local Similarity   41.7%;  Pred. No. 4.2;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 73
US-09-710-279-128
; Sequence 128, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
;   LENGTH: 222
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-09-710-279-128
```

```
  Query Match             29.1%;  Score 46.5;  DB 2;  Length 222;
  Best Local Similarity   40.7%;  Pred. No. 34;
  Matches   11;  Conservative    5;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAK 27
              :||:  ||   |:  |  ||: ||: |
Db        192 FNTLD-NLNIKYQLATSAQDVYNEIKK 217


RESULT 74
US-07-901-707-3
; Sequence 3, Application US/07901707
; Patent No. 5376546
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Composition and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/901,707
;      FILING DATE:  19920619
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5376546and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27129/30910
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-5750
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-901-707-3

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 75
US-07-988-430-3
; Sequence 3, Application US/07988430
; Patent No. 5416202
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,430
;      FILING DATE:  19921209
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5416202and, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-988-430-3

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 76
US-08-425-336-3
; Sequence 3, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
```

```
;       COUNTRY:  USA
;       ZIP:  60606-6402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/425,336
;       FILING DATE:  18-APR-1995
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/064,691
;       FILING DATE:  12-MAY-1993
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Meyers, Thomas C.
;       REGISTRATION NUMBER:  P-36,989
;       REFERENCE/DOCKET NUMBER:  31394
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/474-6300
;       TELEFAX:  312/474-0448
;       TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  280 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-425-336-3

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 77
US-08-425-336-127
; Sequence 127, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-425-336-127

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 78
US-08-425-336-128
; Sequence 128, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
```

```
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  128:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-425-336-128

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 79
US-08-425-336-129
; Sequence 129, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  129:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-425-336-129

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 80
US-08-378-761A-26
; Sequence 26, Application US/08378761A
; Patent No. 5635384
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761A
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-761A-26

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 81
US-08-485-286-26
; Sequence 26, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
```

```
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,286
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/378761
;      FILING DATE:  26-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-485-286-26

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 82
US-08-488-113B-3
; Sequence 3, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-3

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 83
US-08-488-113B-127
; Sequence 127, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-127

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 84
US-08-488-113B-128
; Sequence 128, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  128:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-128

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 85
US-08-488-113B-129
; Sequence 129, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  129:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-129

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 86
US-08-477-484B-3
; Sequence 3, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-3

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 87
US-08-477-484B-127
; Sequence 127, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-127

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
```

```
                  | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 88
US-08-477-484B-128
; Sequence 128, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  128:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-128

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
                | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 89
US-08-477-484B-129
; Sequence 129, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  129:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-129

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
                | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 90
US-08-646-360-3
; Sequence 3, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
```

```
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-360-3

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 91
US-08-646-360-127
; Sequence 127, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-360-127

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 92
US-08-646-360-128
; Sequence 128, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/646,360
;       FILING DATE:  13-MAY-1996
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/05348
;       FILING DATE:  12-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  200-70.P4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  128:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  280 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-646-360-128

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 93
US-08-646-360-129
; Sequence 129, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  129:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-360-129

  Query Match             29.1%;  Score 46.5;  DB 1;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 94
US-08-839-765-3
; Sequence 3, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
```

```
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-3

  Query Match             29.1%;  Score 46.5;  DB 2;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 95
US-08-839-765-127
; Sequence 127, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-127

  Query Match             29.1%;  Score 46.5;  DB 2;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 96
US-08-839-765-128
; Sequence 128, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
```

```
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  128:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-128

  Query Match             29.1%;  Score 46.5;  DB 2;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 97
US-08-839-765-129
; Sequence 129, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  129:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-129

  Query Match             29.1%;  Score 46.5;  DB 2;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 98
US-09-136-389-3
; Sequence 3, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-3

  Query Match             29.1%;  Score 46.5;  DB 2;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 99
US-09-136-389-127
; Sequence 127, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-127

  Query Match             29.1%;  Score 46.5;  DB 2;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37


RESULT 100
US-09-136-389-128
; Sequence 128, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  128:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-128

  Query Match             29.1%;  Score 46.5;  DB 2;  Length 280;
  Best Local Similarity   41.7%;  Pred. No. 44;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;
```

```
Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:    : :| |||  :||:|
Db         14 TATFNVQASSADYATFIAGIRNKL 37
```

Search completed: September 18, 2006, 19:15:31
Job time : 9.5419 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:30:33 ; Search time 42.2346 Seconds
(without alignments)
329.030 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	100.0	30	5	US-10-758-902-1	Sequence 1, Appli
2	160	100.0	149	5	US-10-758-902-9	Sequence 9, Appli
3	160	100.0	250	6	US-11-084-080-1	Sequence 1, Appli
4	160	100.0	250	6	US-11-084-080-11	Sequence 11, Appl
5	160	100.0	250	6	US-11-084-080-12	Sequence 12, Appl
6	160	100.0	250	6	US-11-084-080-13	Sequence 13, Appl
7	160	100.0	250	6	US-11-084-080-14	Sequence 14, Appl
8	160	100.0	250	6	US-11-084-080-129	Sequence 129, App
9	160	100.0	750	6	US-11-084-080-16	Sequence 16, Appl
10	160	100.0	750	6	US-11-084-080-20	Sequence 20, Appl
11	160	100.0	750	6	US-11-084-080-22	Sequence 22, Appl
12	160	100.0	750	6	US-11-084-080-24	Sequence 24, Appl
13	160	100.0	759	6	US-11-084-080-28	Sequence 28, Appl
14	83	51.9	15	6	US-11-084-080-32	Sequence 32, Appl
15	81	50.6	15	6	US-11-084-080-34	Sequence 34, Appl
16	81	50.6	15	6	US-11-084-080-35	Sequence 35, Appl
17	80	50.0	15	6	US-11-084-080-33	Sequence 33, Appl
18	78	48.8	15	6	US-11-084-080-36	Sequence 36, Appl
19	77	48.1	15	6	US-11-084-080-37	Sequence 37, Appl
20	62	38.8	15	6	US-11-084-080-38	Sequence 38, Appl
21	61	38.1	312	5	US-10-467-009-2	Sequence 2, Appli
22	61	38.1	313	6	US-11-106-187-2	Sequence 2, Appli
23	61	38.1	313	6	US-11-010-795-20	Sequence 20, Appl
24	59	36.9	107	4	US-10-424-599-213759	Sequence 213759,
25	59	36.9	261	4	US-10-127-890-9	Sequence 9, Appli
26	59	36.9	261	5	US-10-717-243-9	Sequence 9, Appli
27	57	35.6	324	4	US-10-437-963-146447	Sequence 146447,
28	56	35.0	77	4	US-10-767-701-37927	Sequence 37927, A
29	56	35.0	120	4	US-10-425-115-351081	Sequence 351081,
30	56	35.0	154	3	US-09-978-274A-6	Sequence 6, Appli
31	56	35.0	160	4	US-10-425-115-351080	Sequence 351080,
32	56	35.0	263	3	US-09-978-274A-4	Sequence 4, Appli
33	56	35.0	289	4	US-10-425-115-351084	Sequence 351084,
34	56	35.0	314	3	US-09-978-274A-2	Sequence 2, Appli
35	56	35.0	314	4	US-10-128-713A-16	Sequence 16, Appl
36	54.5	34.1	292	4	US-10-424-599-274703	Sequence 274703,
37	54	33.8	447	4	US-10-424-599-215698	Sequence 215698,
38	53	33.1	1464	6	US-11-097-143-40125	Sequence 40125, A
39	51.5	32.2	757	4	US-10-437-963-136583	Sequence 136583,
40	51	31.9	148	4	US-10-767-701-50462	Sequence 50462, A
41	51	31.9	1416	3	US-09-071-035-404	Sequence 404, App
42	51	31.9	1416	4	US-10-206-576-404	Sequence 404, App
43	51	31.9	1416	5	US-10-912-362-404	Sequence 404, App
44	51	31.9	1448	3	US-09-071-035-402	Sequence 402, App
45	51	31.9	1448	4	US-10-206-576-402	Sequence 402, App
46	51	31.9	1448	5	US-10-912-362-402	Sequence 402, App
47	50.5	31.6	312	4	US-10-028-248A-101	Sequence 101, App
48	50.5	31.6	312	4	US-10-107-782-101	Sequence 101, App
49	50.5	31.6	685	6	US-11-087-099-3131	Sequence 3131, Ap
50	50.5	31.6	1211	5	US-10-474-792-38	Sequence 38, Appl
51	50	31.2	334	4	US-10-369-493-8942	Sequence 8942, Ap
52	50	31.2	366	6	US-11-188-298-8941	Sequence 8941, Ap
53	50	31.2	638	4	US-10-437-963-189354	Sequence 189354,
54	50	31.2	668	5	US-10-732-923-1792	Sequence 1792, Ap
55	49.5	30.9	1610	3	US-09-738-626-6666	Sequence 6666, Ap
56	49.5	30.9	1610	4	US-10-627-476-14	Sequence 14, Appl
57	49.5	30.9	1610	4	US-10-627-476-56	Sequence 56, Appl
58	49	30.6	68	4	US-10-437-963-186472	Sequence 186472,
59	49	30.6	362	5	US-10-739-930-8881	Sequence 8881, Ap
60	49	30.6	447	5	US-10-739-930-8813	Sequence 8813, Ap
61	49	30.6	732	4	US-10-156-761-14353	Sequence 14353, A
62	49	30.6	806	4	US-10-264-049-2841	Sequence 2841, Ap
63	49	30.6	1168	4	US-10-369-493-16733	Sequence 16733, A
64	49	30.6	1850	4	US-10-146-657-5	Sequence 5, Appli
65	49	30.6	2154	4	US-10-695-994-4	Sequence 4, Appli
66	49	30.6	2154	5	US-10-805-684-150	Sequence 150, App
67	49	30.6	2364	4	US-10-170-385-15	Sequence 15, Appl
68	48.5	30.3	62	4	US-10-424-599-182569	Sequence 182569,
69	48.5	30.3	214	4	US-10-282-122A-52871	Sequence 52871, A
70	48.5	30.3	272	4	US-10-231-913-106	Sequence 106, App
71	48.5	30.3	312	4	US-10-028-248A-99	Sequence 99, Appl
72	48.5	30.3	312	4	US-10-231-913-105	Sequence 105, App
73	48.5	30.3	312	4	US-10-107-782-99	Sequence 99, Appl
74	48.5	30.3	312	5	US-10-344-326-34	Sequence 34, Appl
75	48.5	30.3	312	5	US-10-756-149-5517	Sequence 5517, Ap
76	48	30.0	188	4	US-10-191-879-19	Sequence 19, Appl
77	48	30.0	210	4	US-10-191-879-10	Sequence 10, Appl
78	48	30.0	237	5	US-10-732-923-16035	Sequence 16035, A
79	48	30.0	266	5	US-10-501-282-4668	Sequence 4668, Ap
80	48	30.0	269	4	US-10-369-493-64	Sequence 64, Appl
81	48	30.0	300	4	US-10-670-695-26	Sequence 26, Appl
82	48	30.0	303	5	US-10-501-282-4670	Sequence 4670, Ap
83	48	30.0	374	4	US-10-670-695-24	Sequence 24, Appl
84	48	30.0	420	5	US-10-732-923-2574	Sequence 2574, Ap
85	48	30.0	475	4	US-10-425-115-190559	Sequence 190559,
86	48	30.0	514	4	US-10-369-493-13282	Sequence 13282, A
87	48	30.0	712	4	US-10-369-493-1508	Sequence 1508, Ap
88	48	30.0	833	5	US-10-915-002-286	Sequence 286, App
89	48	30.0	931	6	US-11-097-143-3411	Sequence 3411, Ap
90	48	30.0	1228	4	US-10-369-493-23342	Sequence 23342, A
91	48	30.0	2171	5	US-10-739-930-6743	Sequence 6743, Ap
92	47.5	29.7	572	6	US-11-097-143-14550	Sequence 14550, A
93	47.5	29.7	669	4	US-10-437-963-203986	Sequence 203986,
94	47.5	29.7	862	6	US-11-045-004-26	Sequence 26, Appl
95	47	29.4	15	6	US-11-084-080-39	Sequence 39, Appl
96	47	29.4	203	3	US-09-186-276B-36	Sequence 36, Appl
97	47	29.4	203	3	US-09-186-188B-36	Sequence 36, Appl
98	47	29.4	203	4	US-10-253-007-36	Sequence 36, Appl
99	47	29.4	281	4	US-10-282-122A-50612	Sequence 50612, A
100	47	29.4	389	4	US-10-161-051-105	Sequence 105, App

ALIGNMENTS

```
RESULT 1
US-10-758-902-1
; Sequence 1, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-1

  Query Match             100.0%;  Score 160;  DB 5;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 2
US-10-758-902-9
; Sequence 9, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-9

  Query Match             100.0%;  Score 160;  DB 5;  Length 149;
  Best Local Similarity   100.0%;  Pred. No. 1e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 3
US-11-084-080-1
; Sequence 1, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis Wild
US-11-084-080-1

  Query Match             100.0%;  Score 160;  DB 6;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 4
US-11-084-080-11
; Sequence 11, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (123)..(123)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
```

```
;   LOCATION: (127)..(127)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (129)..(129)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (133)..(133)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (152)..(152)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-084-080-11

  Query Match           100.0%;  Score 160;  DB 6;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 5
US-11-084-080-12
; Sequence 12, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (123)..(123)
;   OTHER INFORMATION: Xaa can be T or A or Q
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (127)..(127)
;   OTHER INFORMATION: Xaa can be G or A
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (129)..(129)
;   OTHER INFORMATION: Xaa can be Q or G
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (133)..(133)
;   OTHER INFORMATION: Xaa can be N or D or T or A or R or Q or E or G or H or K or S
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (152)..(152)
;   OTHER INFORMATION: Xaa can be Q or A
US-11-084-080-12

  Query Match           100.0%;  Score 160;  DB 6;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 6
US-11-084-080-13
; Sequence 13, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-13

  Query Match           100.0%;  Score 160;  DB 6;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 7
US-11-084-080-14
; Sequence 14, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
```

```
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-14

  Query Match             100.0%;  Score 160;  DB 6;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 8
US-11-084-080-129
; Sequence 129, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-129

  Query Match             100.0%;  Score 160;  DB 6;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 9
US-11-084-080-16
; Sequence 16, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-16

  Query Match             100.0%;  Score 160;  DB 6;  Length 750;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db        254 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 283


RESULT 10
US-11-084-080-20
; Sequence 20, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-20

  Query Match             100.0%;  Score 160;  DB 6;  Length 750;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db        501 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 530


RESULT 11
US-11-084-080-22
; Sequence 22, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
```

; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald .
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-22

Query Match 100.0%; Score 160; DB 6; Length 750;
Best Local Similarity 100.0%; Pred. No. 6.7e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
||||||||||||||||||||||||||||||
Db 23 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 52

RESULT 12
US-11-084-080-24
; Sequence 24, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-24

Query Match 100.0%; Score 160; DB 6; Length 750;
Best Local Similarity 100.0%; Pred. No. 6.7e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
||||||||||||||||||||||||||||||
Db 270 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 299

RESULT 13
US-11-084-080-28
; Sequence 28, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-011
US-11-084-080-28

Query Match 100.0%; Score 160; DB 6; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.8e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
||||||||||||||||||||||||||||||
Db 263 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 292

RESULT 14
US-11-084-080-32
; Sequence 32, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bougainvillea spectabilis
US-11-084-080-32

Query Match 51.9%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYP 15
              |||||||||||||||
Db          1 YNTVSFNLGEAYEYP 15


RESULT 15
US-11-084-080-34
; Sequence 34, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-34

  Query Match             50.6%;  Score 81;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 5e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDL 21
              |||||||||||||||
Db          1 NLGEAYEYPTFIQDL 15


RESULT 16
US-11-084-080-35
; Sequence 35, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-35

  Query Match             50.6%;  Score 81;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 5e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 EAYEYPTFIQDLRNE 24
              |||||||||||||||
Db          1 EAYEYPTFIQDLRNE 15


RESULT 17
US-11-084-080-33
; Sequence 33, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-33

  Query Match             50.0%;  Score 80;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFI 18
              |||||||||||||||
Db          1 VSFNLGEAYEYPTFI 15


RESULT 18
US-11-084-080-36
; Sequence 36, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
```

```
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-36

  Query Match             48.8%;  Score 78;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.00014;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 EYPTFIQDLRNELAK 27
              |||||||||||||||
Db          1 EYPTFIQDLRNELAK 15


RESULT 19
US-11-084-080-37
; Sequence 37, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-37

  Query Match             48.1%;  Score 77;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 TFIQDLRNELAKGTP 30
              |||||||||||||||
Db          1 TFIQDLRNELAKGTP 15


RESULT 20
US-11-084-080-38
; Sequence 38, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-38

  Query Match             38.8%;  Score 62;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.035;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 QDLRNELAKGTP 30
              ||||||||||||
Db          1 QDLRNELAKGTP 12


RESULT 21
US-10-467-009-2
; Sequence 2, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
;  APPLICANT: RUTGERS, THE STATE UNIVERSITY
;  TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
;  FILE REFERENCE: OCIRS 3.4-076
;  CURRENT APPLICATION NUMBER: US/10/467,009
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: 60/266,396
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-10-467-009-2

  Query Match             38.1%;  Score 61;  DB 5;  Length 312;
  Best Local Similarity   48.0%;  Pred. No. 1.7;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 22
US-11-106-187-2
; Sequence 2, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  WANG, PINGER
;  TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
;  FILE REFERENCE: OCIRS 3.9-060 CONT
;  CURRENT APPLICATION NUMBER: US/11/106,187
;  CURRENT FILING DATE:  2005-04-14
;  PRIOR APPLICATION NUMBER: US/09/721,047
;  PRIOR FILING DATE: 2000-11-22
;  PRIOR APPLICATION NUMBER: PCT/US99/11301
;  PRIOR FILING DATE: 1999-05-21
;  PRIOR APPLICATION NUMBER: 60/086,374
;  PRIOR FILING DATE: 1998-05-22
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
;   LENGTH: 313
;   TYPE: PRT
```

```
;   ORGANISM: Phytolacca americana
US-11-106-187-2

  Query Match           38.1%;  Score 61;  DB 6;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 1.7;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 23
US-11-010-795-20
; Sequence 20, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  DI, RONG
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
;  TITLE OF INVENTION:  RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
;  FILE REFERENCE: OCIRS 3.0-085
;  CURRENT APPLICATION NUMBER: US/11/010,795
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: 60/529,348
;  PRIOR FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 20
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-11-010-795-20

  Query Match           38.1%;  Score 61;  DB 6;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 1.7;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 24
US-10-424-599-213759
; Sequence 213759, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 213759
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_3504C.1.pep
US-10-424-599-213759

  Query Match           36.9%;  Score 59;  DB 4;  Length 107;
  Best Local Similarity   43.6%;  Pred. No. 0.98;
  Matches   17;  Conservative    2;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| |||   ||           | |||  |
Db         36 TVNFN-GETFESPTFCSTLRQAEHAAAGVALNTLAKRGP 73


RESULT 25
US-10-127-890-9
; Sequence 9, Application US/10127890
; Publication No. US20030166196A1
;  GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 173
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/127,890
;            FILING DATE: 23-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,360
;            FILING DATE: 13-MAY-1996
;            APPLICATION NUMBER: PCT/US94/05348
;            FILING DATE: 12-MAY-1994
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 261 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-127-890-9

  Query Match           36.9%;  Score 59;  DB 4;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 2.7;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 26
US-10-717-243-9
; Sequence 9, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
```

```
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 169
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/717,243
;            FILING DATE: 18-Nov-2003
;            CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/839,765
;            FILING DATE: 15-APR-1997
;            APPLICATION NUMBER: US 08/425,336
;            FILING DATE: 18-APR-1995
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 261 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-717-243-9

  Query Match             36.9%;  Score 59;  DB 5;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 2.7;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 27
US-10-437-963-146447
; Sequence 146447, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146447
;   LENGTH: 324
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_47070C.1.pep
US-10-437-963-146447

  Query Match             35.6%;  Score 57;  DB 4;  Length 324;
  Best Local Similarity   41.0%;  Pred. No. 7;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GETFESPAFCSTLRLAEHAAAEVALNELSKRGP 73


RESULT 28
US-10-767-701-37927
; Sequence 37927, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 37927
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-C41259_1.pep
US-10-767-701-37927

  Query Match             35.0%;  Score 56;  DB 4;  Length 77;
  Best Local Similarity   41.0%;  Pred. No. 1.9;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPAFCSTLRQAEHAAAEVALNELSKRGP 73


RESULT 29
US-10-425-115-351081
; Sequence 351081, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351081
;   LENGTH: 120
;   TYPE: PRT
```

```
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83354C.1.pep
US-10-425-115-351081

  Query Match             35.0%;  Score 56;  DB 4;  Length 120;
  Best Local Similarity   41.0%;  Pred. No. 3.1;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps   2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPVFCSTLRQAEHAAAEVALNELSKRGP 73


RESULT 30
US-09-978-274A-6
; Sequence 6, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 154
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-09-978-274A-6

  Query Match             35.0%;  Score 56;  DB 3;  Length 154;
  Best Local Similarity   44.0%;  Pred. No. 4.2;
  Matches   11;  Conservative    7;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: |||:
Db          3 NTITFDAGNATINKYATFMESLRNQ 27


RESULT 31
US-10-425-115-351080
; Sequence 351080, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351080
;   LENGTH: 160
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83353C.1.pep
US-10-425-115-351080

  Query Match             35.0%;  Score 56;  DB 4;  Length 160;
  Best Local Similarity   41.0%;  Pred. No. 4.4;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPVFCSTLRQAEHAAAEVALNELSKRGP 73


RESULT 32
US-09-978-274A-4
; Sequence 4, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 263
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-09-978-274A-4

  Query Match             35.0%;  Score 56;  DB 3;  Length 263;
  Best Local Similarity   44.0%;  Pred. No. 7.8;
  Matches   11;  Conservative    7;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: |||:
Db          3 NTITFDAGNATINKYATFMESLRNQ 27


RESULT 33
US-10-425-115-351084
; Sequence 351084, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351084
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83357C.1.pep
US-10-425-115-351084

  Query Match             35.0%;  Score 56;  DB 4;  Length 289;
  Best Local Similarity   41.0%;  Pred. No. 8.7;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPVFCSTLRQAEHAAAEVALNELSKRGP 73


RESULT 34
US-09-978-274A-2
; Sequence 2, Application US/09978274A
; Patent No. US20020116737A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-09-978-274A-2

  Query Match             35.0%;  Score 56;  DB 3;  Length 314;
  Best Local Similarity   44.0%;  Pred. No. 9.6;
  Matches   11;  Conservative    7;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: |||:
Db         26 NTITFDAGNATINKYATFMESLRNQ 50


RESULT 35
US-10-128-713A-16
; Sequence 16, Application US/10128713A
; Publication No. US20030170847A1
; GENERAL INFORMATION:
;  APPLICANT: Bramucci, Michael G
;  TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production
;  FILE REFERENCE: CL-1788
;  CURRENT APPLICATION NUMBER: US/10/128,713A
;  CURRENT FILING DATE:  2002-04-22
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Rhodococcus erythropolis
US-10-128-713A-16

  Query Match             35.0%;  Score 56;  DB 4;  Length 314;
  Best Local Similarity   45.5%;  Pred. No. 9.6;
  Matches   10;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKG 28
              |||||::   ||:|:  :| :|
Db        174 NLGEAFQLTNFIRDVGEDLDRG 195


RESULT 36
US-10-424-599-274703
; Sequence 274703, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274703
;   LENGTH: 292
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_90078C.1.pep
US-10-424-599-274703

  Query Match             34.1%;  Score 54.5;  DB 4;  Length 292;
  Best Local Similarity   38.7%;  Pred. No. 15;
  Matches   12;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 YNTVSFNL-GEAYEYPTFIQDLRNELAKGTP 30
              |  : ||  || ::|| |   :|: :|  ||
Db         22 YTFLEFNTQGEDFDYPEFRDPIRSPVAWPTP 52


RESULT 37
US-10-424-599-215698
; Sequence 215698, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215698
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(447)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_36803C.1.pep
US-10-424-599-215698

  Query Match             33.8%;  Score 54;  DB 4;  Length 447;
  Best Local Similarity   50.0%;  Pred. No. 29;
  Matches   11;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNEL 25
              |  |   |  | | |:||:||:|
Db        210 VVMNFFEELEPPLFVQDMRNKL 231


RESULT 38
US-11-097-143-40125
; Sequence 40125, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
```

; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40125
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-40125

Query Match 33.1%; Score 53; DB 6; Length 1464;
Best Local Similarity 43.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 7 NLGEAYEYPTFIQDLRNELAKGT 29
:|| ||:| : : || :|||
Db 660 SLGMAYDYDSIMHYARNTFSKGT 682

RESULT 39
US-10-437-963-136583
; Sequence 136583, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 136583
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38148C.1.pep
US-10-437-963-136583

Query Match 32.2%; Score 51.5; DB 4; Length 757;
Best Local Similarity 40.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

Qy 7 NLGEAYEYPTFIQDLRNELAK---GTP 30
|| :| || ::|| :|:| | |
Db 272 NLNQAMSYPPLMEDLGRQLSKKCGGLP 298

RESULT 40
US-10-767-701-50462
; Sequence 50462, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 50462
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3480-009-P1-K1-F12.pep
US-10-767-701-50462

Query Match 31.9%; Score 51; DB 4; Length 148;
Best Local Similarity 40.0%; Pred. No. 23;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 NTVSFNLGEAYEYPTFIQDL 21
: | ||||: ::|: : ||
Db 4 HVVDFNLGDGIQWPSLMSDL 23

RESULT 41
US-09-071-035-404
; Sequence 404, Application US/09071035
; Publication No. US20020045737A1
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-404

Query Match 31.9%; Score 51; DB 3; Length 1416;
Best Local Similarity 38.5%; Pred. No. 3.1e+02;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
||||| | |: | | : |:::
Db 873 YNTVSANAGQIYTETTIDSETLNQMS 898

RESULT 42
US-10-206-576-404
; Sequence 404, Application US/10206576
; Publication No. US20030017495A1

```
;   GENERAL INFORMATION:
;        APPLICANT: Choi et al.
;        TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;        NUMBER OF SEQUENCES: 497
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: Dell Latitude
;             OPERATING SYSTEM: Windows 98
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/206,576
;             FILING DATE: 29-Jul-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/071,035
;             FILING DATE: 1998-05-04
;             APPLICATION NUMBER: US 60/046,655
;             FILING DATE: 1997-05-16
;             APPLICATION NUMBER: US 60/044,031
;             FILING DATE: 1997-05-06
;             APPLICATION NUMBER: US 60/066,009
;             FILING DATE: 1997-11-14
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hyman, Mark J.
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB369P1D1
;   INFORMATION FOR SEQ ID NO: 404:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1416 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 404:
US-10-206-576-404

  Query Match             31.9%;  Score 51;  DB 4;  Length 1416;
  Best Local Similarity   38.5%;  Pred. No. 3.1e+02;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |    |    :  |:::
Db        873 YNTVSANAGQIYTETTIDSETLNQMS 898


RESULT 43
US-10-912-362-404
; Sequence 404, Application US/10912362
; Publication No. US20050043528A1
;   GENERAL INFORMATION:
;        APPLICANT: Choi et al.
;        TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;        NUMBER OF SEQUENCES: 497
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 14200 Shady Grove Road
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: Dell Latitude
;             OPERATING SYSTEM: Windows 2000
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/912,362
;             FILING DATE: 06-Aug-2004
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 10/206,576
;             FILING DATE: 2002-07-29
;             APPLICATION NUMBER: US 09/071,035
;             FILING DATE: 1998-05-04
;             APPLICATION NUMBER: US 60/046,655
;             FILING DATE: 1997-05-16
;             APPLICATION NUMBER: US 60/044,031
;             FILING DATE: 1997-05-06
;             APPLICATION NUMBER: US 60/066,009
;             FILING DATE: 1997-11-14
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hyman, Mark J.
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB369P1D2
;   INFORMATION FOR SEQ ID NO: 404:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1416 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 404:
US-10-912-362-404

  Query Match             31.9%;  Score 51;  DB 5;  Length 1416;
  Best Local Similarity   38.5%;  Pred. No. 3.1e+02;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |    |    :  |:::
Db        873 YNTVSANAGQIYTETTIDSETLNQMS 898


RESULT 44
US-09-071-035-402
; Sequence 402, Application US/09071035
; Publication No. US20020045737A1
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  402:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1448 amino acids
```

```
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-035-402

  Query Match             31.9%;  Score 51;  DB 3;  Length 1448;
  Best Local Similarity   38.5%;  Pred. No. 3.2e+02;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |   |   :  |:::
Db        900 YNTVSANAGQIYTETTIDSETLNQMS 925


RESULT 45
US-10-206-576-402
; Sequence 402, Application US/10206576
; Publication No. US20030017495A1
;   GENERAL INFORMATION:
;        APPLICANT: Choi et al.
;        TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;        NUMBER OF SEQUENCES: 497
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: Dell Latitude
;             OPERATING SYSTEM: Windows 98
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/206,576
;             FILING DATE: 29-Jul-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/071,035
;             FILING DATE: 1998-05-04
;             APPLICATION NUMBER: US 60/046,655
;             FILING DATE: 1997-05-16
;             APPLICATION NUMBER: US 60/044,031
;             FILING DATE: 1997-05-06
;             APPLICATION NUMBER: US 60/066,009
;             FILING DATE: 1997-11-14
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hyman, Mark J.
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB369P1D1
;   INFORMATION FOR SEQ ID NO: 402:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1448 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 402:
US-10-206-576-402

  Query Match             31.9%;  Score 51;  DB 4;  Length 1448;
  Best Local Similarity   38.5%;  Pred. No. 3.2e+02;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |   |   :  |:::
Db        900 YNTVSANAGQIYTETTIDSETLNQMS 925


RESULT 46
US-10-912-362-402
; Sequence 402, Application US/10912362
; Publication No. US20050043528A1
;   GENERAL INFORMATION:
;        APPLICANT: Choi et al.
;        TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;        NUMBER OF SEQUENCES: 497
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 14200 Shady Grove Road
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: Dell Latitude
;             OPERATING SYSTEM: Windows 2000
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/912,362
;             FILING DATE: 06-Aug-2004
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 10/206,576
;             FILING DATE: 2002-07-29
;             APPLICATION NUMBER: US 09/071,035
;             FILING DATE: 1998-05-04
;             APPLICATION NUMBER: US 60/046,655
;             FILING DATE: 1997-05-16
;             APPLICATION NUMBER: US 60/044,031
;             FILING DATE: 1997-05-06
;             APPLICATION NUMBER: US 60/066,009
;             FILING DATE: 1997-11-14
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hyman, Mark J.
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB369P1D2
;   INFORMATION FOR SEQ ID NO: 402:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1448 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 402:
US-10-912-362-402

  Query Match             31.9%;  Score 51;  DB 5;  Length 1448;
  Best Local Similarity   38.5%;  Pred. No. 3.2e+02;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |   |   :  |:::
Db        900 YNTVSANAGQIYTETTIDSETLNQMS 925


RESULT 47
US-10-028-248A-101
; Sequence 101, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Malyankar, Uriel
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Miller, Charles
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Li, Li
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Kekuda, Ramesh
```

; APPLICANT: Smithson, Glennda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-028-248A-101

Query Match 31.6%; Score 50.5; DB 4; Length 312;
Best Local Similarity 45.8%; Pred. No. 64;
Matches 11; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

Qy 7 NLGEAYEYPTF---IQDLRNELAK 27
|:| :|||| : | || | : |
Db 133 NVGMSYEYPEYFLEIPDLDNTIKK 156

RESULT 48
US-10-107-782-101
; Sequence 101, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glennda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zerhusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 101
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-782-101

Query Match 31.6%; Score 50.5; DB 4; Length 312;
Best Local Similarity 45.8%; Pred. No. 64;
Matches 11; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

Qy 7 NLGEAYEYPTF---IQDLRNELAK 27
|:| :|||| : | || | : |
Db 133 NVGMSYEYPEYFLEIPDLDNTIKK 156

RESULT 49
US-11-087-099-3131
; Sequence 3131, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3131
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Leptospira interrogans serovar lai str. 56601
US-11-087-099-3131

Query Match 31.6%; Score 50.5; DB 6; Length 685;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 1;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
| :| : | | : ||||:||| |
Db 242 YGAISSGI---QTYYTKVADLRNDLAKAKP 268

RESULT 50
US-10-474-792-38
; Sequence 38, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagursky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Lourie

; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 1211
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-38

Query Match 31.6%; Score 50.5; DB 5; Length 1211;
Best Local Similarity 41.7%; Pred. No. 3.1e+02;
Matches 10; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 4 VSFNLGEAYEYPTFIQDLRNELAK 27
::|:|| || |: |: |: ||
Db 1178 INFSLG-GNEYEAFVSDITNQQAK 1200

RESULT 51
US-10-369-493-8942
; Sequence 8942, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8942
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Chloroflexus aurantiacus
US-10-369-493-8942

Query Match 31.2%; Score 50; DB 4; Length 334;
Best Local Similarity 50.0%; Pred. No. 82;
Matches 13; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

Qy 4 VSFNLGEAYEYPTFIQDLRNELAKGT 29
:|| | | | ||: ||| ::|||
Db 311 ISF--GTAEENRVFIEVLRNLMSKGT 334

RESULT 52
US-11-188-298-8941
; Sequence 8941, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 8941
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Chloroflexus aurantiacus
US-11-188-298-8941

Query Match 31.2%; Score 50; DB 6; Length 366;
Best Local Similarity 50.0%; Pred. No. 91;
Matches 13; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

Qy 4 VSFNLGEAYEYPTFIQDLRNELAKGT 29
:|| | | | ||: ||| ::|||
Db 336 ISF--GTAEENRVFIEVLRNLMSKGT 359

RESULT 53
US-10-437-963-189354
; Sequence 189354, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189354
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(638)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85872C.1.pep
US-10-437-963-189354

Query Match 31.2%; Score 50; DB 4; Length 638;
Best Local Similarity 38.9%; Pred. No. 1.7e+02;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 12 YEYPTFIQDLRNELAKGT 29
|:|| |: || ::: |:
Db 349 YDYPEFVADLTTQVSNGS 366

RESULT 54
US-10-732-923-1792
; Sequence 1792, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1792
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Drosophila virilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(668)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-1792

Query Match 31.2%; Score 50; DB 5; Length 668;

```
  Best Local Similarity   36.0%;  Pred. No. 1.8e+02;
  Matches    9;  Conservative    7;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              :|: |  | :|  :  :| |:|:||
Db        458 TFSYGVTYIFPAALPIIRREVAEGT 482


RESULT 55
US-09-738-626-6666
; Sequence 6666, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988·
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6666
;   LENGTH: 1610
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-6666

  Query Match             30.9%;  Score 49.5;  DB 3;  Length 1610;
  Best Local Similarity   55.0%;  Pred. No. 6e+02;
  Matches   11;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         11 AYEYPTFIQDLRNELAKGTP 30
              ||||||  |: |   | :| |
Db         71 AYEYPT-IRSLAQRLVEGEP 89


RESULT 56
US-10-627-476-14
; Sequence 14, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schoder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CPCN
;  CURRENT APPLICATION NUMBER: US/10/627,476
;  CURRENT FILING DATE:  2003-07-25
;  PRIOR APPLICATION NUMBER: 09/602,787
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 14
;   LENGTH: 1610
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-627-476-14

  Query Match             30.9%;  Score 49.5;  DB 4;  Length 1610;
  Best Local Similarity   55.0%;  Pred. No. 6e+02;
  Matches   11;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         11 AYEYPTFIQDLRNELAKGTP 30
              ||||||  |: |   | :| |
Db         71 AYEYPT-IRSLAQRLVEGEP 89


RESULT 57
US-10-627-476-56
; Sequence 56, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schoder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CPCN
;  CURRENT APPLICATION NUMBER: US/10/627,476
;  CURRENT FILING DATE:  2003-07-25
;  PRIOR APPLICATION NUMBER: 09/602,787
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 56
;   LENGTH: 1610
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-627-476-56
```

```
  Query Match             30.9%;  Score 49.5;  DB 4;  Length 1610;
  Best Local Similarity   55.0%;  Pred. No. 6e+02;
  Matches   11;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         11 AYEYPTFIQDLRNELAKGTP 30
              |||||| |: |   | :| |
Db         71 AYEYPT-IRSLAQRLVEGEP 89


RESULT 58
US-10-437-963-186472
; Sequence 186472, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 186472
;   LENGTH: 68
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(68)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_8326C.1.pep
US-10-437-963-186472

  Query Match             30.6%;  Score 49;  DB 4;  Length 68;
  Best Local Similarity   39.1%;  Pred. No. 18;
  Matches    9;  Conservative    3;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          8 LGEAYEYPTFIQDLRNELAKGTP 30
              ||  |||  |: |   ::  | |
Db          1 LGYRYEYGYFLPDTNTDMVSGFP 23


RESULT 59
US-10-739-930-8881
; Sequence 8881, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
;  TITLE OF INVENTION:  PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53377)B
;  CURRENT APPLICATION NUMBER: US/10/739,930
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 8881
;   LENGTH: 362
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(362)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: GLYMA-23APR03-C2136_5.p
US-10-739-930-8881

  Query Match             30.6%;  Score 49;  DB 5;  Length 362;
  Best Local Similarity   36.7%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    8;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          2 NTVSFNLG----EAYEYPTFIQDLRNELAK 27
              :|::|:|     || |:|   :|: || :|
Db        155 DTLAFSLAPHPPEAEEFPAXCRDIVNEYSK 184


RESULT 60
US-10-739-930-8813
; Sequence 8813, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
;  TITLE OF INVENTION:  PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53377)B
;  CURRENT APPLICATION NUMBER: US/10/739,930
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 8813
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(447)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: GLYMA-23APR03-C18365_1.p
US-10-739-930-8813

  Query Match             30.6%;  Score 49;  DB 5;  Length 447;
  Best Local Similarity   45.5%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNEL 25
              |  |  |  | | |:||:|::|
Db        210 VVMNFFEELEPPLFVQDMRSKL 231


RESULT 61
US-10-156-761-14353
; Sequence 14353, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;  APPLICANT: OMURA, SATOSHI
;  APPLICANT:  IKEDA, HARUO
;  APPLICANT:  ISHIKAWA, JUN
;  APPLICANT:  HORIKAWA, HIROSHI
;  APPLICANT:  SHIBA, TADAYOSHI
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  APPLICANT:  HATTORI, MASAHIRA
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-262
;  CURRENT APPLICATION NUMBER: US/10/156,761
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: JP 2001-204089
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-272697
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14353
;   LENGTH: 732
;   TYPE: PRT
;   ORGANISM: Streptomyces avermitilis
US-10-156-761-14353

  Query Match             30.6%;  Score 49;  DB 4;  Length 732;
  Best Local Similarity   42.9%;  Pred. No. 2.9e+02;
  Matches    9;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;
```

```
Qy          9 GEAYEYPTFIQDLRNELAKGT 29
              ||  :  | :|||   :|:||
Db        255 GEEIDVKTLVQDLERAVARGT 275
```

RESULT 62
US-10-264-049-2841
; Sequence 2841, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2841
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (19)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-2841

Query Match 30.6%; Score 49; DB 4; Length 806;
Best Local Similarity 40.0%; Pred. No. 3.2e+02;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

```
Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db        344 SHELGQDYEHVTMLQERFREFARDT 368
```

RESULT 63
US-10-369-493-16733
; Sequence 16733, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16733
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-369-493-16733

Query Match 30.6%; Score 49; DB 4; Length 1168;
Best Local Similarity 52.6%; Pred. No. 4.9e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQD 20
              |||  |: |  ||  |||:
Db        805 NTVLANIDETIEYTVFIQN 823
```

RESULT 64
US-10-146-657-5
; Sequence 5, Application US/10146657
; Publication No. US20030143190A1
; GENERAL INFORMATION:
; APPLICANT: Iyer, Subramanian
; APPLICANT: Nguyen, Tay N.
; APPLICANT: Wu, Dauh-Rurng
; APPLICANT: Xing, Ruye
; TITLE OF INVENTION: HIGHLY PURIFIED CYTOKINE ACTIVATING FACTOR AND METHODS
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: 3812-7
; CURRENT APPLICATION NUMBER: US/10/146,657
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/620,093A
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/197,619
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1850
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-146-657-5

Query Match 30.6%; Score 49; DB 4; Length 1850;
Best Local Similarity 38.5%; Pred. No. 8.4e+02;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

```
Qy          4 VSFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ::| || ||  :  ::  | |||
Db        192 VQKSIGMAYIYPCPVDVMKERLTKGT 217
```

RESULT 65
US-10-695-994-4
; Sequence 4, Application US/10695994
; Publication No. US20040142354A1
; GENERAL INFORMATION:
; APPLICANT: MISHRA, LOPA
; TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
; FILE REFERENCE: P04470US1/BAS
; CURRENT APPLICATION NUMBER: US/10/695,994
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 09/431,184
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US98/08656
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 08/841,349
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2154
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-695-994-4

Query Match 30.6%; Score 49; DB 4; Length 2154;
Best Local Similarity 40.0%; Pred. No. 1e+03;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

```
Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
```

```
              |  ||: ||: | :|:   | |: |
Db       1710 SHELGQDYEHVTMLQERFREFARDT 1734


RESULT 66
US-10-805-684-150
; Sequence 150, Application US/10805684
; Publication No. US20050100966A1
; GENERAL INFORMATION:
;  APPLICANT: SAKAMOTO, TAKESHI
;  APPLICANT:  TAKEDA, SHIZU
;  TITLE OF INVENTION: FHOS-INTERACTING PROTEINS AND USE THEREOF
;  FILE REFERENCE: 58748(70342)
;  CURRENT APPLICATION NUMBER: US/10/805,684
;  CURRENT FILING DATE:  2004-03-19
;  PRIOR APPLICATION NUMBER: 60/455,766
;  PRIOR FILING DATE: 2003-03-19
;  PRIOR APPLICATION NUMBER: 60/459,936
;  PRIOR FILING DATE: 2003-04-02
;  PRIOR APPLICATION NUMBER: 60/460,103
;  PRIOR FILING DATE: 2003-04-02
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 150
;   LENGTH: 2154
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-805-684-150

  Query Match             30.6%;  Score 49;  DB 5;  Length 2154;
  Best Local Similarity   40.0%;  Pred. No. 1e+03;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1710 SHELGQDYEHVTMLQERFREFARDT 1734


RESULT 67
US-10-170-385-15
; Sequence 15, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Neil Raymond
;  APPLICANT:  Mundy, Christopher Robert
;  APPLICANT:  Kan, On
;  APPLICANT:  Harris, Robert Alan
;  APPLICANT:  White, Jonathan
;  APPLICANT:  Binley, Katie Mary
;  APPLICANT:  Rayner, William Nigel
;  APPLICANT:  Naylor, Stuart
;  APPLICANT:  Kingsman, Susan Mary
;  APPLICANT:  Krige, David
;  TITLE OF INVENTION: ANALYSIS METHOD
;  FILE REFERENCE: 532682000100
;  CURRENT APPLICATION NUMBER: US/10/170,385
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: PCT/GB02/01662
;  PRIOR FILING DATE: 2002-04-08
;  PRIOR APPLICATION NUMBER: PCT/GB01/05458
;  PRIOR FILING DATE: 2001-12-10
;  NUMBER OF SEQ ID NOS: 549
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-170-385-15

  Query Match             30.6%;  Score 49;  DB 4;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+03;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 68
US-10-424-599-182569
; Sequence 182569, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182569
;   LENGTH: 62
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_135872C.1.pep
US-10-424-599-182569

  Query Match             30.3%;  Score 48.5;  DB 4;  Length 62;
  Best Local Similarity   41.4%;  Pred. No. 19;
  Matches   12;  Conservative    6;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLR---NELAKGT 29
              |||::|::  || ||: :    | | | |
Db         27 VSFSVGKSQAYPVFIRCIHCMDNFLQKTT 55


RESULT 69
US-10-282-122A-52871
; Sequence 52871, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
```

```
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52871
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Clostridium difficile
US-10-282-122A-52871

  Query Match             30.3%;  Score 48.5;  DB 4;  Length 214;
  Best Local Similarity   50.0%;  Pred. No. 82;
  Matches   11;  Conservative    3;  Mismatches    1;  Indels    7;  Gaps    1;

Qy          7 NLGEAYEYPTFIQDLRNELAKG 28
              ||||       :||:: |||||
Db        104 NLGE-------LQDMKEELAKG 118


RESULT 70
US-10-231-913-106
; Sequence 106, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia S.
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Edinger, Schlomit
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Boldog, Ference L.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Eisen, Andrew J.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-216
;  CURRENT APPLICATION NUMBER: US/10/231,913
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/251,660
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 60/255,029
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
;   LENGTH: 272
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (3)
;   OTHER INFORMATION: wherein Xaa is any amino acid
US-10-231-913-106

  Query Match             30.3%;  Score 48.5;  DB 4;  Length 272;
  Best Local Similarity   41.7%;  Pred. No. 1.1e+02;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db         93 NVGMSYEYPEYFLDVPDLDNVIKK 116


RESULT 71
US-10-028-248A-99
; Sequence 99, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Malyankar, Uriel
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Miller, Charles
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Li, Li
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Colman, Steven
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Si, Jingsheng
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Stone, David
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Rothenberg, Mark
;  TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 21402-222
;  CURRENT APPLICATION NUMBER: US/10/028,248A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/256619
;  PRIOR FILING DATE: 2000-12-19
;  PRIOR APPLICATION NUMBER: 60/262959
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/272408
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/285189
;  PRIOR FILING DATE: 2001-04-20
;  PRIOR APPLICATION NUMBER: 60/308039
;  PRIOR FILING DATE: 2001-07-26
;  PRIOR APPLICATION NUMBER: 60/311266
;  PRIOR FILING DATE: 2001-08-09
;  NUMBER OF SEQ ID NOS: 211
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-028-248A-99
```

```
  Query Match             30.3%;  Score 48.5;  DB 4;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 72
US-10-231-913-105
; Sequence 105, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia S.
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Edinger, Schlomit
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Boldog, Ference L.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Eisen, Andrew J.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-216
;  CURRENT APPLICATION NUMBER: US/10/231,913
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/251,660
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 60/255,029
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-231-913-105

  Query Match             30.3%;  Score 48.5;  DB 4;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 73
US-10-107-782-99
; Sequence 99, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
;  APPLICANT: Boldog, Ferenc,
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Colman, Steve,
;  APPLICANT:  Edinger, Shlomit,
;  APPLICANT:  Gangolli, Esha,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Liu, Xiaohong,
;  APPLICANT:  Malyankar, Uriel,
;  APPLICANT:  Miller, Charles,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rothenberg, Mark,
;  APPLICANT:  Sciore, Paul,
;  APPLICANT:  Shenoy, Suresh,
;  APPLICANT:  Shimkets, Richard,
;  APPLICANT:  Si, Jingsheng,
;  APPLICANT:  Smithson, Glennda,
;  APPLICANT:  Spytek, Kimberly,
;  APPLICANT:  Stone, David,
;  APPLICANT:  Taupier, Raymond, jr.,
;  APPLICANT:  Tchernev, Velizar,
;  APPLICANT:  Vernet, Corine,
;  APPLICANT:  Zerhusen, Brian
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
;  FILE REFERENCE: 21402-222CIP
;  CURRENT APPLICATION NUMBER: US/10/107,782
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: 10/028,248
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 60/256,619
;  PRIOR FILING DATE: 2000-12-19
;  PRIOR APPLICATION NUMBER: 60/262,959
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/272,408
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/285,189
;  PRIOR FILING DATE: 2001-04-20
;  PRIOR APPLICATION NUMBER: 60/308,039
;  PRIOR FILING DATE: 2001-07-26
;  PRIOR APPLICATION NUMBER: 60/311,266
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/279,344
;  PRIOR FILING DATE: 2001-03-28
;  NUMBER OF SEQ ID NOS: 215
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 99
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-107-782-99

  Query Match             30.3%;  Score 48.5;  DB 4;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 74
US-10-344-326-34
; Sequence 34, Application US/10344326
; Publication No. US20050089847A1
; GENERAL INFORMATION:
;  APPLICANT: BioNetWorks GmbH
```

```
;  TITLE OF INVENTION: Short chain dehydrogenases/reductases (SDR)
;  FILE REFERENCE: 22854PWO_AS
;  CURRENT APPLICATION NUMBER: US/10/344,326
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US-60/223 436
;  PRIOR FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   OTHER INFORMATION: SD homolog
US-10-344-326-34

  Query Match             30.3%;  Score 48.5;  DB 5;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 75
US-10-756-149-5517
; Sequence 5517, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
;  TITLE OF INVENTION:  METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/756,149
;  CURRENT FILING DATE:  2004-01-12
;  NUMBER OF SEQ ID NOS: 5818
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5517
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-756-149-5517

  Query Match             30.3%;  Score 48.5;  DB 5;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 76
US-10-191-879-19
; Sequence 19, Application US/10191879
; Publication No. US20030084469A1
; GENERAL INFORMATION:
;  APPLICANT: Chang, Chi-Yao
;  APPLICANT:  Ting, Jing-Wen
;  APPLICANT:  Leu, Kuen-Lin
;  APPLICANT:  Lin, Chih-Hung
;  APPLICANT:  Chang, Chia-Ching
;  APPLICANT:  Tsai, Chih-Tung
;  TITLE OF INVENTION: FISH GROWTH HORMONES
;  FILE REFERENCE: 08919-039002
;  CURRENT APPLICATION NUMBER: US/10/191,879
;  CURRENT FILING DATE:  2002-07-09
;  PRIOR APPLICATION NUMBER: US 09/549,831
;  PRIOR FILING DATE: 2000-04-14
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Danio rerio
US-10-191-879-19

  Query Match             30.0%;  Score 48;  DB 4;  Length 188;
  Best Local Similarity   37.9%;  Pred. No. 84;
  Matches   11;  Conservative    5;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          4 VSFNLGEAYEYP--TFIQDLRNELAKGTP 30
              :|| | |::|:|  |    : | |  | |
Db         74 ISFRLIESWEFPSQTLSSTISNSLTIGNP 102


RESULT 77
US-10-191-879-10
; Sequence 10, Application US/10191879
; Publication No. US20030084469A1
; GENERAL INFORMATION:
;  APPLICANT: Chang, Chi-Yao
;  APPLICANT:  Ting, Jing-Wen
;  APPLICANT:  Leu, Kuen-Lin
;  APPLICANT:  Lin, Chih-Hung
;  APPLICANT:  Chang, Chia-Ching
;  APPLICANT:  Tsai, Chih-Tung
;  TITLE OF INVENTION: FISH GROWTH HORMONES
;  FILE REFERENCE: 08919-039002
;  CURRENT APPLICATION NUMBER: US/10/191,879
;  CURRENT FILING DATE:  2002-07-09
;  PRIOR APPLICATION NUMBER: US 09/549,831
;  PRIOR FILING DATE: 2000-04-14
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Danio rerio
US-10-191-879-10

  Query Match             30.0%;  Score 48;  DB 4;  Length 210;
  Best Local Similarity   37.9%;  Pred. No. 95;
  Matches   11;  Conservative    5;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          4 VSFNLGEAYEYP--TFIQDLRNELAKGTP 30
              :|| | |::|:|  |    : | |  | |
Db         96 ISFRLIESWEFPSQTLSSTISNSLTIGNP 124


RESULT 78
US-10-732-923-16035
; Sequence 16035, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;  FILE REFERENCE: 38-15(52796)C
;  CURRENT APPLICATION NUMBER: US/10/732,923
;  CURRENT FILING DATE:  2003-12-10
;  PRIOR APPLICATION NUMBER: 10/310,154
;  PRIOR FILING DATE: 2002-12-04
;  NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 16035
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(237)
;   OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-16035

  Query Match             30.0%;  Score 48;  DB 5;  Length 237;
```

Best Local Similarity 40.7%; Pred. No. 1.1e+02;
Matches 11; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

```
Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAK 27
              |:| | |||:::: |:   ||  | :|
Db         69 YSTHSKNLGKSHQQPSI--DLNGEQSK 93
```

RESULT 79
US-10-501-282-4668
; Sequence 4668, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4668
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-4668

Query Match 30.0%; Score 48; DB 5; Length 266;
Best Local Similarity 43.5%; Pred. No. 1.3e+02;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNE 24
              | ||||  : |   :|:|| | :
Db          5 NLVSFNQTDRYTILSFLQDQRQK 27
```

RESULT 80
US-10-369-493-64
; Sequence 64, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 64
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-10-369-493-64

Query Match 30.0%; Score 48; DB 4; Length 269;
Best Local Similarity 42.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

```
Qy          2 NTVSFNLGEAYEYPT----FIQDLRN 23
              ||| |  |:|| | |    |:: |::
Db         91 NTVKPENGKAYGYNTDWIGFLKSLKS 116
```

RESULT 81
US-10-670-695-26
; Sequence 26, Application US/10670695
; Publication No. US20040058316A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, Wayne A.
; APPLICANT: Lappin, Michael R.
; APPLICANT: Rosen, David K.
; APPLICANT: Andrews, Janet S.
; TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS TO DETERMINE THE IMMUNE
; TITLE OF INVENTION: STATUS OF AN ANIMAL
; FILE REFERENCE: DI-9-1
; CURRENT APPLICATION NUMBER: US/10/670,695
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 09/521,738
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Feline herpesvirus 1
US-10-670-695-26

Query Match 30.0%; Score 48; DB 4; Length 300;
Best Local Similarity 45.8%; Pred. No. 1.4e+02;
Matches 11; Conservative 5; Mismatches 6; Indels 2; Gaps 2;

```
Qy          1 YN-TVS-FNLGEAYEYPTFIQDLR 22
              || |:| | : :  ||| |: |:|
Db         76 YNATISWFKVTQGCEYPMFLMDMR 99
```

RESULT 82
US-10-501-282-4670
; Sequence 4670, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4670
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-4670

Query Match 30.0%; Score 48; DB 5; Length 303;
Best Local Similarity 43.5%; Pred. No. 1.5e+02;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNE 24
              | ||||  : |   :|:|| | :
Db         42 NLVSFNQTDRYTILSFLQDQRQK 64
```

```
RESULT 83
US-10-670-695-24
; Sequence 24, Application US/10670695
; Publication No. US20040058316A1
; GENERAL INFORMATION:
;  APPLICANT: Jensen, Wayne A.
;  APPLICANT:  Lappin, Michael R.
;  APPLICANT:  Rosen, David K.
;  APPLICANT:  Andrews, Janet S.
;  TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS TO DETERMINE THE IMMUNE
;  TITLE OF INVENTION:  STATUS OF AN ANIMAL
;  FILE REFERENCE: DI-9-1
;  CURRENT APPLICATION NUMBER: US/10/670,695
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 09/521,738
;  PRIOR FILING DATE: 2000-03-09
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;    LENGTH: 374
;    TYPE: PRT
;    ORGANISM: Feline herpesvirus 1
US-10-670-695-24

  Query Match             30.0%;  Score 48;  DB 4;  Length 374;
  Best Local Similarity   45.8%;  Pred. No. 1.9e+02;
  Matches   11;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    2;

Qy          1 YN-TVS-FNLGEAYEYPTFIQDLR 22
              || |:| | : :  ||| |: |:|
Db        104 YNATISWFKVTQGCEYPMFLMDMR 127


RESULT 84
US-10-732-923-2574
; Sequence 2574, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;  FILE REFERENCE: 38-15(52796)C
;  CURRENT APPLICATION NUMBER: US/10/732,923
;  CURRENT FILING DATE:  2003-12-10
;  PRIOR APPLICATION NUMBER: 10/310,154
;  PRIOR FILING DATE: 2002-12-04
;  NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 2574
;    LENGTH: 420
;    TYPE: PRT
;    ORGANISM: Chlorohydra viridissima
US-10-732-923-2574

  Query Match             30.0%;  Score 48;  DB 5;  Length 420;
  Best Local Similarity   37.5%;  Pred. No. 2.1e+02;
  Matches    9;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAK 27
              :   | | :| | : ||: | | |
Db        152 IDSKLHEVFELPEYAQDIHNYLKK 175


RESULT 85
US-10-425-115-190559
; Sequence 190559, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 190559
;    LENGTH: 475
;    TYPE: PRT
;    ORGANISM: Zea mays
;    FEATURE:
;    OTHER INFORMATION: Clone ID: MRT4577_105369C.1.pep
US-10-425-115-190559

  Query Match             30.0%;  Score 48;  DB 4;  Length 475;
  Best Local Similarity   41.2%;  Pred. No. 2.5e+02;
  Matches    7;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         12 YEYPTFIQDLRNELAKG 28
              |:|| |: ||  :: :|
Db        184 YDYPEFVADLAKQVKQG 200


RESULT 86
US-10-369-493-13282
; Sequence 13282, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,039
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13282
;    LENGTH: 514
;    TYPE: PRT
;    ORGANISM: Aspergillus nidulans
;    FEATURE:
;    NAME/KEY: unsure
;    LOCATION: (1)..(514)
;    OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-13282

  Query Match             30.0%;  Score 48;  DB 4;  Length 514;
  Best Local Similarity   43.5%;  Pred. No. 2.7e+02;
  Matches   10;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKGT 29
              |||: ||| |    |   |::|:
Db        352 NLGDGYEYGTIAAALVAPLSRGS 374


RESULT 87
US-10-369-493-1508
; Sequence 1508, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
```

; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1508
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1508

Query Match 30.0%; Score 48; DB 4; Length 712;
Best Local Similarity 41.9%; Pred. No. 3.9e+02;
Matches 13; Conservative 5; Mismatches 7; Indels 6; Gaps 2;

Qy 2 NTVSF--NLGEAYEYPTFIQDLRNELAKGTP 30
|:::| |||| || || : | :| |
Db 191 NSINFSKNLGEQKEYITFTK----EQLEGVP 217

RESULT 88
US-10-915-002-286
; Sequence 286, Application US/10915002
; Publication No. US20060078950A1
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTI
; TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
; TITLE OF INVENTION: PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/10/915,002
; CURRENT FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-915-002-286

Query Match 30.0%; Score 48; DB 5; Length 833;
Best Local Similarity 44.4%; Pred. No. 4.7e+02;
Matches 16; Conservative 3; Mismatches 11; Indels 6; Gaps 3;

Qy 1 YN---TVSFNL--GEAYEYPT-FIQDLRNELAKGTP 30
|| :|| | | : | | :|| ||| |||
Db 527 YNPNKNLSFRLSYSEGFRAPQYFDEDLHVELAGGTP 562

RESULT 89
US-11-097-143-3411
; Sequence 3411, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3411
; LENGTH: 931
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-3411

Query Match 30.0%; Score 48; DB 6; Length 931;
Best Local Similarity 36.7%; Pred. No. 5.4e+02;
Matches 11; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
: | | || | : | | ||||
Db 708 HRPVIIRLACEYELPACVSLARREFMKGTP 737

RESULT 90
US-10-369-493-23342
; Sequence 23342, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23342
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23342

Query Match 30.0%; Score 48; DB 4; Length 1228;
Best Local Similarity 41.7%; Pred. No. 7.4e+02;
Matches 15; Conservative 2; Mismatches 13; Indels 6; Gaps 2;

Qy 1 YNTVSFNLGEAYEYPTFIQ---DLRNELAK---GTP 30
|| :: || |||| | || | | || |
Db 636 YNVLAARLGWLPSYPTFNQNGIDLYKEAEKAGAATP 671

RESULT 91
US-10-739-930-6743
; Sequence 6743, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6743
; LENGTH: 2171
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:

```
;   OTHER INFORMATION: Clone ID: ARATH-23APR03-C8263_1.p
US-10-739-930-6743

  Query Match             30.0%;  Score 48;  DB 5;  Length 2171;
  Best Local Similarity   45.5%;  Pred. No. 1.4e+03;
  Matches   10;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 FNLGEAYEYPTFIQDLRNELAK 27
              |:| : ::| |  || : ||||
Db       1042 FSLSDEPKYVTVRQDEKMELAK 1063


RESULT 92
US-11-097-143-14550
; Sequence 14550, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14550
;   LENGTH: 572
;   TYPE: PRT
;   ORGANISM: DROSOPHILA
US-11-097-143-14550

  Query Match             29.7%;  Score 47.5;  DB 6;  Length 572;
  Best Local Similarity   42.3%;  Pred. No. 3.6e+02;
  Matches   11;  Conservative    5;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLRNELAKG 28
              ||| | | |::||  : : .:   |||
Db        516 TVSVNFGPAFKYPEVLVEHK---AKG 538


RESULT 93
US-10-437-963-203986
; Sequence 203986, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203986
;   LENGTH: 669
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_99117C.1.pep
US-10-437-963-203986

  Query Match             29.7%;  Score 47.5;  DB 4;  Length 669;
  Best Local Similarity   47.8%;  Pred. No. 4.3e+02;
  Matches   11;  Conservative    6;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELA 26
              |::|:  | :|  ||:||| :||
Db         18 VNYNI-MADDYSKFIEDLRKKLA 39


RESULT 94
US-11-045-004-26
; Sequence 26, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
;  APPLICANT: BUCHRIESER, CARMEN
;  APPLICANT:  FRANGEUL, LIONEL
;  APPLICANT:  COUVE, ELISABETH
;  APPLICANT:  RUSNIOK, CHRISTOPHE
;  APPLICANT:  FSIHI, HAFIDA
;  APPLICANT:  DEHOUX, PIERRE
;  APPLICANT:  DUSSURGET, OLIVIER
;  APPLICANT:  CHETOUANI, FARID
;  APPLICANT:  NEDJARI, HAFED
;  APPLICANT:  GLASER, PHILIPPE
;  APPLICANT:  KUNST, FRANCK
;  APPLICANT:  COSSART, PASCALE
;  APPLICANT:  DANIELS, JUSTIN
;  APPLICANT:  GOEBEI, WERNER
;  APPLICANT:  KREFT, JURGEN
;  APPLICANT:  KUHN, MICHAEL
;  APPLICANT:  NG, EVA
;  APPLICANT:  VAZQUEZ-BOLAND, ANTONIO
;  APPLICANT:  DOMINGUEZ-BERNAL, GUSTAVO
;  APPLICANT:  GARRIDO-GARCIA, PATRICIA
;  APPLICANT:  TIERREZ-MARTINEZ, ALBERTO
;  APPLICANT:  AMEND, ALEXANDRA
;  APPLICANT:  CHAKRABORTY, TRINAD
;  APPLICANT:  DOMANN, EUGEN
;  APPLICANT:  HAIN, THORSTEN
;  APPLICANT:  BERCHE, PATRICK
;  APPLICANT:  CHARBIT, ALAIN
;  APPLICANT:  DURANT, LIONEL
;  APPLICANT:  PEREZ-DIAZ, JOSE-CLAUDIO
;  APPLICANT:  BAQUERO, FERNANDO
;  APPLICANT:  GARCIA DEL PORTILLO, FRANCISCO
;  APPLICANT:  GOMEZ-LOPEZ, NURIA
;  APPLICANT:  MADUENIO, ENCARNA
;  APPLICANT:  PABLOS, BETRIZ DE
;  APPLICANT:  WEHLAND, JURGEN
;  APPLICANT:  KARST, UWE
;  APPLICANT:  ENTIAN, KARL-DIETER
;  APPLICANT:  HAUF, JORG
;  APPLICANT:  ROSE, MATTHIAS
;  APPLICANT:  VOSS, HAMUT
;  TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
;  FILE REFERENCE: 05394.0018-02
;  CURRENT APPLICATION NUMBER: US/11/045,004
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: 10/637,657
;  PRIOR FILING DATE: 2003-08-11
;  PRIOR APPLICATION NUMBER: 10/257,023
```

; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-26

Query Match 29.7%; Score 47.5; DB 6; Length 862;
Best Local Similarity 44.0%; Pred. No. 5.8e+02;
Matches 11; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

Qy 8 LGEAY---EYPTFIQDLRNELAKGT 29
||| | || : :: |:| |||
Db 707 LGETSSTDEEPTILLEIENDLKKGT 731

RESULT 95
US-11-084-080-39
; Sequence 39, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bougainvillea spectabilis
US-11-084-080-39

Query Match 29.4%; Score 47; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 RNELAKGTP 30
|||||||||
Db 1 RNELAKGTP 9

RESULT 96
US-09-186-276B-36
; Sequence 36, Application US/09186276B
; Publication No. US20020019996A1
; GENERAL INFORMATION:
; APPLICANT: Benfey, Philip
; APPLICANT: DiLaurenzio, Laura
; APPLICANT: Wysocka-Diller, Joanna
; APPLICANT: Malamy, Jocelyn E.
; APPLICANT: Pysh, Leonard
; APPLICANT: Helariutta, Yrjo
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof
; FILE REFERENCE: 5914-075-999
; CURRENT APPLICATION NUMBER: US/09/186,276B
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 08/842,445
; PRIOR FILING DATE: 1997-04-24
; PRIOR APPLICATION NUMBER: 08/638,617
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Oryza sp.
US-09-186-276B-36

Query Match 29.4%; Score 47; DB 3; Length 203;
Best Local Similarity 29.6%; Pred. No. 1.3e+02;
Matches 8; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NTVSFNLGEAYEYPTFIQDLRNELAKG 28
: : |||| :: :|:|:| : |
Db 78 HVIDFNLGVGGQWASFLQELAHRRGAG 104

RESULT 97
US-09-186-188B-36
; Sequence 36, Application US/09186188B
; Publication No. US20020032917A1
; GENERAL INFORMATION:
; APPLICANT: Benfey et al.
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5914-074-999
; CURRENT APPLICATION NUMBER: US/09/186,188B
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 08/842,445
; PRIOR FILING DATE: 1997-04-24
; PRIOR APPLICATION NUMBER: 08/638,617
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Plant
US-09-186-188B-36

Query Match 29.4%; Score 47; DB 3; Length 203;
Best Local Similarity 29.6%; Pred. No. 1.3e+02;
Matches 8; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NTVSFNLGEAYEYPTFIQDLRNELAKG 28
: : |||| :: :|:|:| : |
Db 78 HVIDFNLGVGGQWASFLQELAHRRGAG 104

RESULT 98
US-10-253-007-36
; Sequence 36, Application US/10253007
; Publication No. US20030088073A1
; GENERAL INFORMATION:
; APPLICANT: Benfey et al.
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5914-074-999
; CURRENT APPLICATION NUMBER: US/10/253,007
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/186,188
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 08/842,445
; PRIOR FILING DATE: 1997-04-24
; PRIOR APPLICATION NUMBER: 08/638,617
; PRIOR FILING DATE: 1996-04-26

```
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
;    LENGTH: 203
;    TYPE: PRT
;    ORGANISM: Plant
US-10-253-007-36

  Query Match             29.4%;  Score 47;  DB 4;  Length 203;
  Best Local Similarity   29.6%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    8;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKG 28
              : : ||||   :: :|:|:| :    |
Db         78 HVIDFNLGVGGQWASFLQELAHRRGAG 104


RESULT 99
US-10-282-122A-50612
; Sequence 50612, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50612
;    LENGTH: 281
;    TYPE: PRT
;    ORGANISM: Burkholderia mallei
US-10-282-122A-50612

  Query Match             29.4%;  Score 47;  DB 4;  Length 281;
  Best Local Similarity   47.1%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         11 AYEYPTFIQDLRNELAK 27
              ||| | |::||  ::|:
Db        227 AYENPKFVEDLVRDVAR 243


RESULT 100
US-10-161-051-105
; Sequence 105, Application US/10161051
; Publication No. US20030152945A1
; GENERAL INFORMATION:
;  APPLICANT: Peter Deak
;  APPLICANT:  David M Glover
;  APPLICANT:  Carol Midgley
;  TITLE OF INVENTION: Cell cycle progression proteins
;  FILE REFERENCE: CCI-021CP
;  CURRENT APPLICATION NUMBER: US/10/161,051
;  CURRENT FILING DATE:  2002-05-30
;  PRIOR APPLICATION NUMBER: GB 0007268.6
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 194
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
;    LENGTH: 389
;    TYPE: PRT
;    ORGANISM: Drosophila melanogaster
US-10-161-051-105

  Query Match             29.4%;  Score 47;  DB 4;  Length 389;
  Best Local Similarity   31.0%;  Pred. No. 2.7e+02;
  Matches   13;  Conservative    9;  Mismatches    6;  Indels   14;  Gaps    2;

Qy          2 NTVS-FNLGEAYEYPTFIQ----------DLRNELAKGT 29
              :||| |   |  :||||::           :||::: ||:
Db        203 DTVSTFTSYELMDYPTFVRYTVYVAMIALPRNELRDKVIKGS 244


Search completed: September 18, 2006, 19:35:30
Job time : 44.7346 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:31:32 ; Search time 7.03911 Seconds
(without alignments)
301.092 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 256596 seqs, 70647373 residues

Total number of hits satisfying chosen parameters: 256596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51.5	32.2	386	6	US-10-449-902-44047	Sequence 44047, A
2	51.5	32.2	386	6	US-10-449-902-45250	Sequence 45250, A
3	50	31.2	644	6	US-10-449-902-50668	Sequence 50668, A
4	49	30.6	368	7	US-11-174-307B-4568	Sequence 4568, Ap
5	49	30.6	2364	7	US-11-289-102-242	Sequence 242, App
6	48	30.0	1471	6	US-10-537-642-22	Sequence 22, Appl
7	47.5	29.7	601	6	US-10-471-571A-4686	Sequence 4686, Ap
8	47	29.4	474	7	US-11-330-403-3613	Sequence 3613, Ap
9	47	29.4	507	7	US-11-330-403-3082	Sequence 3082, Ap
10	47	29.4	2177	6	US-10-713-648A-64	Sequence 64, Appl
11	46	28.7	715	6	US-10-449-902-53933	Sequence 53933, A
12	45.5	28.4	277	6	US-10-953-349-30545	Sequence 30545, A
13	45.5	28.4	277	7	US-11-056-355B-61236	Sequence 61236, A
14	45.5	28.4	281	6	US-10-953-349-30544	Sequence 30544, A
15	45.5	28.4	281	7	US-11-056-355B-61235	Sequence 61235, A
16	45.5	28.4	298	6	US-10-953-349-30543	Sequence 30543, A
17	45.5	28.4	298	7	US-11-056-355B-61234	Sequence 61234, A
18	45.5	28.4	357	7	US-11-056-355B-98415	Sequence 98415, A
19	45.5	28.4	357	7	US-11-056-355B-109654	Sequence 109654,
20	45.5	28.4	359	7	US-11-056-355B-50007	Sequence 50007, A
21	45.5	28.4	359	7	US-11-056-355B-71347	Sequence 71347, A
22	45.5	28.4	384	7	US-11-056-355B-73361	Sequence 73361, A
23	45.5	28.4	393	7	US-11-056-355B-98647	Sequence 98647, A
24	45.5	28.4	393	7	US-11-056-355B-109886	Sequence 109886,
25	45.5	28.4	676	6	US-10-449-902-56715	Sequence 56715, A
26	45.5	28.4	697	7	US-11-330-403-15327	Sequence 15327, A
27	45	28.1	210	7	US-11-429-276-1150	Sequence 1150, Ap
28	45	28.1	225	6	US-10-953-349-32986	Sequence 32986, A
29	45	28.1	277	7	US-11-330-403-17205	Sequence 17205, A
30	45	28.1	592	7	US-11-056-355B-30657	Sequence 30657, A
31	45	28.1	592	7	US-11-056-355B-34247	Sequence 34247, A
32	45	28.1	600	6	US-10-953-349-4610	Sequence 4610, Ap
33	45	28.1	600	7	US-11-056-355B-20860	Sequence 20860, A
34	45	28.1	612	6	US-10-953-349-4609	Sequence 4609, Ap
35	45	28.1	612	7	US-11-056-355B-20859	Sequence 20859, A
36	45	28.1	650	7	US-11-056-355B-30656	Sequence 30656, A
37	45	28.1	650	7	US-11-056-355B-34246	Sequence 34246, A
38	45	28.1	670	6	US-10-953-349-4608	Sequence 4608, Ap
39	45	28.1	670	7	US-11-056-355B-20858	Sequence 20858, A
40	45	28.1	727	7	US-11-056-355B-30655	Sequence 30655, A
41	45	28.1	727	7	US-11-056-355B-34245	Sequence 34245, A
42	45	28.1	2186	6	US-10-471-571A-860	Sequence 860, App
43	44.5	27.8	397	7	US-11-416-490-135	Sequence 135, App
44	44	27.5	145	7	US-11-056-355B-42844	Sequence 42844, A
45	44	27.5	258	7	US-11-056-355B-42843	Sequence 42843, A
46	44	27.5	378	6	US-10-511-244-22	Sequence 22, Appl
47	44	27.5	416	7	US-11-056-355B-45540	Sequence 45540, A
48	44	27.5	455	6	US-10-953-349-32220	Sequence 32220, A
49	44	27.5	455	7	US-11-056-355B-68604	Sequence 68604, A
50	44	27.5	850	7	US-11-121-154-153	Sequence 153, App
51	44	27.5	1001	6	US-10-449-902-41315	Sequence 41315, A
52	44	27.5	1363	6	US-10-374-780A-1324	Sequence 1324, Ap
53	43.5	27.2	364	6	US-10-449-902-31435	Sequence 31435, A
54	43.5	27.2	367	6	US-10-953-349-20088	Sequence 20088, A
55	43.5	27.2	372	6	US-10-953-349-20087	Sequence 20087, A
56	43.5	27.2	408	6	US-10-953-349-20086	Sequence 20086, A
57	43.5	27.2	411	7	US-11-056-355B-55414	Sequence 55414, A
58	43.5	27.2	414	7	US-11-056-355B-55413	Sequence 55413, A
59	43.5	27.2	434	7	US-11-056-355B-96500	Sequence 96500, A
60	43.5	27.2	485	7	US-11-056-355B-55412	Sequence 55412, A
61	43.5	27.2	787	7	US-11-056-355B-100946	Sequence 100946,
62	43.5	27.2	787	7	US-11-056-355B-112185	Sequence 112185,
63	43.5	27.2	880	7	US-11-056-355B-100945	Sequence 100945,
64	43.5	27.2	880	7	US-11-056-355B-112184	Sequence 112184,
65	43.5	27.2	911	7	US-11-056-355B-100944	Sequence 100944,
66	43.5	27.2	911	7	US-11-056-355B-112183	Sequence 112183,
67	43.5	27.2	981	6	US-10-449-902-43097	Sequence 43097, A
68	43.5	27.2	1176	6	US-10-479-834-26	Sequence 26, Appl
69	43.5	27.2	1176	7	US-11-273-537-19	Sequence 19, Appl
70	43	26.9	445	7	US-11-330-403-2492	Sequence 2492, Ap
71	43	26.9	553	6	US-10-449-902-31529	Sequence 31529, A
72	43	26.9	553	6	US-10-449-902-45402	Sequence 45402, A
73	43	26.9	711	6	US-10-449-902-53657	Sequence 53657, A
74	43	26.9	725	7	US-11-056-355B-80327	Sequence 80327, A
75	43	26.9	753	6	US-10-449-902-46787	Sequence 46787, A
76	43	26.9	753	7	US-11-330-403-4451	Sequence 4451, Ap
77	43	26.9	767	6	US-10-449-902-53326	Sequence 53326, A
78	43	26.9	797	7	US-11-056-355B-80326	Sequence 80326, A
79	43	26.9	804	6	US-10-449-902-55004	Sequence 55004, A
80	43	26.9	855	7	US-11-056-355B-80325	Sequence 80325, A
81	42.5	26.6	229	6	US-10-374-780A-1453	Sequence 1453, Ap
82	42.5	26.6	397	7	US-11-416-490-137	Sequence 137, App
83	42.5	26.6	496	7	US-11-056-355B-48930	Sequence 48930, A
84	42.5	26.6	496	7	US-11-056-355B-79165	Sequence 79165, A
85	42.5	26.6	539	7	US-11-330-403-3810	Sequence 3810, Ap
86	42.5	26.6	539	7	US-11-330-403-3828	Sequence 3828, Ap
87	42.5	26.6	547	7	US-11-330-403-4997	Sequence 4997, Ap
88	42.5	26.6	547	7	US-11-330-403-6530	Sequence 6530, Ap
89	42.5	26.6	586	7	US-11-056-355B-79164	Sequence 79164, A
90	42.5	26.6	617	7	US-11-056-355B-48929	Sequence 48929, A
91	42.5	26.6	649	6	US-10-953-349-5336	Sequence 5336, Ap
92	42.5	26.6	694	6	US-10-953-349-5335	Sequence 5335, Ap
93	42.5	26.6	731	6	US-10-953-349-5334	Sequence 5334, Ap
94	42.5	26.6	760	7	US-11-056-355B-79163	Sequence 79163, A
95	42.5	26.6	791	7	US-11-056-355B-48928	Sequence 48928, A
96	42	26.2	233	7	US-11-330-403-18353	Sequence 18353, A
97	42	26.2	318	6	US-10-449-902-31941	Sequence 31941, A
98	42	26.2	318	6	US-10-449-902-44562	Sequence 44562, A

99	42	26.2	318	6	US-10-449-902-46734	Sequence 46734, A
100	42	26.2	326	7	US-11-330-403-4313	Sequence 4313, Ap

ALIGNMENTS

RESULT 1
US-10-449-902-44047
; Sequence 44047, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44047
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44047

Query Match 32.2%; Score 51.5; DB 6; Length 386;
Best Local Similarity 40.7%; Pred. No. 10;
Matches 11; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

```
Qy          7 NLGEAYEYPTFIQDLRNELAK---GTP 30
              || :|  ||  ::||  :|:|   | |
Db        189 NLNQAMSYPPLMEDLGRQLSKKCGGLP 215
```

RESULT 2
US-10-449-902-45250
; Sequence 45250, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45250
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45250

Query Match 32.2%; Score 51.5; DB 6; Length 386;
Best Local Similarity 40.7%; Pred. No. 10;
Matches 11; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

```
Qy          7 NLGEAYEYPTFIQDLRNELAK---GTP 30
              || :|  ||  ::||  :|:|   | |
Db        189 NLNQAMSYPPLMEDLGRQLSKKCGGLP 215
```

RESULT 3
US-10-449-902-50668
; Sequence 50668, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50668
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50668

Query Match 31.2%; Score 50; DB 6; Length 644;
Best Local Similarity 38.9%; Pred. No. 31;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

```
Qy         12 YEYPTFIQDLRNELAKGT 29
              |:|| |: ||  ::: |:
Db        355 YDYPEFVADLTTQVSNGS 372
```

RESULT 4
US-11-174-307B-4568
; Sequence 4568, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 4568
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: PFam Name: 2OG-FeII_Oxy; PFam Description: 2OG-Fe(II)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 30102640; NR Description: At1g06620 [Arabidopsis
; OTHER INFORMATION: thaliana] >gi|30679748|ref|NP_172147.2| 2-oxoglutarate-dependent
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 5031283; NR Description: unknown [Prunus armeniaca]
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 66730858; NR Description: 2-oxoglutarate-dependent
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 8885558; NR Description: leucoanthocyanidin
; OTHER INFORMATION: dioxygenase-like protein [Arabidopsis thaliana]
; OTHER INFORMATION: >gi|15983483|gb|AAL11609.1| AT5g59540/f2o15_200 [Arabidopsis
; OTHER INFORMATION: thaliana] >gi|15238459|ref|NP_200762.1| oxidoreductase, 2OG-Fe(II
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 3201612; NR Description: putative dioxygenase
; OTHER INFORMATION: [Arabidopsis thaliana] >gi|15224576|ref|NP_180642.1|
; OTHER INFORMATION: 2-oxoglutarate-dependent dioxygenase, putative [Arabidopsis
; OTHER INFORMATION: thaliana] >gi|25285697|pir||D84713 probable dioxygenase [imported
US-11-174-307B-4568

  Query Match 30.6%; Score 49; DB 7; Length 368;
  Best Local Similarity 36.7%; Pred. No. 23;
  Matches 11; Conservative 8; Mismatches 7; Indels 4; Gaps 1;

Qy 2 NTVSFNLG----EAYEYPTFIQDLRNELAK 27
Db 161 DTLAFSLAPHPPEAEEFPAVCRDIVNEYSK 190

RESULT 5
US-11-289-102-242
; Sequence 242, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 242
; LENGTH: 2364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-242

  Query Match 30.6%; Score 49; DB 7; Length 2364;
  Best Local Similarity 40.0%; Pred. No. 2e+02;
  Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 5 SFNLGEAYEYPTFIQDLRNELAKGT 29
Db 1723 SHELGQDYEHVTMLQERFREFARDT 1747

RESULT 6
US-10-537-642-22
; Sequence 22, Application US/10537642
; Publication No. US20060165719A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doolan, Denise L.
; APPLICANT: Carucci, Daniel J.
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
; FILE REFERENCE: EPI-103X
; CURRENT APPLICATION NUMBER: US/10/537,642
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US 60/431,494
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1161
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 1471
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-537-642-22

  Query Match 30.0%; Score 48; DB 6; Length 1471;
  Best Local Similarity 44.8%; Pred. No. 1.6e+02;
  Matches 13; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

Qy 1 YNTVSFNLGEAYEYPTFIQ--DLRNELAK 27
Db 758 YNNVSFNSSAYYEYHSDIDLIHFSNNLKK 786

RESULT 7
US-10-471-571A-4686
; Sequence 4686, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4686
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(601)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-4686

  Query Match 29.7%; Score 47.5; DB 6; Length 601;
  Best Local Similarity 42.3%; Pred. No. 67;
  Matches 11; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Qy 5 SFNLGEAYEYPTFI-QDLRNELAKGT 29
Db 363 AFNLAEQYQCPVIVLSDLQLSLGKQT 388

RESULT 8
US-11-330-403-3613
; Sequence 3613, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 3613
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Campylobacter jejuni subsp. jejuni NCTC 11168
US-11-330-403-3613

Query Match 29.4%; Score 47; DB 7; Length 474;
Best Local Similarity 34.8%; Pred. No. 60;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNE 24
              || :| : :||::| ||   : :
Db        125 NTPTFFIRDAYKFPDFIHTQKRD 147
```

RESULT 9
US-11-330-403-3082
; Sequence 3082, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 3082
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-11-330-403-3082

Query Match 29.4%; Score 47; DB 7; Length 507;
Best Local Similarity 34.8%; Pred. No. 65;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNE 24
              || :| : :||::| ||   : :
Db        125 NTPTFFIRDAYKFPDFIHTQKRD 147
```

RESULT 10
US-10-713-648A-64
; Sequence 64, Application US/10713648A
; Publication No. US20060107344A1
; GENERAL INFORMATION:
; APPLICANT: POSCO
; APPLICANT: POSTECH
; APPLICANT: An, Gynheung
; APPLICANT: Ryu, Choong-Hwan
; APPLICANT: Han, Jong-Jin
; APPLICANT: Kang, Hong-Gyu
; APPLICANT: An, Kyungsook
; TITLE OF INVENTION: ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
; TITLE OF INVENTION: MUTAGENESIS OF RICE
; FILE REFERENCE: 20010-04USA
; CURRENT APPLICATION NUMBER: US/10/713,648A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/427,166
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 2177
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: line 1C-109-51 polypeptide sequence
US-10-713-648A-64

Query Match 29.4%; Score 47; DB 6; Length 2177;
Best Local Similarity 45.5%; Pred. No. 3.5e+02;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

```
Qy          6 FNLGEAYEYPTFIQDLRNELAK 27
              |:| | ::| :  || : ||||
Db       1053 FSLSEEFKYVSVRQDEKMELAK 1074
```

RESULT 11
US-10-449-902-53933
; Sequence 53933, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53933
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53933

Query Match 28.7%; Score 46; DB 6; Length 715;
Best Local Similarity 29.6%; Pred. No. 1.4e+02;
Matches 8; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKG 28
              : : |:||   :: :|:|:| :  | |
Db        464 HVIDFDLGVGGQWASFLQELAHRRAAG 490
```

RESULT 12
US-10-953-349-30545
; Sequence 30545, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30545
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30545

Query Match 28.4%; Score 45.5; DB 6; Length 277;
Best Local Similarity 41.7%; Pred. No. 54;
Matches 10; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

```
Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL 25
              | :||:   : :| |||  :||:|
Db         11 TATFNVQASSTDYVTFITGIRNKL 34
```

RESULT 13
US-11-056-355B-61236
; Sequence 61236, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby

; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61236
; LENGTH: 277
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 13661990
US-11-056-355B-61236

Query Match 28.4%; Score 45.5; DB 7; Length 277;
Best Local Similarity 41.7%; Pred. No. 54;
Matches 10; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 3 TVSFNL-GEAYEYPTFIQDLRNEL 25
| :||: : :| ||| :||:|
Db 11 TATFNVQASSTDYVTFITGIRNKL 34

RESULT 14
US-10-953-349-30544
; Sequence 30544, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30544
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30544

Query Match 28.4%; Score 45.5; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 54;
Matches 10; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 3 TVSFNL-GEAYEYPTFIQDLRNEL 25
| :||: : :| ||| :||:|
Db 15 TATFNVQASSTDYVTFITGIRNKL 38

RESULT 15
US-11-056-355B-61235
; Sequence 61235, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61235
; LENGTH: 281
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(281)
; OTHER INFORMATION: Ceres Seq. ID no. 13661989
US-11-056-355B-61235

Query Match 28.4%; Score 45.5; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 54;
Matches 10; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 3 TVSFNL-GEAYEYPTFIQDLRNEL 25
| :||: : :| ||| :||:|
Db 15 TATFNVQASSTDYVTFITGIRNKL 38

RESULT 16
US-10-953-349-30543
; Sequence 30543, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30543
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30543

Query Match 28.4%; Score 45.5; DB 6; Length 298;
Best Local Similarity 41.7%; Pred. No. 58;
Matches 10; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 3 TVSFNL-GEAYEYPTFIQDLRNEL 25
| :||: : :| ||| :||:|
Db 32 TATFNVQASSTDYVTFITGIRNKL 55

RESULT 17
US-11-056-355B-61234
; Sequence 61234, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61234
; LENGTH: 298
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(298)
; OTHER INFORMATION: Ceres Seq. ID no. 13661988
US-11-056-355B-61234

Query Match 28.4%; Score 45.5; DB 7; Length 298;
Best Local Similarity 41.7%; Pred. No. 58;
Matches 10; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 3 TVSFNL-GEAYEYPTFIQDLRNEL 25
| :||: : :| ||| :||:|

```
Db         32 TATFNVQASSTDYVTFITGIRNKL 55


RESULT 18
US-11-056-355B-98415
; Sequence 98415, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 98415
;   LENGTH: 357
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(357)
;   OTHER INFORMATION: Ceres Seq. ID no. 13593580
US-11-056-355B-98415

  Query Match             28.4%;  Score 45.5;  DB 7;  Length 357;
  Best Local Similarity   50.0%;  Pred. No. 72;
  Matches   10;  Conservative    4;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLR 22
              :|:|| || :| ||:   ||
Db         36 SVNFN-GEIFESPTYCSTLR 54


RESULT 19
US-11-056-355B-109654
; Sequence 109654, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 109654
;   LENGTH: 357
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(357)
;   OTHER INFORMATION: Ceres Seq. ID no. 13593580
US-11-056-355B-109654

  Query Match             28.4%;  Score 45.5;  DB 7;  Length 357;
  Best Local Similarity   50.0%;  Pred. No. 72;
  Matches   10;  Conservative    4;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLR 22
              :|:|| || :| ||:   ||
Db         36 SVNFN-GEIFESPTYCSTLR 54


RESULT 20
US-11-056-355B-50007
; Sequence 50007, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 50007
;   LENGTH: 359
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(359)
;   OTHER INFORMATION: Ceres Seq. ID no. 15220525
US-11-056-355B-50007

  Query Match             28.4%;  Score 45.5;  DB 7;  Length 359;
  Best Local Similarity   50.0%;  Pred. No. 72;
  Matches   10;  Conservative    4;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLR 22
              :|:|| || :| ||:   ||
Db         36 SVNFN-GEIFESPTYCSTLR 54


RESULT 21
US-11-056-355B-71347
; Sequence 71347, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 71347
;   LENGTH: 359
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(359)
;   OTHER INFORMATION: Ceres Seq. ID.no. 3094824
US-11-056-355B-71347

  Query Match             28.4%;  Score 45.5;  DB 7;  Length 359;
  Best Local Similarity   50.0%;  Pred. No. 72;
  Matches   10;  Conservative    4;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLR 22
              :|:|| || :| ||:   ||
Db         36 SVNFN-GEIFESPTYCSTLR 54


RESULT 22
US-11-056-355B-73361
; Sequence 73361, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
```

; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 73361
; LENGTH: 384
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(384)
; OTHER INFORMATION: Ceres Seq. ID no. 4964092
US-11-056-355B-73361

Query Match 28.4%; Score 45.5; DB 7; Length 384;
Best Local Similarity 50.0%; Pred. No. 78;
Matches 10; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 3 TVSFNLGEAYEYPTFIQDLR 22
:|:|| || :| ||: ||
Db 36 SVNFN-GEIFESPTYCSTLR 54

RESULT 23
US-11-056-355B-98647
; Sequence 98647, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 98647
; LENGTH: 393
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(393)
; OTHER INFORMATION: Ceres Seq. ID no. 13601198
US-11-056-355B-98647

Query Match 28.4%; Score 45.5; DB 7; Length 393;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 10; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 3 TVSFNLGEAYEYPTFIQDLR 22
:|:|| || :| ||: ||
Db 36 SVNFN-GEIFESPTYCSTLR 54

RESULT 24
US-11-056-355B-109886
; Sequence 109886, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 109886
; LENGTH: 393
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(393)
; OTHER INFORMATION: Ceres Seq. ID no. 13601198
US-11-056-355B-109886

Query Match 28.4%; Score 45.5; DB 7; Length 393;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 10; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 3 TVSFNLGEAYEYPTFIQDLR 22
:|:|| || :| ||: ||
Db 36 SVNFN-GEIFESPTYCSTLR 54

RESULT 25
US-10-449-902-56715
; Sequence 56715, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56715
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-56715

Query Match 28.4%; Score 45.5; DB 6; Length 676;
Best Local Similarity 39.4%; Pred. No. 1.5e+02;
Matches 13; Conservative 4; Mismatches 7; Indels 9; Gaps 1;

Qy 3 TVSFNLGE---------AYEYPTFIQDLRNELA 26
:: :||| | | | |||||:|
Db 590 SIEKSLGEYRDKIPAEVASEIETAIADLRNEMA 622

RESULT 26
US-11-330-403-15327
; Sequence 15327, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 15327
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Desulfovibrio vulgaris subsp. vulgaris (strain Hildenborough)
US-11-330-403-15327

```
  Query Match             28.4%;  Score 45.5;  DB 7;  Length 697;
  Best Local Similarity   52.2%;  Pred. No. 1.6e+02;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    5;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL 25
              |: || || | ||    ||| :|
Db         76 TLVFN-GEIYNYP----DLRRDL 93


RESULT 27
US-11-429-276-1150
; Sequence 1150, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564
;  CURRENT APPLICATION NUMBER: US/11/429,276
;  CURRENT FILING DATE:  2006-05-08
;  PRIOR APPLICATION NUMBER: 10/775,204
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: PCT/US02/40891
;  PRIOR FILING DATE: 2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1150
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Salmo salar
US-11-429-276-1150

  Query Match             28.1%;  Score 45;  DB 7;  Length 210;
  Best Local Similarity   40.9%;  Pred. No. 46;
  Matches    9;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNEL 25
              :|| | |::|||:    : | |
Db         96 ISFRLIESWEYPSQTLTISNSL 117


RESULT 28
US-10-953-349-32986
; Sequence 32986, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32986
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-32986

  Query Match             28.1%;  Score 45;  DB 6;  Length 225;
  Best Local Similarity   40.7%;  Pred. No. 50;
  Matches   11;  Conservative    7;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAK 27
              |:| | |||:::: |:   ||  | :|
Db         69 YSTHSKNLGKSHQQPSI--DLNVEQSK 93


RESULT 29
US-11-330-403-17205
; Sequence 17205, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 17205
;   LENGTH: 277
;   TYPE: PRT
;   ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-330-403-17205

  Query Match             28.1%;  Score 45;  DB 7;  Length 277;
  Best Local Similarity   45.5%;  Pred. No. 63;
  Matches   10;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          9 GEAYEYPTFIQDLRNELAKGTP 30
              |   |: : |||||::  || |
Db        153 GNPTEHISAIQDLRSQDPKGLP 174


RESULT 30
US-11-056-355B-30657
; Sequence 30657, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 30657
;   LENGTH: 592
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(592)
;   OTHER INFORMATION: Ceres Seq. ID no. 12327296
US-11-056-355B-30657

  Query Match             28.1%;  Score 45;  DB 7;  Length 592;
  Best Local Similarity   30.8%;  Pred. No. 1.5e+02;
  Matches    8;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :: : |: :|  || ||  |: : :|
Db        198 NYRIPESPKYSVFITDLIKEMLQASP 223


RESULT 31
```

```
US-11-056-355B-34247
; Sequence 34247, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 34247
;   LENGTH: 592
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(592)
;   OTHER INFORMATION: Ceres Seq. ID no. 12327296
US-11-056-355B-34247

  Query Match             28.1%;  Score 45;  DB 7;  Length 592;
  Best Local Similarity   30.8%;  Pred. No. 1.5e+02;
  Matches    8;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :: : |: :|  || ||  |: : :|
Db        198 NYRIPESPKYSVFITDLIKEMLQASP 223


RESULT 32
US-10-953-349-4610
; Sequence 4610, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4610
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-4610

  Query Match             28.1%;  Score 45;  DB 6;  Length 600;
  Best Local Similarity   30.8%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :: : |: :|  || ||  |: : :|
Db        186 NYRIPESPKYSVFITDLIKEMLQASP 211


RESULT 33
US-11-056-355B-20860
; Sequence 20860, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 20860
;   LENGTH: 600
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(600)
;   OTHER INFORMATION: Ceres Seq. ID no. 13491875
US-11-056-355B-20860

  Query Match             28.1%;  Score 45;  DB 7;  Length 600;
  Best Local Similarity   30.8%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :: : |: :|  || ||  |: : :|
Db        186 NYRIPESPKYSVFITDLIKEMLQASP 211


RESULT 34
US-10-953-349-4609
; Sequence 4609, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4609
;   LENGTH: 612
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-4609

  Query Match             28.1%;  Score 45;  DB 6;  Length 612;
  Best Local Similarity   30.8%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :: : |: :|  || ||  |: : :|
Db        198 NYRIPESPKYSVFITDLIKEMLQASP 223


RESULT 35
US-11-056-355B-20859
; Sequence 20859, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 20859
;   LENGTH: 612
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(612)
;   OTHER INFORMATION: Ceres Seq. ID no. 13491874
```

US-11-056-355B-20859

Query Match 28.1%; Score 45; DB 7; Length 612;
Best Local Similarity 30.8%; Pred. No. 1.6e+02;
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
:: : |: :| || || |: : :|
Db 198 NYRIPESPKYSVFITDLIKEMLQASP 223

RESULT 36
US-11-056-355B-30656
; Sequence 30656, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 30656
; LENGTH: 650
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(650)
; OTHER INFORMATION: Ceres Seq. ID no. 12327295
US-11-056-355B-30656

Query Match 28.1%; Score 45; DB 7; Length 650;
Best Local Similarity 30.8%; Pred. No. 1.7e+02;
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
:: : |: :| || || |: : :|
Db 256 NYRIPESPKYSVFITDLIKEMLQASP 281

RESULT 37
US-11-056-355B-34246
; Sequence 34246, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 34246
; LENGTH: 650
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(650)
; OTHER INFORMATION: Ceres Seq. ID no. 12327295
US-11-056-355B-34246

Query Match 28.1%; Score 45; DB 7; Length 650;
Best Local Similarity 30.8%; Pred. No. 1.7e+02;
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
:: : |: :| || || |: : :|
Db 256 NYRIPESPKYSVFITDLIKEMLQASP 281

RESULT 38
US-10-953-349-4608
; Sequence 4608, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4608
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4608

Query Match 28.1%; Score 45; DB 6; Length 670;
Best Local Similarity 30.8%; Pred. No. 1.8e+02;
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
:: : |: :| || || |: : :|
Db 256 NYRIPESPKYSVFITDLIKEMLQASP 281

RESULT 39
US-11-056-355B-20858
; Sequence 20858, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 20858
; LENGTH: 670
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(670)
; OTHER INFORMATION: Ceres Seq. ID no. 13491873
US-11-056-355B-20858

Query Match 28.1%; Score 45; DB 7; Length 670;
Best Local Similarity 30.8%; Pred. No. 1.8e+02;
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
:: : |: :| || || |: : :|
Db 256 NYRIPESPKYSVFITDLIKEMLQASP 281

RESULT 40
US-11-056-355B-30655
; Sequence 30655, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

```
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 30655
;   LENGTH: 727
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(727)
;   OTHER INFORMATION: Ceres Seq. ID no. 12327294
US-11-056-355B-30655

  Query Match             28.1%;  Score 45;  DB 7;  Length 727;
  Best Local Similarity   30.8%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :: : |: :|  || ||  |: : :|
Db        333 NYRIPESPKYSVFITDLIKEMLQASP 358


RESULT 41
US-11-056-355B-34245
; Sequence 34245, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 34245
;   LENGTH: 727
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(727)
;   OTHER INFORMATION: Ceres Seq. ID no. 12327294
US-11-056-355B-34245

  Query Match             28.1%;  Score 45;  DB 7;  Length 727;
  Best Local Similarity   30.8%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :: : |: :|  || ||  |: : :|
Db        333 NYRIPESPKYSVFITDLIKEMLQASP 358


RESULT 42
US-10-471-571A-860
; Sequence 860, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 860
;   LENGTH: 2186
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(2186)
;   OTHER INFORMATION: Mrp protein [Staphylococcus
US-10-471-571A-860

  Query Match             28.1%;  Score 45;  DB 6;  Length 2186;
  Best Local Similarity   44.0%;  Pred. No. 6.9e+02;
  Matches   11;  Conservative    3;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLRNELAK 27
              ||:||  |   | |: ||  |  |:
Db        552 TVTFN--ETLTYKTYTQDFINSAAE 574


RESULT 43
US-11-416-490-135
; Sequence 135, Application US/11416490
; Publication No. US20060195935A1
; GENERAL INFORMATION:
;  APPLICANT: ChromaGenics B.V.
;  APPLICANT:  Otte, Arie P.
;  APPLICANT:  Kwaks, Theodorus H.J.
;  APPLICANT:  Sewalt, Richard G.A.B.
;  APPLICANT:  van Blokland, Rik
;  TITLE OF INVENTION: Selection of host cells expressing protein at high levels
;  FILE REFERENCE: 0117 B US P00 CIP
;  CURRENT APPLICATION NUMBER: US/11/416,490
;  CURRENT FILING DATE:  2006-05-02
;  PRIOR APPLICATION NUMBER: US 11/269,525
;  PRIOR FILING DATE: 2005-11-07
;  PRIOR APPLICATION NUMBER: US 11/359,953
;  PRIOR FILING DATE: 2006-02-21
;  PRIOR APPLICATION NUMBER: US 60/626,301
;  PRIOR FILING DATE: 2004-11-08
;  PRIOR APPLICATION NUMBER: US 60/696,610
;  PRIOR FILING DATE: 2005-07-05
;  PRIOR APPLICATION NUMBER: EP 04105593.0
;  PRIOR FILING DATE: 2004-11-08
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 135
;   LENGTH: 397
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-11-416-490-135

  Query Match             27.8%;  Score 44.5;  DB 7;  Length 397;
  Best Local Similarity   28.1%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    8;  Mismatches   12;  Indels    3;  Gaps    1;

Qy          1 YNTVSFNLGEA---YEYPTFIQDLRNELAKGT 29
              | |  : || |   : ||| ::: :  : : |
Db        181 YETAHYMLGTAAGPHPYPTIVREFQRMIGEET 212


RESULT 44
US-11-056-355B-42844
; Sequence 42844, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
```

```
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 42844
;   LENGTH: 145
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(145)
;   OTHER INFORMATION: Ceres Seq. ID no. 12604798
US-11-056-355B-42844

  Query Match             27.5%;  Score 44;  DB 7;  Length 145;
  Best Local Similarity   40.9%;  Pred. No. 42;
  Matches    9;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKG 28
              |:| | |||  : :: | |  |
Db         12 NVGAALEYPITVLNVENILVIG 33


RESULT 45
US-11-056-355B-42843
; Sequence 42843, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 42843
;   LENGTH: 258
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(258)
;   OTHER INFORMATION: Ceres Seq. ID no. 12604797
US-11-056-355B-42843

  Query Match             27.5%;  Score 44;  DB 7;  Length 258;
  Best Local Similarity   40.9%;  Pred. No. 82;
  Matches    9;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKG 28
              |:| | |||  : :: | |  |
Db        125 NVGAALEYPITVLNVENILVIG 146


RESULT 46
US-10-511-244-22
; Sequence 22, Application US/10511244
; Publication No. US20060183116A1
; GENERAL INFORMATION:
;  APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
;  APPLICANT:  THE UNIVERSITY OF BRITISH COLUMBIA
;  APPLICANT:  SAREEN, Dipti
;  APPLICANT:  NEWTON, Gerald L.
;  APPLICANT:  FAHEY, Robert C.
;  APPLICANT:  BUCHMEIER, Nancy
;  APPLICANT:  STEFFEK, Micah
;  APPLICANT:  AV-GAY, Yossef
;  APPLICANT:  RAWAT, Mamta
;  APPLICANT:  KOLEDIN, Teresa
;  TITLE OF INVENTION: METHODS OF USE OF THE ENZYMES OF MYCOTHIOL SYNTHESIS
;  FILE REFERENCE: UCSD1420-1
;  CURRENT APPLICATION NUMBER: US/10/511,244
;  CURRENT FILING DATE:  2004-10-13
;  PRIOR APPLICATION NUMBER: PCT/US 03/11539
;  PRIOR FILING DATE: 2003-04-15
;  PRIOR APPLICATION NUMBER: US 60/373,890
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/373,079
;  PRIOR FILING DATE: 2002-04-15
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 378
;   TYPE: PRT
;   ORGANISM: Mycobacterium tuberculosis
US-10-511-244-22

  Query Match             27.5%;  Score 44;  DB 6;  Length 378;
  Best Local Similarity   36.4%;  Pred. No. 1.3e+02;
  Matches   12;  Conservative    3;  Mismatches    8;  Indels   10;  Gaps    1;

Qy          8 LGEAY----------EYPTFIQDLRNELAKGTP 30
              | |||          |: || | ::  || | |
Db        265 LAEAYASMDVFVHSGEHETFCQVVQEALASGLP 297


RESULT 47
US-11-056-355B-45540
; Sequence 45540, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 45540
;   LENGTH: 416
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(416)
;   OTHER INFORMATION: Ceres Seq. ID no. 15219074
US-11-056-355B-45540

  Query Match             27.5%;  Score 44;  DB 7;  Length 416;
  Best Local Similarity   47.8%;  Pred. No. 1.4e+02;
  Matches   11;  Conservative    1;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          8 LGEAYEYPTFIQDLRNELAKGTP 30
              :| |  | | | || | |  | | |
Db        187 VGIARRYSTTITDLMNVVNAMGAP 209


RESULT 48
US-10-953-349-32220
; Sequence 32220, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
```

```
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32220
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-10-953-349-32220

  Query Match           27.5%;  Score 44;  DB 6;  Length 455;
  Best Local Similarity   38.1%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 FNLGEAYEYPTFIQDLRNELA 26
              : ||:|  :|| :: |:  ||
Db         55 YELGDADGFPTVVERLKRALA 75


RESULT 49
US-11-056-355B-68604
; Sequence 68604, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 68604
;   LENGTH: 455
;   TYPE: prt
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(455)
;   OTHER INFORMATION: Ceres Seq. ID no. 14303593
US-11-056-355B-68604

  Query Match           27.5%;  Score 44;  DB 7;  Length 455;
  Best Local Similarity   38.1%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 FNLGEAYEYPTFIQDLRNELA 26
              : ||:|  :|| :: |:  ||
Db         55 YELGDADGFPTVVERLKRALA 75


RESULT 50
US-11-121-154-153
; Sequence 153, Application US/11121154
; Publication No. US20060105914A1
; GENERAL INFORMATION:
;  APPLICANT: TAYLOR, LARRY EDMUND
;  APPLICANT:  WEINER, RONALD M.
;  APPLICANT:  HUTCHESON, STEVEN WAYNE
;  APPLICANT:  EKBORG, NATHAN A.
;  APPLICANT:  HOWARD, MICHAEL
;  TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
;  FILE REFERENCE: 108172-00121
;  CURRENT APPLICATION NUMBER: US/11/121,154
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,971
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 214
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 153
;   LENGTH: 850
;   TYPE: PRT
;   ORGANISM: Microbulbifer degradans
US-11-121-154-153

  Query Match           27.5%;  Score 44;  DB 7;  Length 850;
  Best Local Similarity   58.3%;  Pred. No. 3.3e+02;
  Matches    7;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 GEAYEYPTFIQD 20
              |:|:||  |:||
Db        673 GQAFEYQLFLQD 684


RESULT 51
US-10-449-902-41315
; Sequence 41315, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41315
;   LENGTH: 1001
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-41315

  Query Match           27.5%;  Score 44;  DB 6;  Length 1001;
  Best Local Similarity   40.9%;  Pred. No. 3.9e+02;
  Matches    9;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          8 LGEAYEYPTFIQDLRNELAKGT 29
              ||| :: | | ||  :|: : |
Db        971 LGEWFKQPMFPQDPGDEVVRST 992


RESULT 52
US-10-374-780A-1324
; Sequence 1324, Application US/10374780A
; Publication No. US20060162006A9
; GENERAL INFORMATION:
;  APPLICANT: Sherman, Bradley K
;  APPLICANT:  Riechmann, Jose Luis
;  APPLICANT:  Jiang, Cai-Zhong
;  APPLICANT:  Heard, Jacqueline E
;  APPLICANT:  Haake, Volker
;  APPLICANT:  Creelman, Robert A
;  APPLICANT:  Ratcliffe, Oliver
;  APPLICANT:  Adam, Luc J
;  APPLICANT:  Reuber, T. Lynne
;  APPLICANT:  Keddie, James
;  APPLICANT:  Broun, Pierre E
;  APPLICANT:  Pilgrim, Marsha L
;  APPLICANT:  Dubell III, Arnold T
;  APPLICANT:  Pineda, Omaira
;  APPLICANT:  Yu, Guo-Liang
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
;  FILE REFERENCE: MBI-0047 CIP
;  CURRENT APPLICATION NUMBER: US/10/374,780A
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: 09/837,944
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: 60/310,847
;  PRIOR FILING DATE: 2001-08-09
```

```
;  PRIOR APPLICATION NUMBER: 09/934,455
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: 60/336,049
;  PRIOR FILING DATE: 2001-11-19
;  PRIOR APPLICATION NUMBER: 60/338,692
;  PRIOR FILING DATE: 2001-12-11
;  PRIOR APPLICATION NUMBER: 10/171,468
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: 10/225,066
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 10/225,067
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 10/225,068
;  PRIOR FILING DATE: 2002-08-09
;  NUMBER OF SEQ ID NOS: 2906
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1324
;   LENGTH: 1363
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Orthologous to G987
US-10-374-780A-1324

  Query Match             27.5%;  Score 44;  DB 6;  Length 1363;
  Best Local Similarity   37.0%;  Pred. No. 5.6e+02;
  Matches   10;  Conservative    6;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAKGTP 30
              | | :   :::|: || | ||  :| |
Db        468 VHFGICTGFQWPSLIQRLANE--EGGP 492


RESULT 53
US-10-449-902-31435
; Sequence 31435, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31435
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-31435

  Query Match             27.2%;  Score 43.5;  DB 6;  Length 364;
  Best Local Similarity   45.8%;  Pred. No. 1.4e+02;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    5;  Gaps    1;

Qy          4 VSFNLGE-----AYEYPTFIQDLR 22
              ||||||      :: :  | ||||
Db        150 VSFNLGSLGFLTSHNFEGFRQDLR 173


RESULT 54
US-10-953-349-20088
; Sequence 20088, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20088
;   LENGTH: 367
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-20088

  Query Match             27.2%;  Score 43.5;  DB 6;  Length 367;
  Best Local Similarity   40.9%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    6;  Mismatches    2;  Indels    5;  Gaps    1;

Qy          8 LGEAYE-----YPTFIQDLRNE 24
              | ||||     :| |:::|:|:
Db        329 LHEAYEKMNGVFPVFLRELQNK 350


RESULT 55
US-10-953-349-20087
; Sequence 20087, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20087
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-20087

  Query Match             27.2%;  Score 43.5;  DB 6;  Length 372;
  Best Local Similarity   40.9%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    6;  Mismatches    2;  Indels    5;  Gaps    1;

Qy          8 LGEAYE-----YPTFIQDLRNE 24
              | ||||     :| |:::|:|:
Db        334 LHEAYEKMNGVFPVFLRELQNK 355


RESULT 56
US-10-953-349-20086
; Sequence 20086, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20086
;   LENGTH: 408
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-20086

  Query Match             27.2%;  Score 43.5;  DB 6;  Length 408;
  Best Local Similarity   40.9%;  Pred. No. 1.6e+02;
  Matches    9;  Conservative    6;  Mismatches    2;  Indels    5;  Gaps    1;
```

```
Qy          8 LGEAYE-----YPTFIQDLRNE 24
              | ||||     :| |:::|:|:
Db        370 LHEAYEKMNGVFPVFLRELQNK 391


RESULT 57
US-11-056-355B-55414
; Sequence 55414, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 55414
;   LENGTH: 411
;   TYPE: prt
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(411)
;   OTHER INFORMATION: Ceres Seq. ID no. 12581699
US-11-056-355B-55414

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 411;
  Best Local Similarity   41.7%;  Pred. No. 1.7e+02;
  Matches   10;  Conservative    5;  Mismatches    4;  Indels    5;  Gaps    1;

Qy          4 VSFNLGE-----AYEYPTFIQDLR 22
              ||||||      ::::  : ||||
Db        196 VSFNLGSLGFLTSHDFEDYKQDLR 219


RESULT 58
US-11-056-355B-55413
; Sequence 55413, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 55413
;   LENGTH: 414
;   TYPE: prt
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(414)
;   OTHER INFORMATION: Ceres Seq. ID no. 12581698
US-11-056-355B-55413

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 414;
  Best Local Similarity   41.7%;  Pred. No. 1.7e+02;
  Matches   10;  Conservative    5;  Mismatches    4;  Indels    5;  Gaps    1;

Qy          4 VSFNLGE-----AYEYPTFIQDLR 22
              ||||||      ::::  : ||||
Db        199 VSFNLGSLGFLTSHDFEDYKQDLR 222


RESULT 59
US-11-056-355B-96500
; Sequence 96500, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 96500
;   LENGTH: 434
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(434)
;   OTHER INFORMATION: Ceres Seq. ID no. 12733586
US-11-056-355B-96500

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 434;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+02;
  Matches   10;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLR 22
              ||:|| ||.:| | :   ||
Db         36 TVNFN-GEIFESPQYCSTLR 54


RESULT 60
US-11-056-355B-55412
; Sequence 55412, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 55412
;   LENGTH: 485
;   TYPE: prt
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(485)
;   OTHER INFORMATION: Ceres Seq. ID no. 12581697
US-11-056-355B-55412

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 485;
  Best Local Similarity   41.7%;  Pred. No. 2e+02;
  Matches   10;  Conservative    5;  Mismatches    4;  Indels    5;  Gaps    1;

Qy          4 VSFNLGE-----AYEYPTFIQDLR 22
              ||||||      ::::  : ||||
Db        270 VSFNLGSLGFLTSHDFEDYKQDLR 293


RESULT 61
US-11-056-355B-100946
; Sequence 100946, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 100946
;   LENGTH: 787
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(787)
;   OTHER INFORMATION: Ceres Seq. ID no. 13606445
US-11-056-355B-100946

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 787;
  Best Local Similarity   46.2%;  Pred. No. 3.5e+02;
  Matches   12;  Conservative    3;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          5 SFNLGEAYEYPT-FIQDLRNELAKGT 29
              | ||| || |      :||| :| |:
Db        678 SRNLGPAYSYQAQGTNNLRNFMAHGS 703


RESULT 62
US-11-056-355B-112185
; Sequence 112185, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 112185
;   LENGTH: 787
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(787)
;   OTHER INFORMATION: Ceres Seq. ID no. 13606445
US-11-056-355B-112185

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 787;
  Best Local Similarity   46.2%;  Pred. No. 3.5e+02;
  Matches   12;  Conservative    3;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          5 SFNLGEAYEYPT-FIQDLRNELAKGT 29
              | ||| || |      :||| :| |:
Db        678 SRNLGPAYSYQAQGTNNLRNFMAHGS 703


RESULT 63
US-11-056-355B-100945
; Sequence 100945, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 100945
;   LENGTH: 880
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(880)
;   OTHER INFORMATION: Ceres Seq. ID no. 13606444
US-11-056-355B-100945

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 880;
  Best Local Similarity   46.2%;  Pred. No. 4e+02;
  Matches   12;  Conservative    3;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          5 SFNLGEAYEYPT-FIQDLRNELAKGT 29
              | ||| || |      :||| :| |:
Db        771 SRNLGPAYSYQAQGTNNLRNFMAHGS 796


RESULT 64
US-11-056-355B-112184
; Sequence 112184, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 112184
;   LENGTH: 880
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(880)
;   OTHER INFORMATION: Ceres Seq. ID no. 13606444
US-11-056-355B-112184

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 880;
  Best Local Similarity   46.2%;  Pred. No. 4e+02;
  Matches   12;  Conservative    3;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          5 SFNLGEAYEYPT-FIQDLRNELAKGT 29
              | ||| || |      :||| :| |:
Db        771 SRNLGPAYSYQAQGTNNLRNFMAHGS 796


RESULT 65
US-11-056-355B-100944
; Sequence 100944, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
```

```
; SEQ ID NO 100944
;   LENGTH: 911
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(911)
;   OTHER INFORMATION: Ceres Seq. ID no. 13606443
US-11-056-355B-100944

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 911;
  Best Local Similarity   46.2%;  Pred. No. 4.2e+02;
  Matches   12;  Conservative    3;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          5 SFNLGEAYEYPT-FIQDLRNELAKGT 29
              | ||| || |      :||| :| |:
Db        802 SRNLGPAYSYQAQGTNNLRNFMAHGS 827


RESULT 66
US-11-056-355B-112183
; Sequence 112183, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 112183
;   LENGTH: 911
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(911)
;   OTHER INFORMATION: Ceres Seq. ID no. 13606443
US-11-056-355B-112183

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 911;
  Best Local Similarity   46.2%;  Pred. No. 4.2e+02;
  Matches   12;  Conservative    3;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          5 SFNLGEAYEYPT-FIQDLRNELAKGT 29
              | ||| || |      :||| :| |:
Db        802 SRNLGPAYSYQAQGTNNLRNFMAHGS 827


RESULT 67
US-10-449-902-43097
; Sequence 43097, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43097
;   LENGTH: 981
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-43097

  Query Match             27.2%;  Score 43.5;  DB 6;  Length 981;
  Best Local Similarity   45.8%;  Pred. No. 4.5e+02;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    5;  Gaps    1;

Qy          4 VSFNLGE-----AYEYPTFIQDLR 22
              ||||||      :: :  | ||||
Db        767 VSFNLGSLGFLTSHNFEGFRQDLR 790


RESULT 68
US-10-479-834-26
; Sequence 26, Application US/10479834
; Publication No. US20060185030A1
; GENERAL INFORMATION:
;  APPLICANT: Sheen, Jen
;  APPLICANT:  Hwang, Iidoo
;  TITLE OF INVENTION: Cytokinin Response Regulators and Uses
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 00786/402002
;  CURRENT APPLICATION NUMBER: US/10/479,834
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/US02/18066
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/296,554
;  PRIOR FILING DATE: 2001-06-06
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 1176
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-479-834-26

  Query Match             27.2%;  Score 43.5;  DB 6;  Length 1176;
  Best Local Similarity   33.3%;  Pred. No. 5.6e+02;
  Matches    8;  Conservative    9;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLRNELA 26
              |: : || :|: |: :: | ::||
Db        455 TIGY-LGASYDMPSLVEKLLHQLA 477


RESULT 69
US-11-273-537-19
; Sequence 19, Application US/11273537
; Publication No. US20060137033A1
; GENERAL INFORMATION:
;  APPLICANT: Meister, Robert J.
;  APPLICANT:  Sivasankar, Shoba
;  TITLE OF INVENTION: Cytokinin-Sensing Histidine Kinases and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: 1746
;  CURRENT APPLICATION NUMBER: US/11/273,537
;  CURRENT FILING DATE:  2005-11-14
;  PRIOR APPLICATION NUMBER: US 60/627,394
;  PRIOR FILING DATE: 2004-11-12
;  PRIOR APPLICATION NUMBER: US 60/706,787
;  PRIOR FILING DATE: 2005-08-09
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 1176
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-11-273-537-19

  Query Match             27.2%;  Score 43.5;  DB 7;  Length 1176;
  Best Local Similarity   33.3%;  Pred. No. 5.6e+02;
```

```
  Matches    8;  Conservative    9;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLRNELA 26
              |: : || :|: |: :: | ::||
Db        455 TIGY-LGASYDMPSLVEKLLHQLA 477


RESULT 70
US-11-330-403-2492
; Sequence 2492, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 2492
;   LENGTH: 445
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-11-330-403-2492

  Query Match             26.9%;  Score 43;  DB 7;  Length 445;
  Best Local Similarity   34.8%;  Pred. No. 2.2e+02;
  Matches    8;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          8 LGEAYEYPTFIQDLRNELAKGTP 30
              |   : :|  || ::: || | |
Db         65 LALGHNHPAVIQSIQDTLASGLP 87


RESULT 71
US-10-449-902-31529
; Sequence 31529, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31529
;   LENGTH: 553
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-31529

  Query Match             26.9%;  Score 43;  DB 6;  Length 553;
  Best Local Similarity   33.3%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAK 27
              : |:: :  :| | || |:|   |
Db        294 IDFDINQGSQYITLIQFLKNNANK 317


RESULT 72
US-10-449-902-45402
; Sequence 45402, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45402
;   LENGTH: 553
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-45402

  Query Match             26.9%;  Score 43;  DB 6;  Length 553;
  Best Local Similarity   33.3%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAK 27
              : |:: :  :| | || |:|   |
Db        294 IDFDINQGSQYITLIQFLKNNANK 317


RESULT 73
US-10-449-902-53657
; Sequence 53657, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53657
;   LENGTH: 711
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-53657

  Query Match             26.9%;  Score 43;  DB 6;  Length 711;
  Best Local Similarity   28.0%;  Pred. No. 3.7e+02;
  Matches    7;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAKG 28
              : |:||   :: :|:|:| :    |
Db        463 IDFDLGVGGQWASFLQELAHRCGSG 487


RESULT 74
US-11-056-355B-80327
; Sequence 80327, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
```

```
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 80327
;   LENGTH: 725
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(725)
;   OTHER INFORMATION: Ceres Seq. ID no. 12655380
US-11-056-355B-80327

  Query Match            26.9%;  Score 43;  DB 7;  Length 725;
  Best Local Similarity  26.5%;  Pred. No. 3.8e+02;
  Matches   13;  Conservative    3;  Mismatches    9;  Indels   24;  Gaps    1;

Qy          6 FNLGEAYEYPTFIQD-----------------------LRNELAKGTP 30
              :|  |   :|  | :|                       | ||||||  |
Db        445 WNYGSKLKYETEVQKKLPMDLLRELGSNLGTIRAPGIGLLYNELAKGVP 493


RESULT 75
US-10-449-902-46787
; Sequence 46787, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46787
;   LENGTH: 753
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-46787

  Query Match            26.9%;  Score 43;  DB 6;  Length 753;
  Best Local Similarity  53.3%;  Pred. No. 4e+02;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         13 EYPTFIQDLRNELAK 27
              ||  |:||   |:||
Db        308 EYARFLQDTAKEMAK 322


RESULT 76
US-11-330-403-4451
; Sequence 4451, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4451
;   LENGTH: 753
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-11-330-403-4451

  Query Match            26.9%;  Score 43;  DB 7;  Length 753;
  Best Local Similarity  29.2%;  Pred. No. 4e+02;
  Matches    7;  Conservative    9;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNE 24
              :||  | : :|:::| |:  :: |
Db        201 HNTPIFFIQDAHKFPDFVHAVKPE 224


RESULT 77
US-10-449-902-53326
; Sequence 53326, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53326
;   LENGTH: 767
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-53326

  Query Match            26.9%;  Score 43;  DB 6;  Length 767;
  Best Local Similarity  53.3%;  Pred. No. 4e+02;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         13 EYPTFIQDLRNELAK 27
              ||  |:||   |:||
Db        316 EYAKFLQDTAKEMAK 330


RESULT 78
US-11-056-355B-80326
; Sequence 80326, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 80326
;   LENGTH: 797
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(797)
;   OTHER INFORMATION: Ceres Seq. ID no. 12655379
US-11-056-355B-80326

  Query Match            26.9%;  Score 43;  DB 7;  Length 797;
  Best Local Similarity  26.5%;  Pred. No. 4.2e+02;
  Matches   13;  Conservative    3;  Mismatches    9;  Indels   24;  Gaps    1;
```

```
Qy          6 FNLGEAYEYPTFIQD-----------------------LRNELAKGTP 30
              :| |   :| | :|                        | ||||||  |
Db        517 WNYGSKLKYETEVQKKLPMDLLRELGSNLGTIRAPGIGLLYNELAKGVP 565
```

RESULT 79
US-10-449-902-55004
; Sequence 55004, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55004
; LENGTH: 804
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55004

Query Match 26.9%; Score 43; DB 6; Length 804;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```
Qy         13 EYPTFIQDLRNELAKG 28
              | |:|:||| |   :|
Db        786 ELPSFMQDLTNHQRQG 801
```

RESULT 80
US-11-056-355B-80325
; Sequence 80325, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 80325
; LENGTH: 855
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(855)
; OTHER INFORMATION: Ceres Seq. ID no. 12655378
US-11-056-355B-80325

Query Match 26.9%; Score 43; DB 7; Length 855;
Best Local Similarity 26.5%; Pred. No. 4.6e+02;
Matches 13; Conservative 3; Mismatches 9; Indels 24; Gaps 1;

```
Qy          6 FNLGEAYEYPTFIQD-----------------------LRNELAKGTP 30
              :| |   :| | :|                        | ||||||  |
Db        575 WNYGSKLKYETEVQKKLPMDLLRELGSNLGTIRAPGIGLLYNELAKGVP 623
```

RESULT 81
US-10-374-780A-1453
; Sequence 1453, Application US/10374780A
; Publication No. US20060162006A9
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1453
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to G1140
US-10-374-780A-1453

Query Match 26.6%; Score 42.5; DB 6; Length 229;
Best Local Similarity 51.9%; Pred. No. 1.2e+02;
Matches 14; Conservative 3; Mismatches 7; Indels 3; Gaps 2;

```
Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAK 27
              ||| | |||:| | |:   ||  | :|
Db         69 YNTHSNNLGKA-EQPSL--DLNLEHSK 92
```

RESULT 82
US-11-416-490-137
; Sequence 137, Application US/11416490
; Publication No. US20060195935A1
; GENERAL INFORMATION:
; APPLICANT: ChromaGenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kwaks, Theodorus H.J.
; APPLICANT: Sewalt, Richard G.A.B.
; APPLICANT: van Blokland, Rik
; TITLE OF INVENTION: Selection of host cells expressing protein at high levels
; FILE REFERENCE: 0117 B US P00 CIP

```
;  CURRENT APPLICATION NUMBER: US/11/416,490
;  CURRENT FILING DATE:  2006-05-02
;  PRIOR APPLICATION NUMBER: US 11/269,525
;  PRIOR FILING DATE: 2005-11-07
;  PRIOR APPLICATION NUMBER: US 11/359,953
;  PRIOR FILING DATE: 2006-02-21
;  PRIOR APPLICATION NUMBER: US 60/626,301
;  PRIOR FILING DATE: 2004-11-08
;  PRIOR APPLICATION NUMBER: US 60/696,610
;  PRIOR FILING DATE: 2005-07-05
;  PRIOR APPLICATION NUMBER: EP 04105593.0
;  PRIOR FILING DATE: 2004-11-08
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 137
;   LENGTH: 397
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-11-416-490-137

  Query Match             26.6%;  Score 42.5;  DB 7;  Length 397;
  Best Local Similarity   28.1%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    8;  Mismatches   12;  Indels    3;  Gaps    1;

Qy          1 YNTVSFNLGEA---YEYPTFIQDLRNELAKGT 29
              | |  : || |   : ||| ::: :  : : |
Db        181 YETAHYLLGTAAGPHPYPTIVREFQRIIGEET 212


RESULT 83
US-11-056-355B-48930
; Sequence 48930, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 48930
;   LENGTH: 496
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(496)
;   OTHER INFORMATION: Ceres Seq. ID no. 13579123
US-11-056-355B-48930

  Query Match             26.6%;  Score 42.5;  DB 7;  Length 496;
  Best Local Similarity   31.0%;  Pred. No. 2.9e+02;
  Matches    9;  Conservative    8;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          2 NTVSFN-LGEAYEYPTFIQDLRNELAKGT 29
              | :||| :|:   :   |: |:|::   |
Db        440 NILSFNRIGQKQRFKIVIKPLKNQVMNAT 468


RESULT 84
US-11-056-355B-79165
; Sequence 79165, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 79165
;   LENGTH: 496
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(496)
;   OTHER INFORMATION: Ceres Seq. ID no. 12649501
US-11-056-355B-79165

  Query Match             26.6%;  Score 42.5;  DB 7;  Length 496;
  Best Local Similarity   31.0%;  Pred. No. 2.9e+02;
  Matches    9;  Conservative    8;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          2 NTVSFN-LGEAYEYPTFIQDLRNELAKGT 29
              | :||| :|:   :   |: |:|::   |
Db        440 NILSFNRIGQKQRFKIVIKPLKNQVMNAT 468


RESULT 85
US-11-330-403-3810
; Sequence 3810, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 3810
;   LENGTH: 539
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-11-330-403-3810

  Query Match             26.6%;  Score 42.5;  DB 7;  Length 539;
  Best Local Similarity   52.9%;  Pred. No. 3.2e+02;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          6 FNLG---EAYEYPTFIQ 19
              :|||   |||: ||:|
Db        474 YNLGMLMAAYEHKTFVQ 490


RESULT 86
US-11-330-403-3828
; Sequence 3828, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 3828
;   LENGTH: 539
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-11-330-403-3828

  Query Match             26.6%;  Score 42.5;  DB 7;  Length 539;
  Best Local Similarity   52.9%;  Pred. No. 3.2e+02;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    3;  Gaps    1;
```

```
Qy          6 FNLG---EAYEYPTFIQ 19
              :|||    |||: ||:|
Db        474 YNLGMLMAAYEHKTFVQ 490
```

RESULT 87
US-11-330-403-4997
; Sequence 4997, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4997
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Neisseria meningitidis MC58
US-11-330-403-4997

Query Match 26.6%; Score 42.5; DB 7; Length 547;
Best Local Similarity 52.9%; Pred. No. 3.2e+02;
Matches 9; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

```
Qy          6 FNLG---EAYEYPTFIQ 19
              :|||    |||: ||:|
Db        474 YNLGMLMAAYEHKTFVQ 490
```

RESULT 88
US-11-330-403-6530
; Sequence 6530, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 6530
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Neisseria meningitidis Z2491
US-11-330-403-6530

Query Match 26.6%; Score 42.5; DB 7; Length 547;
Best Local Similarity 52.9%; Pred. No. 3.2e+02;
Matches 9; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

```
Qy          6 FNLG---EAYEYPTFIQ 19
              :|||    |||: ||:|
Db        474 YNLGMLMAAYEHKTFVQ 490
```

RESULT 89
US-11-056-355B-79164
; Sequence 79164, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 79164
; LENGTH: 586
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(586)
; OTHER INFORMATION: Ceres Seq. ID no. 12649500
US-11-056-355B-79164

Query Match 26.6%; Score 42.5; DB 7; Length 586;
Best Local Similarity 31.0%; Pred. No. 3.5e+02;
Matches 9; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

```
Qy          2 NTVSFN-LGEAYEYPTFIQDLRNELAKGT 29
              | :||| :|:   :   |: |:|::   |
Db        530 NILSFNRIGQKQRFKIVIKPLKNQVMNAT 558
```

RESULT 90
US-11-056-355B-48929
; Sequence 48929, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 48929
; LENGTH: 617
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(617)
; OTHER INFORMATION: Ceres Seq. ID no. 13579122
US-11-056-355B-48929

Query Match 26.6%; Score 42.5; DB 7; Length 617;
Best Local Similarity 31.0%; Pred. No. 3.7e+02;
Matches 9; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

```
Qy          2 NTVSFN-LGEAYEYPTFIQDLRNELAKGT 29
              | :||| :|:   :   |: |:|::   |
Db        561 NILSFNRIGQKQRFKIVIKPLKNQVMNAT 589
```

RESULT 91
US-10-953-349-5336
; Sequence 5336, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5336
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5336

Query Match 26.6%; Score 42.5; DB 6; Length 649;
Best Local Similarity 46.2%; Pred. No. 3.9e+02;

Matches 12; Conservative 1; Mismatches 10; Indels 3; Gaps 1;

```
Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              |  | | |    |:|  | || | ||
Db        365 YKAVHFYL---QEHPDIINDLLNVLA 387
```

RESULT 92
US-10-953-349-5335
; Sequence 5335, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5335
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5335

Query Match 26.6%; Score 42.5; DB 6; Length 694;
Best Local Similarity 46.2%; Pred. No. 4.3e+02;
Matches 12; Conservative 1; Mismatches 10; Indels 3; Gaps 1;

```
Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              |  | | |    |:|  | || | ||
Db        410 YKAVHFYL---QEHPDIINDLLNVLA 432
```

RESULT 93
US-10-953-349-5334
; Sequence 5334, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5334
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5334

Query Match 26.6%; Score 42.5; DB 6; Length 731;
Best Local Similarity 46.2%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 10; Indels 3; Gaps 1;

```
Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              |  | | |    |:|  | || | ||
Db        447 YKAVHFYL---QEHPDIINDLLNVLA 469
```

RESULT 94
US-11-056-355B-79163
; Sequence 79163, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 79163
; LENGTH: 760
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(760)
; OTHER INFORMATION: Ceres Seq. ID no. 12649499
US-11-056-355B-79163

Query Match 26.6%; Score 42.5; DB 7; Length 760;
Best Local Similarity 31.0%; Pred. No. 4.7e+02;
Matches 9; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

```
Qy          2 NTVSFN-LGEAYEYPTFIQDLRNELAKGT 29
              | :||| :|:   :   |: |:|::   |
Db        704 NILSFNRIGQKQRFKIVIKPLKNQVMNAT 732
```

RESULT 95
US-11-056-355B-48928
; Sequence 48928, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 48928
; LENGTH: 791
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(791)
; OTHER INFORMATION: Ceres Seq. ID no. 13579121
US-11-056-355B-48928

Query Match 26.6%; Score 42.5; DB 7; Length 791;
Best Local Similarity 31.0%; Pred. No. 5e+02;
Matches 9; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

```
Qy          2 NTVSFN-LGEAYEYPTFIQDLRNELAKGT 29
              | :||| :|:   :   |: |:|::   |
Db        735 NILSFNRIGQKQRFKIVIKPLKNQVMNAT 763
```

RESULT 96
US-11-330-403-18353
; Sequence 18353, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 18353
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Bacillus subtilis subsp. subtilis str. 168

US-11-330-403-18353

Query Match 26.2%; Score 42; DB 7; Length 233;
Best Local Similarity 28.6%; Pred. No. 1.4e+02;
Matches 8; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

```
Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKG 28
              | |: | |    :| | ::::|  :  |
Db        119 YVTIGFGLRNVPDYLTVLKEMRRVVKPG 146
```

RESULT 97
US-10-449-902-31941
; Sequence 31941, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31941
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31941

Query Match 26.2%; Score 42; DB 6; Length 318;
Best Local Similarity 32.1%; Pred. No. 2e+02;
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKGT 29
              :|||  :|:||   |::      : :||
Db        198 DTVSSEIGKAYGRTTYLVTTLKVVPRGT 225
```

RESULT 98
US-10-449-902-44562
; Sequence 44562, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44562
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44562

Query Match 26.2%; Score 42; DB 6; Length 318;
Best Local Similarity 32.1%; Pred. No. 2e+02;
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKGT 29
              :|||  :|:||   |::      : :||
Db        198 DTVSSEIGKAYGRTTYLVTTLKVVPRGT 225
```

RESULT 99
US-10-449-902-46734
; Sequence 46734, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46734
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46734

Query Match 26.2%; Score 42; DB 6; Length 318;
Best Local Similarity 32.1%; Pred. No. 2e+02;
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

```
Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKGT 29
              :|||  :|:||   |::      : :||
Db        198 DTVSSEIGKAYGRTTYLVTTLKVVPRGT 225
```

RESULT 100
US-11-330-403-4313
; Sequence 4313, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4313
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-330-403-4313

Query Match 26.2%; Score 42; DB 7; Length 326;
Best Local Similarity 28.6%; Pred. No. 2.1e+02;
Matches 10; Conservative 4; Mismatches 13; Indels 8; Gaps 1;

```
Qy          4 VSFNLGEAYEYPTFIQD--------LRNELAKGTP 30
              |  | |     | |: |         ||: : |:|
Db        139 VDLNTGSTTVLPAFLSDNGNLPAPNTRNKFSDGSP 173
```

Search completed: September 18, 2006, 19:36:18
Job time : 9.03911 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:14:52 ; Search time 145.307 Seconds
(without alignments)
315.254 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending_Patents_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/paa/PCTUS_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/paa/US066_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/paa/US073_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/paa/US074_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/paa/US075_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/paa/US076_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/paa/US077_COMB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/paa/US078_COMB.pep:*
9: /EMC_Celerra_SIDS3/ptodata/2/paa/US079_COMB.pep:*
10: /EMC_Celerra_SIDS3/ptodata/2/paa/US080_COMB.pep:*
11: /EMC_Celerra_SIDS3/ptodata/2/paa/US081_COMB.pep:*
12: /EMC_Celerra_SIDS3/ptodata/2/paa/US082_COMB.pep:*
13: /EMC_Celerra_SIDS3/ptodata/2/paa/US083_COMB.pep:*
14: /EMC_Celerra_SIDS3/ptodata/2/paa/US084_COMB.pep:*
15: /EMC_Celerra_SIDS3/ptodata/2/paa/US085_COMB.pep:*
16: /EMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*
17: /EMC_Celerra_SIDS3/ptodata/2/paa/US087_COMB.pep:*
18: /EMC_Celerra_SIDS3/ptodata/2/paa/US088_COMB.pep:*
19: /EMC_Celerra_SIDS3/ptodata/2/paa/US089_COMB.pep:*
20: /EMC_Celerra_SIDS3/ptodata/2/paa/US090_COMB.pep:*
21: /EMC_Celerra_SIDS3/ptodata/2/paa/US091_COMB.pep:*
22: /EMC_Celerra_SIDS3/ptodata/2/paa/US092_COMB.pep:*
23: /EMC_Celerra_SIDS3/ptodata/2/paa/US093_COMB.pep:*
24: /EMC_Celerra_SIDS3/ptodata/2/paa/US094_COMB.pep:*
25: /EMC_Celerra_SIDS3/ptodata/2/paa/US095_COMB.pep:*
26: /EMC_Celerra_SIDS3/ptodata/2/paa/US096_COMB.pep:*
27: /EMC_Celerra_SIDS3/ptodata/2/paa/US097_COMB.pep:*
28: /EMC_Celerra_SIDS3/ptodata/2/paa/US098_COMB.pep:*
29: /EMC_Celerra_SIDS3/ptodata/2/paa/US099_COMB.pep:*
30: /EMC_Celerra_SIDS3/ptodata/2/paa/US100_COMB.pep:*
31: /EMC_Celerra_SIDS3/ptodata/2/paa/US101_COMB.pep:*
32: /EMC_Celerra_SIDS3/ptodata/2/paa/US102_COMB.pep:*
33: /EMC_Celerra_SIDS3/ptodata/2/paa/US103_COMB.pep:*
34: /EMC_Celerra_SIDS3/ptodata/2/paa/US104_COMB.pep:*
35: /EMC_Celerra_SIDS3/ptodata/2/paa/US105_COMB.pep:*
36: /EMC_Celerra_SIDS3/ptodata/2/paa/US106_COMB.pep:*
37: /EMC_Celerra_SIDS3/ptodata/2/paa/US107_COMB.pep:*
38: /EMC_Celerra_SIDS3/ptodata/2/paa/US108_COMB.pep:*
39: /EMC_Celerra_SIDS3/ptodata/2/paa/US109_COMB.pep:*
40: /EMC_Celerra_SIDS3/ptodata/2/paa/US110_COMB.pep:*
41: /EMC_Celerra_SIDS3/ptodata/2/paa/US111_COMB.pep:*
42: /EMC_Celerra_SIDS3/ptodata/2/paa/US112_COMB.pep:*
43: /EMC_Celerra_SIDS3/ptodata/2/paa/US113_COMB.pep:*
44: /EMC_Celerra_SIDS3/ptodata/2/paa/US114_COMB.pep:*
45: /EMC_Celerra_SIDS3/ptodata/2/paa/US600_COMB.pep:*
46: /EMC_Celerra_SIDS3/ptodata/2/paa/US601_COMB.pep:*
47: /EMC_Celerra_SIDS3/ptodata/2/paa/US602_COMB.pep:*
48: /EMC_Celerra_SIDS3/ptodata/2/paa/US603_COMB.pep:*
49: /EMC_Celerra_SIDS3/ptodata/2/paa/US604_COMB.pep:*
50: /EMC_Celerra_SIDS3/ptodata/2/paa/US605_COMB.pep:*
51: /EMC_Celerra_SIDS3/ptodata/2/paa/US606_COMB.pep:*
52: /EMC_Celerra_SIDS3/ptodata/2/paa/US607_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	100.0	30	37	US-10-758-902-1	Sequence 1, Appli
2	160	100.0	149	24	US-09-446-351B-1	Sequence 1, Appli
3	160	100.0	149	24	US-09-446-351D-1	Sequence 1, Appli
4	160	100.0	149	37	US-10-758-902-9	Sequence 9, Appli
5	160	100.0	250	40	US-11-084-080-1	Sequence 1, Appli
6	160	100.0	250	40	US-11-084-080-11	Sequence 11, Appl
7	160	100.0	250	40	US-11-084-080-12	Sequence 12, Appl
8	160	100.0	250	40	US-11-084-080-13	Sequence 13, Appl
9	160	100.0	250	40	US-11-084-080-14	Sequence 14, Appl
10	160	100.0	250	40	US-11-084-080-129	Sequence 129, App
11	160	100.0	750	40	US-11-084-080-16	Sequence 16, Appl
12	160	100.0	750	40	US-11-084-080-20	Sequence 20, Appl
13	160	100.0	750	40	US-11-084-080-22	Sequence 22, Appl
14	160	100.0	750	40	US-11-084-080-24	Sequence 24, Appl
15	160	100.0	759	40	US-11-084-080-28	Sequence 28, Appl
16	83	51.9	15	40	US-11-084-080-32	Sequence 32, Appl
17	81	50.6	15	40	US-11-084-080-34	Sequence 34, Appl
18	81	50.6	15	40	US-11-084-080-35	Sequence 35, Appl
19	80	50.0	15	40	US-11-084-080-33	Sequence 33, Appl
20	78	48.8	15	40	US-11-084-080-36	Sequence 36, Appl
21	77	48.1	15	40	US-11-084-080-37	Sequence 37, Appl
22	62	38.8	15	40	US-11-084-080-38	Sequence 38, Appl
23	62	38.8	569	27	US-09-791-537-94189	Sequence 94189, A
24	61	38.1	262	27	US-09-791-537-21233	Sequence 21233, A
25	61	38.1	292	27	US-09-791-537-63089	Sequence 63089, A
26	61	38.1	312	1	PCT-US02-02792-2	Sequence 2, Appli
27	61	38.1	312	34	US-10-467-009-2	Sequence 2, Appli
28	61	38.1	313	10	US-08-049-075-2	Sequence 2, Appli
29	61	38.1	313	15	US-08-501-253-2	Sequence 2, Appli
30	61	38.1	313	27	US-09-791-537-36414	Sequence 36414, A
31	61	38.1	313	40	US-11-010-795-20	Sequence 20, Appl
32	61	38.1	313	41	US-11-106-187-2	Sequence 2, Appli
33	59.5	37.2	449	43	US-11-360-355-121143	Sequence 121143,
34	59.5	37.2	449	51	US-60-655-875-121143	Sequence 121143,
35	59	36.9	107	34	US-10-424-599-213759	Sequence 213759,
36	59	36.9	261	7	US-07-787-567A-9	Sequence 9, Appli
37	59	36.9	261	27	US-09-791-537-3998	Sequence 3998, Ap
38	59	36.9	261	31	US-10-127-890-9	Sequence 9, Appli
39	59	36.9	261	36	US-10-613-755-9	Sequence 9, Appli
40	59	36.9	261	37	US-10-717-243-9	Sequence 9, Appli
41	57.5	35.9	225	34	US-10-417-884-7302	Sequence 7302, Ap
42	57.5	35.9	225	34	US-10-417-884A-7302	Sequence 7302, Ap
43	57	35.6	324	34	US-10-437-963-146447	Sequence 146447,
44	56	35.0	77	37	US-10-767-701-37927	Sequence 37927, A
45	56	35.0	120	34	US-10-425-115-351081	Sequence 351081,
46	56	35.0	154	29	US-09-978-274A-6	Sequence 6, Appli
47	56	35.0	160	34	US-10-425-115-351080	Sequence 351080,
48	56	35.0	263	29	US-09-978-274A-4	Sequence 4, Appli
49	56	35.0	289	32	US-10-219-999-61450	Sequence 61450, A
50	56	35.0	289	34	US-10-425-115-351084	Sequence 351084,
51	56	35.0	289	48	US-60-324-109-29945	Sequence 29945, A
52	56	35.0	292	17	US-08-715-074A-2	Sequence 2, Appli
53	56	35.0	314	1	PCT-US02-15033A-16	Sequence 16, Appl
54	56	35.0	314	27	US-09-791-537-91800	Sequence 91800, A

55	56	35.0	314	29	US-09-978-274A-2	Sequence 2, Appli
56	55	34.4	280	37	US-10-703-032-113730	Sequence 113730,
57	54.5	34.1	292	34	US-10-424-599-274703	Sequence 274703,
58	54.5	34.1	608	43	US-11-311-940-8052	Sequence 8052, Ap
59	54.5	34.1	608	43	US-11-311-940A-8052	Sequence 8052, Ap
60	54.5	34.1	608	50	US-60-581-351-12408	Sequence 12408, A
61	54.5	34.1	608	51	US-60-638-099-45698	Sequence 45698, A
62	54.5	34.1	608	52	US-60-752-355-50174	Sequence 50174, A
63	54	33.8	29	13	US-08-378-761-28	Sequence 28, Appl
64	54	33.8	237	37	US-10-767-795-77750	Sequence 77750, A
65	54	33.8	447	34	US-10-424-599-215698	Sequence 215698,
66	54	33.8	563	27	US-09-791-537-78226	Sequence 78226, A
67	54	33.8	563	27	US-09-791-537-79846	Sequence 79846, A
68	53	33.1	470	42	US-11-241-607-52631	GENERAL INFORMATI
69	53	33.1	857	46	US-60-147-189-955	Sequence 955, App
70	53	33.1	1309	46	US-60-167-217-15106	Sequence 15106, A
71	53	33.1	1309	46	US-60-173-464-12311	Sequence 12311, A
72	53	33.1	1464	26	US-09-614-150-40125	Sequence 40125, A
73	53	33.1	1464	26	US-09-614-150A-40125	Sequence 40125, A
74	53	33.1	1464	27	US-09-791-537-8878	Sequence 8878, Ap
75	53	33.1	1464	27	US-09-791-537-119059	Sequence 119059,
76	53	33.1	1464	27	US-09-791-537-146213	Sequence 146213,
77	53	33.1	1464	40	US-11-097-143-40125	Sequence 40125, A
78	53	33.1	1464	46	US-60-191-637-39757	Sequence 39757, A
79	53	33.1	1464	46	US-60-191-681-30787	Sequence 30787, A
80	52	32.5	67	27	US-09-791-537-1700	Sequence 1700, Ap
81	52	32.5	376	27	US-09-791-537-14085	Sequence 14085, A
82	52	32.5	459	40	US-11-031-175-10583	Sequence 10583, A
83	51.5	32.2	238	40	US-11-031-175-16037	Sequence 16037, A
84	51.5	32.2	386	34	US-10-449-902-44047	Sequence 44047, A
85	51.5	32.2	386	34	US-10-449-902-45250	Sequence 45250, A
86	51.5	32.2	757	34	US-10-437-963-136583	Sequence 136583,
87	51	31.9	32	11	US-08-141-891-1	Sequence 1, Appli
88	51	31.9	148	37	US-10-767-701-50462	Sequence 50462, A
89	51	31.9	334	27	US-09-791-537-782	Sequence 782, App
90	51	31.9	545	27	US-09-791-537-5912	Sequence 5912, Ap
91	51	31.9	1233	34	US-10-434-665-4971	Sequence 4971, Ap
92	51	31.9	1416	39	US-10-912-362-404	Sequence 404, App
93	51	31.9	1448	39	US-10-912-362-402	Sequence 402, App
94	51	31.9	1945	27	US-09-708-427-16943	Sequence 16943, A
95	51	31.9	2049	27	US-09-708-427-16942	Sequence 16942, A
96	51	31.9	2172	27	US-09-708-427-16941	Sequence 16941, A
97	50.5	31.6	291	1	PCT-US05-11532-1717	Sequence 1717, Ap
98	50.5	31.6	291	27	US-09-791-537-91812	Sequence 91812, A
99	50.5	31.6	291	32	US-10-219-051B-8973	Sequence 8973, Ap
100	50.5	31.6	291	32	US-10-219-051B-8977	Sequence 8977, Ap

ALIGNMENTS

```
RESULT 1
US-10-758-902-1
; Sequence 1, Application US/10758902
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-1

  Query Match             100.0%;  Score 160;  DB 37;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 2
US-09-446-351B-1
; Sequence 1, Application US/09446351B
; GENERAL INFORMATION:
;  APPLICANT: De Boer, Mark
;  APPLICANT:  Den Hartog, Marcel Theodorus
;  TITLE OF INVENTION: Anti-CD40L Immunotoxins for the Treatment of Diseases
;  FILE REFERENCE: DE BOER
;  CURRENT APPLICATION NUMBER: US/09/446,351B
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: PCT/NL98/00357
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EP 97201895
;  PRIOR FILING DATE: 1997-06-20
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 1
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;   LOCATION: 143
;   OTHER INFORMATION: Trp uncertain
US-09-446-351B-1

  Query Match             100.0%;  Score 160;  DB 24;  Length 149;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 3
US-09-446-351D-1
; Sequence 1, Application US/09446351D
; GENERAL INFORMATION:
;  APPLICANT: TANOX PHARMA, INC.
;  APPLICANT:  De Boer, Mark
;  APPLICANT:  MARCEL, Theodorus
;  TITLE OF INVENTION: ANTI-CD40L IMMUNOTOXINS FOR THE TREATMENT OF DISEASES
;  FILE REFERENCE: TNXPHARMA00357
;  CURRENT APPLICATION NUMBER: US/09/446,351D
;  CURRENT FILING DATE:  2000-02-07
;  PRIOR APPLICATION NUMBER: EP97201895.6
;  PRIOR FILING DATE: 1997-06-20
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-09-446-351D-1

  Query Match             100.0%;  Score 160;  DB 24;  Length 149;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
```

```
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 4
US-10-758-902-9
; Sequence 9, Application US/10758902
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-9

  Query Match           100.0%;  Score 160;  DB 37;  Length 149;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 5
US-11-084-080-1
; Sequence 1, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis Wild
US-11-084-080-1

  Query Match           100.0%;  Score 160;  DB 40;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 6
US-11-084-080-11
; Sequence 11, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (123)..(123)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (127)..(127)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (129)..(129)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (133)..(133)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (152)..(152)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-084-080-11

  Query Match           100.0%;  Score 160;  DB 40;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 7
US-11-084-080-12
; Sequence 12, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
```

```
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (123)..(123)
;   OTHER INFORMATION: Xaa can be T or A or Q
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (127)..(127)
;   OTHER INFORMATION: Xaa can be G or A
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (129)..(129)
;   OTHER INFORMATION: Xaa can be Q or G
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (133)..(133)
;   OTHER INFORMATION: Xaa can be N or D or T or A or R or Q or E or G or H or K or S
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (152)..(152)
;   OTHER INFORMATION: Xaa can be Q or A
US-11-084-080-12

  Query Match           100.0%;  Score 160;  DB 40;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 8
US-11-084-080-13
; Sequence 13, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-13

  Query Match           100.0%;  Score 160;  DB 40;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 9
US-11-084-080-14
; Sequence 14, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-14

  Query Match           100.0%;  Score 160;  DB 40;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 10
US-11-084-080-129
; Sequence 129, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129
;   LENGTH: 250
;   TYPE: PRT
```

```
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-129

  Query Match            100.0%;  Score 160;  DB 40;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 11
US-11-084-080-16
; Sequence 16, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-16

  Query Match            100.0%;  Score 160;  DB 40;  Length 750;
  Best Local Similarity   100.0%;  Pred. No. 3e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db        254 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 283


RESULT 12
US-11-084-080-20
; Sequence 20, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-20

  Query Match            100.0%;  Score 160;  DB 40;  Length 750;
  Best Local Similarity   100.0%;  Pred. No. 3e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db        501 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 530


RESULT 13
US-11-084-080-22
; Sequence 22, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-22

  Query Match            100.0%;  Score 160;  DB 40;  Length 750;
  Best Local Similarity   100.0%;  Pred. No. 3e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db         23 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 52


RESULT 14
US-11-084-080-24
; Sequence 24, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
```

; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-24

Query Match 100.0%; Score 160; DB 40; Length 750;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
||||||||||||||||||||||||||||||
Db 270 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 299

RESULT 15
US-11-084-080-28
; Sequence 28, Application US/11084080
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-011
US-11-084-080-28

Query Match 100.0%; Score 160; DB 40; Length 759;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
||||||||||||||||||||||||||||||
Db 263 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 292

RESULT 16
US-11-084-080-32
; Sequence 32, Application US/11084080
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bougainvillea spectabilis
US-11-084-080-32

Query Match 51.9%; Score 83; DB 40; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTVSFNLGEAYEYP 15
|||||||||||||||
Db 1 YNTVSFNLGEAYEYP 15

RESULT 17
US-11-084-080-34
; Sequence 34, Application US/11084080
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bougainvillea spectabilis
US-11-084-080-34

Query Match 50.6%; Score 81; DB 40; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NLGEAYEYPTFIQDL 21
|||||||||||||||
Db 1 NLGEAYEYPTFIQDL 15

RESULT 18
US-11-084-080-35
; Sequence 35, Application US/11084080
; GENERAL INFORMATION:

```
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-35

  Query Match             50.6%;  Score 81;  DB 40;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0052;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 EAYEYPTFIQDLRNE 24
              |||||||||||||||
Db          1 EAYEYPTFIQDLRNE 15


RESULT 19
US-11-084-080-33
; Sequence 33, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-33

  Query Match             50.0%;  Score 80;  DB 40;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0071;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFI 18
              |||||||||||||||
Db          1 VSFNLGEAYEYPTFI 15


RESULT 20
US-11-084-080-36
; Sequence 36, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-36

  Query Match             48.8%;  Score 78;  DB 40;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 EYPTFIQDLRNELAK 27
              |||||||||||||||
Db          1 EYPTFIQDLRNELAK 15


RESULT 21
US-11-084-080-37
; Sequence 37, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-37

  Query Match             48.1%;  Score 77;  DB 40;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 TFIQDLRNELAKGTP 30
              |||||||||||||||
Db          1 TFIQDLRNELAKGTP 15
```

```
RESULT 22
US-11-084-080-38
; Sequence 38, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-38

  Query Match             38.8%;  Score 62;  DB 40;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 QDLRNELAKGTP 30
              ||||||||||||
Db          1 QDLRNELAKGTP 12


RESULT 23
US-09-791-537-94189
; Sequence 94189, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 94189
;   LENGTH: 569
;   TYPE: PRT
;   ORGANISM: Sambucus nigra
US-09-791-537-94189

  Query Match             38.8%;  Score 62;  DB 27;  Length 569;
  Best Local Similarity   48.4%;  Pred. No. 32;
  Matches   15;  Conservative    6;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGT 29
              | :||||| ||   ||  |:|:|| ::  |:
Db         34 YPSVSFNLTEANSNEYRHFLQELRGKVILGS 64


RESULT 24
US-09-791-537-21233
; Sequence 21233, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21233
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: pdb 1PAFA
US-09-791-537-21233

  Query Match             38.1%;  Score 61;  DB 27;  Length 262;
  Best Local Similarity   48.0%;  Pred. No. 24;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db          2 NTIIYNVGSTTISKYATFLNDLRNE 26


RESULT 25
US-09-791-537-63089
; Sequence 63089, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63089
;   LENGTH: 292
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-09-791-537-63089

  Query Match             38.1%;  Score 61;  DB 27;  Length 292;
  Best Local Similarity   48.0%;  Pred. No. 26;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db          3 NTIIYNVGSTTISKYATFLNDLRNE 27


RESULT 26
PCT-US02-02792-2
; Sequence 2, Application PC/TUS0202792
; GENERAL INFORMATION:
;  APPLICANT: RUTGERS, THE STATE UNIVERSITY
;  TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
;  FILE REFERENCE: OCIRS 3.4-076
;  CURRENT APPLICATION NUMBER: PCT/US02/02792
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: 60/266,396
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
PCT-US02-02792-2
```

```
  Query Match             38.1%;  Score 61;  DB 1;  Length 312;
  Best Local Similarity   48.0%;  Pred. No. 27;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 27
US-10-467-009-2
; Sequence 2, Application US/10467009
; GENERAL INFORMATION:
;  APPLICANT: RUTGERS, THE STATE UNIVERSITY
;  TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
;  FILE REFERENCE: OCIRS 3.4-076
;  CURRENT APPLICATION NUMBER: US/10/467,009
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: 60/266,396
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-10-467-009-2

  Query Match             38.1%;  Score 61;  DB 34;  Length 312;
  Best Local Similarity   48.0%;  Pred. No. 27;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 28
US-08-049-075-2
; Sequence 2, Application US/08049075
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Man-Keun
;    APPLICANT:  Lee, Kwan-Ho
;    APPLICANT:  Na, Byeong-Kook
;    APPLICANT:  Jeong, Han-Seung
;    APPLICANT:  Choi, Kyu-Whan
;    APPLICANT:  Moon, Young-Ho
;    APPLICANT:  Jeon, Hong-Seob
;    TITLE OF INVENTION:  Expression Vector for Phytolacca
;    TITLE OF INVENTION:  Antiviral Protein and Process for Preparing Transgenic
;    TITLE OF INVENTION:  Plant Transformed Thereof
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby
;      STREET:  805 Third Ave.
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/049,075
;      FILING DATE:  20-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, S. Peter
;      REGISTRATION NUMBER:  25,351
;      REFERENCE/DOCKET NUMBER:  0136/07986
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)527-7700
;      TELEFAX:  (212)753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  313 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Phytolacca americana
;      TISSUE TYPE:  leaf
US-08-049-075-2

  Query Match             38.1%;  Score 61;  DB 10;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 29
US-08-501-253-2
; Sequence 2, Application US/08501253
;  GENERAL INFORMATION:
;    APPLICANT:  Uckun, Fatih
;    APPLICANT:  Tumer, Nilgun
;    TITLE OF INVENTION:  Biotherapeutic Agents Comprising
;    TITLE OF INVENTION:  Recombinant PAp and PAP Mutants
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  90 South 7th Street, 3100 Norwest Center
;      CITY:  Minneapolis
;      STATE:  MM
;      COUNTRY:  US
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/501,253
;      FILING DATE:  11-JUL-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M.
;      REGISTRATION NUMBER:  33,924
;      REFERENCE/DOCKET NUMBER:  600.323US01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  313 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-501-253-2

  Query Match             38.1%;  Score 61;  DB 15;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48
```

```
RESULT 30
US-09-791-537-36414
; Sequence 36414, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36414
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-09-791-537-36414

  Query Match             38.1%;  Score 61;  DB 27;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 31
US-11-010-795-20
; Sequence 20, Application US/11010795
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  DI, RONG
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
;  TITLE OF INVENTION:  RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
;  FILE REFERENCE: OCIRS 3.0-085
;  CURRENT APPLICATION NUMBER: US/11/010,795
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: 60/529,348
;  PRIOR FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 20
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-11-010-795-20

  Query Match             38.1%;  Score 61;  DB 40;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 32
US-11-106-187-2
; Sequence 2, Application US/11106187
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  WANG, PINGER
;  TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
;  FILE REFERENCE: OCIRS 3.9-060 CONT
;  CURRENT APPLICATION NUMBER: US/11/106,187
;  CURRENT FILING DATE:  2005-04-14
;  PRIOR APPLICATION NUMBER: US/09/721,047
;  PRIOR FILING DATE: 2000-11-22
;  PRIOR APPLICATION NUMBER: PCT/US99/11301
;  PRIOR FILING DATE: 1999-05-21
;  PRIOR APPLICATION NUMBER: 60/086,374
;  PRIOR FILING DATE: 1998-05-22
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-11-106-187-2

  Query Match             38.1%;  Score 61;  DB 41;  Length 313;
  Best Local Similarity   48.0%;  Pred. No. 28;
  Matches   12;  Conservative    5;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: |||||
Db         24 NTIIYNVGSTTISKYATFLNDLRNE 48


RESULT 33
US-11-360-355-121143
; Sequence 121143, Application US/11360355
; GENERAL INFORMATION:
;  APPLICANT: Boukharov, Andrey
;  APPLICANT:  Du, Zijing
;  APPLICANT:  Guo, Liang
;  APPLICANT:  Kovalic, David
;  APPLICANT:  Lu, Maolong
;  APPLICANT:  McCarter, James
;  APPLICANT:  Miller, Nancy
;  APPLICANT:  Williams, Deryck
;  APPLICANT:  Vaudin, Mark
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
;  TITLE OF INVENTION:  IN PLANTS AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 38-21(53885)
;  CURRENT APPLICATION NUMBER: US/11/360,355
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 121143
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Heterodera glycines
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (439)..(439)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_47566; Strand=-; Position=1
;   OTHER INFORMATION: -190,943-1180,1244-1382,1432-1632,1712-1816,2371-2535,2682-2800,29
;   OTHER INFORMATION: -3066
;   FEATURE:
;   OTHER INFORMATION: Homolog annotation: Hit_ID=NP_497675.1; Match level="QueryCoverage
;   OTHER INFORMATION: =88%, HitCoverage=87%, E-value=2e-94, Identity=48%"; Hit descripti
;   OTHER INFORMATION: =nadh dehydrogenase (48.3 kD) (3E332) [Caenorhabditis elegans]
;   OTHER INFORMATION: gb|AAF59528.2| Hypothetical protein Y53G8AL
;   FEATURE:
;   OTHER INFORMATION: Essential gene: C elegans homolog=Y53G8AL.2; Phenotype=Emb,Lva
US-11-360-355-121143

  Query Match             37.2%;  Score 59.5;  DB 43;  Length 449;
  Best Local Similarity   42.9%;  Pred. No. 58;
  Matches   12;  Conservative    4;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          2 NTVSFNLGEA-YEYPTFIQDLRNELAKG 28
              |  :|| ||  |: | |: |  |: | |
Db        255 NVYTFNAGEGIYKMPLFVNDFVNDFADG 282


RESULT 34
US-60-655-875-121143
; Sequence 121143, Application US/60655875
```

```
; GENERAL INFORMATION:
;  APPLICANT: Boukharov, Andrey
;  APPLICANT:  Du, Zijing
;  APPLICANT:  Guo, Liang
;  APPLICANT:  Kovalic, David
;  APPLICANT:  Lu, Maolong
;  APPLICANT:  McCarter, James
;  APPLICANT:  Miller, Nancy
;  APPLICANT:  Williams, Deryck
;  APPLICANT:  Vaudin, Mark
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
;  TITLE OF INVENTION:  IN PLANTS AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 38-21(53885)
;  CURRENT APPLICATION NUMBER: US/60/655,875
;  CURRENT FILING DATE:  2005-02-24
;  NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 121143
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Heterodera glycines
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (439)..(439)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_47566; Strand=-; Position=1
;   OTHER INFORMATION: -190,943-1180,1244-1382,1432-1632,1712-1816,2371-2535,2682-2800,2
;   OTHER INFORMATION: -3066
;   FEATURE:
;   OTHER INFORMATION: Homolog annotation: Hit_ID=NP_497675.1; Match level="QueryCoverag
;   OTHER INFORMATION: =88%, HitCoverage=87%, E-value=2e-94, Identity=48%"; Hit descript
;   OTHER INFORMATION: =nadh dehydrogenase (48.3 kD) (3E332) [Caenorhabditis elegans]
;   OTHER INFORMATION: gb|AAF59528.2| Hypothetical protein Y53G8AL
;   FEATURE:
;   OTHER INFORMATION: Essential gene: C elegans homolog=Y53G8AL.2; Phenotype=Emb,Lva
US-60-655-875-121143

  Query Match             37.2%;  Score 59.5;  DB 51;  Length 449;
  Best Local Similarity   42.9%;  Pred. No. 58;
  Matches   12;  Conservative    4;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          2 NTVSFNLGEA-YEYPTFIQDLRNELAKG 28
              |  :|| ||  |: | |: |  |: | |
Db        255 NVYTFNAGEGIYKMPLFVNDFVNDFADG 282


RESULT 35
US-10-424-599-213759
; Sequence 213759, Application US/10424599
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 213759
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_3504C.1.pep
US-10-424-599-213759

  Query Match             36.9%;  Score 59;  DB 34;  Length 107;
  Best Local Similarity   43.6%;  Pred. No. 22;
  Matches   17;  Conservative    2;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| |||   ||          | |||  |
Db         36 TVNFN-GETFESPTFCSTLRQAEHAAAGVALNTLAKRGP 73


RESULT 36
US-07-787-567A-9
; Sequence 9, Application US/07787567A
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/787,567A
;      FILING DATE:  19911104
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gruber, Lewis S.
;      REGISTRATION NUMBER:  30,060
;      REFERENCE/DOCKET NUMBER:  27129/30545
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-787-567A-9

  Query Match             36.9%;  Score 59;  DB 7;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 44;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 37
US-09-791-537-3998
; Sequence 3998, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3998
```

```
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-09-791-537-3998

  Query Match             36.9%;  Score 59;  DB 27;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 44;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 38
US-10-127-890-9
; Sequence 9, Application US/10127890
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 261 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-127-890-9

  Query Match             36.9%;  Score 59;  DB 31;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 44;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 39
US-10-613-755-9
; Sequence 9, Application US/10613755
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/613,755
;             FILING DATE: 02-Jul-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 261 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-613-755-9

  Query Match             36.9%;  Score 59;  DB 36;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 44;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 40
US-10-717-243-9
```

```
; Sequence 9, Application US/10717243
;  GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 169
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/717,243
;            FILING DATE: 18-Nov-2003
;            CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/839,765
;            FILING DATE: 15-APR-1997
;            APPLICATION NUMBER: US 08/425,336
;            FILING DATE: 18-APR-1995
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;  INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 261 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-717-243-9

  Query Match             36.9%;  Score 59;  DB 37;  Length 261;
  Best Local Similarity   48.0%;  Pred. No. 44;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: ||||
Db          2 NTITFDAGNATINKYATFMESLRNE 26


RESULT 41
US-10-417-884-7302
; Sequence 7302, Application US/10417884
;  GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/417,884
;            FILING DATE: 17-Apr-2003
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;  INFORMATION FOR SEQ ID NO: 7302:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 225 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: YES
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...225
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7302:
US-10-417-884-7302

  Query Match             35.9%;  Score 57.5;  DB 34;  Length 225;
  Best Local Similarity   31.4%;  Pred. No. 62;
  Matches   11;  Conservative   11;  Mismatches    8;  Indels    5;  Gaps    1;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA-----KGTP 30
              ::  | :||| |::  |::|  :|::     :|||
Db         38 FSKTSMDLGERYDFKGFMEDKMDEVSSREIPEGTP 72


RESULT 42
US-10-417-884A-7302
; Sequence 7302, Application US/10417884A
;  GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/417,884A
```

```
;            FILING DATE: 17-Apr-2003
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532
;            FILING DATE: 30-Jun-1998
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 7302:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 225 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: YES
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...225
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7302:
US-10-417-884A-7302

  Query Match             35.9%;  Score 57.5;  DB 34;  Length 225;
  Best Local Similarity   31.4%;  Pred. No. 62;
  Matches   11;  Conservative   11;  Mismatches    8;  Indels    5;  Gaps    1;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA-----KGTP 30
              ::  | :||| |::  |::|  :|::     :|||
Db         38 FSKTSMDLGERYDFKGFMEDKMDEVSSREIPEGTP 72


RESULT 43
US-10-437-963-146447
; Sequence 146447, Application US/10437963
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146447
;   LENGTH: 324
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_47070C.1.pep
US-10-437-963-146447

  Query Match             35.6%;  Score 57;  DB 34;  Length 324;
  Best Local Similarity   41.0%;  Pred. No. 97;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GETFESPAFCSTLRLAEHAAAEVALNELSKRGP 73


RESULT 44
US-10-767-701-37927
; Sequence 37927, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 37927
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-C41259_1.pep
US-10-767-701-37927

  Query Match             35.0%;  Score 56;  DB 37;  Length 77;
  Best Local Similarity   41.0%;  Pred. No. 43;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPAFCSTLRQAEHAAAEVALNELSKRGP 73


RESULT 45
US-10-425-115-351081
; Sequence 351081, Application US/10425115
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351081
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83354C.1.pep
US-10-425-115-351081

  Query Match             35.0%;  Score 56;  DB 34;  Length 120;
  Best Local Similarity   41.0%;  Pred. No. 60;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPVFCSTLRQAEHAAAEVALNELSKRGP 73


RESULT 46
US-09-978-274A-6
; Sequence 6, Application US/09978274A
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
```

```
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 154
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-09-978-274A-6

  Query Match             35.0%;  Score 56;  DB 29;  Length 154;
  Best Local Similarity   44.0%;  Pred. No. 74;
  Matches   11;  Conservative    7;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: |||:
Db          3 NTITFDAGNATINKYATFMESLRNQ 27


RESULT 47
US-10-425-115-351080
; Sequence 351080, Application US/10425115
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351080
;   LENGTH: 160
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83353C.1.pep
US-10-425-115-351080

  Query Match             35.0%;  Score 56;  DB 34;  Length 160;
  Best Local Similarity   41.0%;  Pred. No. 76;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR-----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPVFCSTLRQAEHAAAEVALNELSKRGP 73


RESULT 48
US-09-978-274A-4
; Sequence 4, Application US/09978274A
; GENERAL INFORMATION:
;  APPLICANT: Thomas, Christopher
;  APPLICANT:  McPherson, Michael
;  APPLICANT:  Atkinson, Howard
;  APPLICANT:  Neelam, Anil
;  TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
;  FILE REFERENCE: 9341-028
;  CURRENT APPLICATION NUMBER: US/09/978,274A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 0025225.4
;  PRIOR FILING DATE: 2000-10-14
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 263
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
US-09-978-274A-4

  Query Match             35.0%;  Score 56;  DB 29;  Length 263;
  Best Local Similarity   44.0%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    7;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: |||:
Db          3 NTITFDAGNATINKYATFMESLRNQ 27


RESULT 49
US-10-219-999-61450
; Sequence 61450, Application US/10219999
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Edgerton, Michael D
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  Stein, Joshua
;  TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-10(52726)C
;  CURRENT APPLICATION NUMBER: US/10/219,999
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: US 60/324,109
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: US 60/312,544
;  PRIOR FILING DATE: 2001-08-15
;  NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 61450
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Zea mays
US-10-219-999-61450

  Query Match             35.0%;  Score 56;  DB 32;  Length 289;
  Best Local Similarity   41.0%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR-----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPVFCSTLRQAEHAAAEVALNELSKRGP 73


RESULT 50
US-10-425-115-351084
; Sequence 351084, Application US/10425115
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351084
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_83357C.1.pep
US-10-425-115-351084

  Query Match             35.0%;  Score 56;  DB 34;  Length 289;
  Best Local Similarity   41.0%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR-----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPVFCSTLRQAEHAAAEVALNELSKRGP 73
```

```
RESULT 51
US-60-324-109-29945
; Sequence 29945, Application US/60324109
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Edgerton, Michael D
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  Stein, Joshua
;  TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-10(52726)B
;  CURRENT APPLICATION NUMBER: US/60/324,109
;  CURRENT FILING DATE:  2001-09-21
;  NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 29945
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
US-60-324-109-29945

  Query Match             35.0%;  Score 56;  DB 48;  Length 289;
  Best Local Similarity   41.0%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    3;  Mismatches    8;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| || :| | |   ||           |||:|  |
Db         36 TVNFN-GEMFESPVFCSTLRQAEHAAAEVALNELSKRGP 73


RESULT 52
US-08-715-074A-2
; Sequence 2, Application US/08715074A
;  GENERAL INFORMATION:
;    APPLICANT:  MOON, YOUNG-HO
;    APPLICANT:  CHOI, JIN-NAM
;    APPLICANT:  YUN, YOUNG-CHAE
;    APPLICANT:  JIN, JUNG-HUN
;    APPLICANT:  HONG, EUN-JU
;    APPLICANT:  LEE, JEONG-HO
;    APPLICANT:  CHOI, KYU-WHAN
;    APPLICANT:  LEE, JONG-SEOB
;    APPLICANT:  SONG, SANG-KEE
;    APPLICANT:  CHOI, YANG-DO ET AL.
;    TITLE OF INVENTION:  NOVEL GENES ENCODING ANTIVIRAL
;    TITLE OF INVENTION:  PROTEINS OF PHYTOLACCA...
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby, P.C.
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/715,074A
;      FILING DATE:  19-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  96-17404
;      FILING DATE:  22-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LUDWIG  S., PETER
;      REGISTRATION NUMBER:  25,351
;      REFERENCE/DOCKET NUMBER:  0136/0C430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  292 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-715-074A-2

  Query Match             35.0%;  Score 56;  DB 17;  Length 292;
  Best Local Similarity   44.0%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    6;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|     :| ||: :||||
Db          3 NTIIYNVGSTTISKYATFLDNLRNE 27


RESULT 53
PCT-US02-15033A-16
; Sequence 16, Application PC/TUS0215033A
; GENERAL INFORMATION:
;  APPLICANT: E. I. du Pont de Nemours & Company
;  APPLICANT:  Bramucci, Michael G
;  APPLICANT:  Brzostowicz, Patricia C.
;  APPLICANT:  Cheng, Qiong
;  APPLICANT:  Kostichka, Kristy N.
;  APPLICANT:  Nagarajan, Vasantha
;  APPLICANT:  Rouviere, Pierre E.
;  APPLICANT:  Tao, Luan
;  APPLICANT:  Thomas, Stuart M.
;  TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production
;  FILE REFERENCE: CL1788 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/15033A
;  CURRENT FILING DATE:  2002-04-24
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Rhodococcus erythropolis
PCT-US02-15033A-16

  Query Match             35.0%;  Score 56;  DB 1;  Length 314;
  Best Local Similarity   45.5%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKG 28
              |||||::   ||:|:  :| :|
Db        174 NLGEAFQLTNFIRDVGEDLDRG 195


RESULT 54
US-09-791-537-91800
; Sequence 91800, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBEF
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91800
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Phytolacca americana
```

US-09-791-537-91800

Query Match 35.0%; Score 56; DB 27; Length 314;
Best Local Similarity 44.0%; Pred. No. 1.3e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

```
Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: |||:
Db         26 NTITFDAGNATINKYATFMESLRNQ 50
```

RESULT 55
US-09-978-274A-2
; Sequence 2, Application US/09978274A
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Phytolacca americana
US-09-978-274A-2

Query Match 35.0%; Score 56; DB 29; Length 314;
Best Local Similarity 44.0%; Pred. No. 1.3e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

```
Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||::|: | |   :| ||:: |||:
Db         26 NTITFDAGNATINKYATFMESLRNQ 50
```

RESULT 56
US-10-703-032-113730
; Sequence 113730, Application US/10703032
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Cao, Yongwei
; APPLICANT: Masucci, James D.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53374)B
; CURRENT APPLICATION NUMBER: US/10/703,032
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 10/020,338
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 211164
; SEQ ID NO 113730
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_TA_8148.pep
US-10-703-032-113730

Query Match 34.4%; Score 55; DB 37; Length 280;
Best Local Similarity 41.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 4; Mismatches 7; Indels 12; Gaps 2;

```
Qy          3 TVSFNLGEAYEYPTFIQDLR----------NELAKGTP 30
              ||:|| ||::| | |   ||          |||:|  |
Db         25 TVTFN-GESFESPGFYPTLRQAEHAAAEVALNELSKRGP 62
```

RESULT 57
US-10-424-599-274703
; Sequence 274703, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274703
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90078C.1.pep
US-10-424-599-274703

Query Match 34.1%; Score 54.5; DB 34; Length 292;
Best Local Similarity 38.7%; Pred. No. 1.9e+02;
Matches 12; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

```
Qy          1 YNTVSFNL-GEAYEYPTFIQDLRNELAKGTP 30
              |  : ||  || ::|| |   :|: :|  ||
Db         22 YTFLEFNTQGEDFDYPEFRDPIRSPVAWPTP 52
```

RESULT 58
US-11-311-940-8052
; Sequence 8052, Application US/11311940
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al
; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
; FILE REFERENCE: 38-21(53720)
; CURRENT APPLICATION NUMBER: US/11/311,940
; CURRENT FILING DATE: 2005-12-19
; NUMBER OF SEQ ID NOS: 10032
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8052
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Magnetospirillum magnetotacticum MS-1
US-11-311-940-8052

Query Match 34.1%; Score 54.5; DB 43; Length 608;
Best Local Similarity 60.9%; Pred. No. 3.5e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 5; Gaps 2;

```
Qy          3 TVSFNLGEAYEYPTFIQDLRNEL 25
              |||:| || | ||    ||| ||
Db         66 TVSYN-GEIYNYP----DLRREL 83
```

RESULT 59
US-11-311-940A-8052
; Sequence 8052, Application US/11311940A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al
; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
; FILE REFERENCE: 38-21(53720)
; CURRENT APPLICATION NUMBER: US/11/311,940A
; CURRENT FILING DATE: 2005-12-19
; NUMBER OF SEQ ID NOS: 10032
; SOFTWARE: PatentIn version 3.3

```
; SEQ ID NO 8052
;   LENGTH: 608
;   TYPE: PRT
;   ORGANISM: Magnetospirillum magnetotacticum MS-1
US-11-311-940A-8052

  Query Match             34.1%;  Score 54.5;  DB 43;  Length 608;
  Best Local Similarity   60.9%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    5;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL 25
              |||:| || | ||    ||| ||
Db         66 TVSYN-GEIYNYP----DLRREL 83


RESULT 60
US-60-581-351-12408
; Sequence 12408, Application US/60581351
; GENERAL INFORMATION:
;  APPLICANT: Laurie, Cathy C
;  TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
;  FILE REFERENCE: 38-21(53372)B
;  CURRENT APPLICATION NUMBER: US/60/581,351
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: US 60/479,962
;  PRIOR FILING DATE: 2003-06-19
;  NUMBER OF SEQ ID NOS: 13980
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12408
;   LENGTH: 608
;   TYPE: PRT
;   ORGANISM: Magnetospirillum magnetotacticum
US-60-581-351-12408

  Query Match             34.1%;  Score 54.5;  DB 50;  Length 608;
  Best Local Similarity   60.9%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    5;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL 25
              |||:| || | ||    ||| ||
Db         66 TVSYN-GEIYNYP----DLRREL 83


RESULT 61
US-60-638-099-45698
; Sequence 45698, Application US/60638099
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  TITLE OF INVENTION: Transgenic Plants with Enhanced Agronomic Phenotypes
;  FILE REFERENCE: 38-21(53720)
;  CURRENT APPLICATION NUMBER: US/60/638,099
;  CURRENT FILING DATE:  2004-12-21
;  NUMBER OF SEQ ID NOS: 48056
; SEQ ID NO 45698
;   LENGTH: 608
;   TYPE: PRT
;   ORGANISM: Magnetospirillum magnetotacticum
US-60-638-099-45698

  Query Match             34.1%;  Score 54.5;  DB 51;  Length 608;
  Best Local Similarity   60.9%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    5;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL 25
              |||:| || | ||    ||| ||
Db         66 TVSYN-GEIYNYP----DLRREL 83


RESULT 62
US-60-752-355-50174
; Sequence 50174, Application US/60752355
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(53720)B
;  CURRENT APPLICATION NUMBER: US/60/752,355
;  CURRENT FILING DATE:  2005-12-21
;  NUMBER OF SEQ ID NOS: 52803
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50174
;   LENGTH: 608
;   TYPE: PRT
;   ORGANISM: Magnetospirillum magnetotacticum MS-1
US-60-752-355-50174

  Query Match             34.1%;  Score 54.5;  DB 52;  Length 608;
  Best Local Similarity   60.9%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    5;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL 25
              |||:| || | ||    ||| ||
Db         66 TVSYN-GEIYNYP----DLRREL 83


RESULT 63
US-08-378-761-28
; Sequence 28, Application US/08378761
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  THOMAS D. ZINDRICK
;      STREET:  9002 PURDUE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268-1189
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/987927
;      FILING DATE:  09-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ZINDRICK, THOMAS D
;      REGISTRATION NUMBER:  32185
;      REFERENCE/DOCKET NUMBER:  38272A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (517) 636-1869
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-761-28

  Query Match             33.8%;  Score 54;  DB 13;  Length 29;
  Best Local Similarity   44.0%;  Pred. No. 36;
  Matches   11;  Conservative    5;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNE 24
              ||: :|:|      | ||: :||||
Db          2 NTIIYNVGSTTISNYATFMDNLRNE 26
```

```
RESULT 64
US-10-767-795-77750
; Sequence 77750, Application US/10767795
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Zhou, Yihua
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53534)B
;  CURRENT APPLICATION NUMBER: US/10/767,795
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 77750
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(237)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C81314_2.pep
US-10-767-795-77750

  Query Match             33.8%;  Score 54;  DB 37;  Length 237;
  Best Local Similarity   41.0%;  Pred. No. 1.9e+02;
  Matches   16;  Conservative    2;  Mismatches    9;  Indels   12;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLR-----------NELAKGTP 30
              ||:|| || :| |||    ||           | ||   |
Db         36 TVNFN-GETFESPTFCSTLRQAEHAAAEVALNTLANRGP 73


RESULT 65
US-10-424-599-215698
; Sequence 215698, Application US/10424599
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215698
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(447)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_36803C.1.pep
US-10-424-599-215698

  Query Match             33.8%;  Score 54;  DB 34;  Length 447;
  Best Local Similarity   50.0%;  Pred. No. 3.2e+02;
  Matches   11;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNEL 25
              |  |  |  | | |:||:||:|
Db        210 VVMNFFEELEPPLFVQDMRNKL 231


RESULT 66
US-09-791-537-78226
; Sequence 78226, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 78226
;   LENGTH: 563
;   TYPE: PRT
;   ORGANISM: Sambucus nigra
US-09-791-537-78226

  Query Match             33.8%;  Score 54;  DB 27;  Length 563;
  Best Local Similarity   45.2%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 YNTVSFNLGEAYE--YPTFIQDLRNELAKGT 29
              | :|||||  |    |  |:::||  :| ||
Db         28 YPSVSFNLAGAKSATYRDFLKNLRTIVATGT 58


RESULT 67
US-09-791-537-79846
; Sequence 79846, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79846
;   LENGTH: 563
;   TYPE: PRT
;   ORGANISM: Sambucus nigra
US-09-791-537-79846

  Query Match             33.8%;  Score 54;  DB 27;  Length 563;
  Best Local Similarity   41.9%;  Pred. No. 3.8e+02;
  Matches   13;  Conservative    6;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 YNTVSFNL--GEAYEYPTFIQDLRNELAKGT 29
              | :|||||   ::  |  |: :||  :| ||
Db         28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGT 58


RESULT 68
US-11-241-607-52631
; GENERAL INFORMATION:
;  APPLICANT: Makarov, Vladimir
;  APPLICANT:  Brover, Vyacheslav
;  APPLICANT:  Feldmann, Kenneth
;  APPLICANT:  Swaller, Timothy
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  FILE REFERENCE: 2750-1609PUS2
;  CURRENT APPLICATION NUMBER: US/11/241,607
;  CURRENT FILING DATE:  2005-09-30
;  PRIOR APPLICATION NUMBER: US 60/615,270
;  PRIOR FILING DATE: 2004-09-30
;  PRIOR APPLICATION NUMBER: US 60/635,140
;  PRIOR FILING DATE: 2004-12-08
;  PRIOR APPLICATION NUMBER: US 60/637,104
;  PRIOR FILING DATE: 2004-12-16
```

```
;  PRIOR APPLICATION NUMBER: US 60/638,820
;  PRIOR FILING DATE: 2004-12-22
;  PRIOR APPLICATION NUMBER: US 60/637,210
;  PRIOR FILING DATE: 2004-12-16
;  PRIOR APPLICATION NUMBER: US 60/615,055
;  PRIOR FILING DATE: 2004-09-30
;  PRIOR APPLICATION NUMBER: US 60/614,271
;  PRIOR FILING DATE: 2004-09-30
;  PRIOR APPLICATION NUMBER: US 60/614,332
;  PRIOR FILING DATE: 2004-09-30
;  PRIOR APPLICATION NUMBER: US 60/627,206
;  PRIOR FILING DATE: 2004-11-12
;  PRIOR APPLICATION NUMBER: US 60/615,080
;  PRIOR FILING DATE: 2004-09-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 66429
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 26451075; NR Description:  RGA1 [Arabidopsis thaliana]
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 37624736; NR Description: gibberellic acid insensitive
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 20334379; NR Description: GAI protein 1 [Vitis vinifer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 60656561; NR Description: DELLA protein [Brassica rapa
US-11-241-607-52631

  Query Match             33.1%;  Score 53;  DB 42;  Length 470;
  Best Local Similarity   40.0%;  Pred. No. 4.5e+02;
  Matches    8;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 NTVSFNLGEAYEYPTFIQDL 21
              : : |||||  ::|: : ||
Db        211 HVIDFNLGEGVQWPSLMSDL 230


RESULT 69
US-60-147-189-955
; Sequence 955, Application US/60147189
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
;  TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL000072
;  CURRENT APPLICATION NUMBER: US/60/147,189
;  CURRENT FILING DATE: 1999-08-08
;  NUMBER OF SEQ ID NOS: 1115
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 955
;   LENGTH: 857
;   TYPE: PRT
;   ORGANISM: Drosophila
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(857)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-60-147-189-955

  Query Match             33.1%;  Score 53;  DB 46;  Length 857;
  Best Local Similarity   43.5%;  Pred. No. 7.2e+02;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKGT 29
              :|| ||:| : :   ||  :|||
Db        133 SLGMAYDYDSIMHYARNTFSKGT 155


RESULT 70
US-60-167-217-15106
; Sequence 15106, Application US/60167217
; GENERAL INFORMATION:
;  APPLICANT: Li, Peter W. D.
;  TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLEUCLES ENCODING DROSOPHILA PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL000152
;  CURRENT APPLICATION NUMBER: US/60/167,217
;  CURRENT FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 23195
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15106
;   LENGTH: 1309
;   TYPE: PRT
;   ORGANISM: Drosophila
US-60-167-217-15106

  Query Match             33.1%;  Score 53;  DB 46;  Length 1309;
  Best Local Similarity   43.5%;  Pred. No. 1e+03;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKGT 29
              :|| ||:| : :   ||  :|||
Db        505 SLGMAYDYDSIMHYARNTFSKGT 527


RESULT 71
US-60-173-464-12311
; Sequence 12311, Application US/60173464
; GENERAL INFORMATION:
;  APPLICANT: Li, Peter W.D.
;  TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL000173
;  CURRENT APPLICATION NUMBER: US/60/173,464
;  CURRENT FILING DATE: 1999-12-29
;  NUMBER OF SEQ ID NOS: 30269
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12311
;   LENGTH: 1309
;   TYPE: PRT
;   ORGANISM: Drosophila
US-60-173-464-12311

  Query Match             33.1%;  Score 53;  DB 46;  Length 1309;
  Best Local Similarity   43.5%;  Pred. No. 1e+03;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKGT 29
              :|| ||:| : :   ||  :|||
Db        505 SLGMAYDYDSIMHYARNTFSKGT 527


RESULT 72
US-09-614-150-40125
; Sequence 40125, Application US/09614150
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/09/614,150
;  CURRENT FILING DATE:  2000-07-11
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
```

```
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40125
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: DROSOPHILA
US-09-614-150-40125

  Query Match             33.1%;  Score 53;  DB 26;  Length 1464;
  Best Local Similarity   43.5%;  Pred. No. 1.1e+03;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKGT 29
              :|| ||:| : :   ||  :|||
Db        660 SLGMAYDYDSIMHYARNTFSKGT 682


RESULT 73
US-09-614-150A-40125
; Sequence 40125, Application US/09614150A
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/09/614,150A
;  CURRENT FILING DATE:  2000-07-11
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40125
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: DROSOPHILA
US-09-614-150A-40125

  Query Match             33.1%;  Score 53;  DB 26;  Length 1464;
  Best Local Similarity   43.5%;  Pred. No. 1.1e+03;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKGT 29
              :|| ||:| : :   ||  :|||
Db        660 SLGMAYDYDSIMHYARNTFSKGT 682


RESULT 74
US-09-791-537-8878
; Sequence 8878, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8878
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-791-537-8878

  Query Match             33.1%;  Score 53;  DB 27;  Length 1464;
  Best Local Similarity   43.5%;  Pred. No. 1.1e+03;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKGT 29
              :|| ||:| : :   ||  :|||
Db        660 SLGMAYDYDSIMHYARNTFSKGT 682


RESULT 75
US-09-791-537-119059
; Sequence 119059, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 119059
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-791-537-119059

  Query Match             33.1%;  Score 53;  DB 27;  Length 1464;
  Best Local Similarity   43.5%;  Pred. No. 1.1e+03;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKGT 29
              :|| ||:| : :   ||  :|||
Db        660 SLGMAYDYDSIMHYARNTFSKGT 682


RESULT 76
US-09-791-537-146213
; Sequence 146213, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
```

; SEQ ID NO 146213
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-791-537-146213

Query Match 33.1%; Score 53; DB 27; Length 1464;
Best Local Similarity 43.5%; Pred. No. 1.1e+03;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 7 NLGEAYEYPTFIQDLRNELAKGT 29
:|| ||:| : : || :|||
Db 660 SLGMAYDYDSIMHYARNTFSKGT 682

RESULT 77
US-11-097-143-40125
; Sequence 40125, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40125
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-40125

Query Match 33.1%; Score 53; DB 40; Length 1464;
Best Local Similarity 43.5%; Pred. No. 1.1e+03;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 7 NLGEAYEYPTFIQDLRNELAKGT 29
:|| ||:| : : || :|||
Db 660 SLGMAYDYDSIMHYARNTFSKGT 682

RESULT 78
US-60-191-637-39757
; Sequence 39757, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 42660
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 39757
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-191-637-39757

Query Match 33.1%; Score 53; DB 46; Length 1464;
Best Local Similarity 43.5%; Pred. No. 1.1e+03;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 7 NLGEAYEYPTFIQDLRNELAKGT 29
:|| ||:| : : || :|||
Db 660 SLGMAYDYDSIMHYARNTFSKGT 682

RESULT 79
US-60-191-681-30787
; Sequence 30787, Application US/60191681
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
; TITLE OF INVENTION: USES THEREOF.
; FILE REFERENCE: cl000390
; CURRENT APPLICATION NUMBER: US/60/191,681
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 30973
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30787
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-191-681-30787

Query Match 33.1%; Score 53; DB 46; Length 1464;
Best Local Similarity 43.5%; Pred. No. 1.1e+03;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 7 NLGEAYEYPTFIQDLRNELAKGT 29
:|| ||:| : : || :|||
Db 660 SLGMAYDYDSIMHYARNTFSKGT 682

RESULT 80
US-09-791-537-1700
; Sequence 1700, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1700
; LENGTH: 67
; TYPE: PRT
; ORGANISM: coliphage T4
US-09-791-537-1700

Query Match 32.5%; Score 52; DB 27; Length 67;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 9; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 6 FNLGEAYEYPTFIQDLRNELAKGT 29
|::||| |: | :|:|::: |
Db 26 FDMGEAEEFKTRFKDIRDKIQSDT 49

RESULT 81

```
US-09-791-537-14085
; Sequence 14085, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14085
;   LENGTH: 376
;   TYPE: PRT
;   ORGANISM: Piromyces rhizinflata
US-09-791-537-14085

  Query Match             32.5%;  Score 52;  DB 27;  Length 376;
  Best Local Similarity   38.5%;  Pred. No. 5.1e+02;
  Matches   10;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTP 30
              :| | | |  | ||::: : : | ||
Db         50 NFFLNEIYANPKFIEEVEDSIEKLTP 75


RESULT 82
US-11-031-175-10583
; Sequence 10583, Application US/11031175
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/11/031,175
;  CURRENT FILING DATE:  2005-01-08
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10583
;   LENGTH: 459
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-11-031-175-10583

  Query Match             32.5%;  Score 52;  DB 40;  Length 459;
  Best Local Similarity   47.6%;  Pred. No. 6e+02;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          8 LGEAYEYPTFIQDLRNELAKG 28
              | | ||:|  :::||| | :|
Db        336 LFEGYEWPGNVRELRNVLERG 356


RESULT 83
US-11-031-175-16037
; Sequence 16037, Application US/11031175
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/11/031,175
;  CURRENT FILING DATE:  2005-01-08
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16037
;   LENGTH: 238
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-11-031-175-16037

  Query Match             32.2%;  Score 51.5;  DB 40;  Length 238;
  Best Local Similarity   43.8%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    4;  Mismatches   11;  Indels    3;  Gaps    2;

Qy          1 YNTV--SFNLGEAYEYPTFIQDLRNELAKGTP 30
                | |:  ||  ||    || ::|:|  || | |
Db         60 YKTLGGSFT-GELVVDPTHLRDMRRRLAAGEP 90


RESULT 84
US-10-449-902-44047
; Sequence 44047, Application US/10449902
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44047
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-44047

  Query Match             32.2%;  Score 51.5;  DB 34;  Length 386;
  Best Local Similarity   40.7%;  Pred. No. 6.1e+02;
  Matches   11;  Conservative    5;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTFIQDLRNELAK---GTP 30
              || :|  ||  ::||  :|:|   | |
Db        189 NLNQAMSYPPLMEDLGRQLSKKCGGLP 215


RESULT 85
US-10-449-902-45250
; Sequence 45250, Application US/10449902
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45250
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-45250

  Query Match             32.2%;  Score 51.5;  DB 34;  Length 386;
```

```
  Best Local Similarity   40.7%;  Pred. No. 6.1e+02;
  Matches   11;  Conservative    5;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTFIQDLRNELAK---GTP 30
              || :|  ||  ::||  :|:|    | |
Db        189 NLNQAMSYPPLMEDLGRQLSKKCGGLP 215


RESULT 86
US-10-437-963-136583
; Sequence 136583, Application US/10437963
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 136583
;   LENGTH: 757
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_38148C.1.pep
US-10-437-963-136583

  Query Match             32.2%;  Score 51.5;  DB 34;  Length 757;
  Best Local Similarity   40.7%;  Pred. No. 1e+03;
  Matches   11;  Conservative    5;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTFIQDLRNELAK---GTP 30
              || :|  ||  ::||  :|:|    | |
Db        272 NLNQAMSYPPLMEDLGRQLSKKCGGLP 298


RESULT 87
US-08-141-891-1
; Sequence 1, Application US/08141891
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    APPLICANT:  Gawlak, Susan L.
;    APPLICANT:  Marquardt, Hans
;    TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;    TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONIA DIOICA
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/141,891
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-728-4800
;      TELEFAX:  206-727-3601
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
;      TISSUE TYPE:  Root
US-08-141-891-1

  Query Match             31.9%;  Score 51;  DB 11;  Length 32;
  Best Local Similarity   58.8%;  Pred. No. 99;
  Matches   10;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         14 YPTFIQDLRNELAKGTP 30
              | |||::||  |  |||
Db         15 YKTFIRNLRTTLTVGTP 31


RESULT 88
US-10-767-701-50462
; Sequence 50462, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 50462
;   LENGTH: 148
;   TYPE: PRT
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3480-009-P1-K1-F12.pep
US-10-767-701-50462

  Query Match             31.9%;  Score 51;  DB 37;  Length 148;
  Best Local Similarity   40.0%;  Pred. No. 3.3e+02;
  Matches    8;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 NTVSFNLGEAYEYPTFIQDL 21
              : | ||||:  ::|: : ||
Db          4 HVVDFNLGDGIQWPSLMSDL 23


RESULT 89
US-09-791-537-782
; Sequence 782, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBEI
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 782
;   LENGTH: 334
;   TYPE: PRT
```

```
;   ORGANISM: Chlamydia muridarum
US-09-791-537-782

  Query Match             31.9%;  Score 51;  DB 27;  Length 334;
  Best Local Similarity   40.7%;  Pred. No. 6.3e+02;
  Matches   11;  Conservative    5;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          3 TVSFNLGEAYEYPTFIQDLRNELAKGT 29
              |::|     |:||   : | ||: |||
Db        153 TIAF----LYQYPDKFEALLNEIIKGT 175


RESULT 90
US-09-791-537-5912
; Sequence 5912, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5912
;   LENGTH: 545
;   TYPE: PRT
;   ORGANISM: Cinnamomum camphora
US-09-791-537-5912

  Query Match             31.9%;  Score 51;  DB 27;  Length 545;
  Best Local Similarity   43.3%;  Pred. No. 9.3e+02;
  Matches   13;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 YNTVSFNLGEAYE--YPTFIQDLRNELAKG 28
              | ||:|   :| :  |  ||: || :|| |
Db          1 YQTVTFTTKKATKTSYTQFIEALRAQLASG 30


RESULT 91
US-10-434-665-4971
; Sequence 4971, Application US/10434665
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: PATH03-09
;  CURRENT APPLICATION NUMBER: US/10/434,665
;  CURRENT FILING DATE:  2003-05-14
;  PRIOR APPLICATION NUMBER: US 09/134,000
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4971
;   LENGTH: 1233
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-10-434-665-4971

  Query Match             31.9%;  Score 51;  DB 34;  Length 1233;
  Best Local Similarity   38.5%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |   |   :  |:::
Db        904 YNTVSANAGQIYTETTIDSETLNQMS 929


RESULT 92
US-10-912-362-404
; Sequence 404, Application US/10912362
;   GENERAL INFORMATION:
;        APPLICANT: Choi et al.
;        TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;        NUMBER OF SEQUENCES: 497
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 14200 Shady Grove Road
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: Dell Latitude
;             OPERATING SYSTEM: Windows 2000
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/912,362
;             FILING DATE: 06-Aug-2004
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 10/206,576
;             FILING DATE: 2002-07-29
;             APPLICATION NUMBER: US 09/071,035
;             FILING DATE: 1998-05-04
;             APPLICATION NUMBER: US 60/046,655
;             FILING DATE: 1997-05-16
;             APPLICATION NUMBER: US 60/044,031
;             FILING DATE: 1997-05-06
;             APPLICATION NUMBER: US 60/066,009
;             FILING DATE: 1997-11-14
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hyman, Mark J.
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB369P1D2
;   INFORMATION FOR SEQ ID NO: 404:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1416 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 404:
US-10-912-362-404

  Query Match             31.9%;  Score 51;  DB 39;  Length 1416;
  Best Local Similarity   38.5%;  Pred. No. 2e+03;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |   |   :  |:::
Db        873 YNTVSANAGQIYTETTIDSETLNQMS 898


RESULT 93
US-10-912-362-402
; Sequence 402, Application US/10912362
;   GENERAL INFORMATION:
;        APPLICANT: Choi et al.
;        TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
;        NUMBER OF SEQUENCES: 497
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 14200 Shady Grove Road
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: Dell Latitude
;             OPERATING SYSTEM: Windows 2000
```

```
;            SOFTWARE: ASCII Text
;         CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/912,362
;            FILING DATE: 06-Aug-2004
;         PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 10/206,576
;            FILING DATE: 2002-07-29
;            APPLICATION NUMBER: US 09/071,035
;            FILING DATE: 1998-05-04
;            APPLICATION NUMBER: US 60/046,655
;            FILING DATE: 1997-05-16
;            APPLICATION NUMBER: US 60/044,031
;            FILING DATE: 1997-05-06
;            APPLICATION NUMBER: US 60/066,009
;            FILING DATE: 1997-11-14
;         ATTORNEY/AGENT INFORMATION:
;            NAME: Hyman, Mark J.
;            REGISTRATION NUMBER: 46,789
;            REFERENCE/DOCKET NUMBER: PB369P1D2
;      INFORMATION FOR SEQ ID NO: 402:
;         SEQUENCE CHARACTERISTICS:
;            LENGTH: 1448 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 402:
US-10-912-362-402

  Query Match             31.9%;  Score 51;  DB 39;  Length 1448;
  Best Local Similarity   38.5%;  Pred. No. 2e+03;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELA 26
              ||||| | |: |   |    :  |:::
Db        900 YNTVSANAGQIYTETTIDSETLNQMS 925


RESULT 94
US-09-708-427-16943
; Sequence 16943, Application US/09708427
; GENERAL INFORMATION:
;  APPLICANT: N. ALEXANDROV et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  THEREBY
;  FILE REFERENCE: 2750-1243P
;  CURRENT APPLICATION NUMBER: US/09/708,427
;  CURRENT FILING DATE:  2000-11-09
;  NUMBER OF SEQ ID NOS: 85364
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16943
;   LENGTH: 1945
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1..1945
;   OTHER INFORMATION: Xaa is any amino acid
;   NAME/KEY: misc_feature
;   LOCATION: 1..1945
;   OTHER INFORMATION: Ceres Seq. ID 1831487
US-09-708-427-16943

  Query Match             31.9%;  Score 51;  DB 27;  Length 1945;
  Best Local Similarity   50.0%;  Pred. No. 2.6e+03;
  Matches   11;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 FNLGEAYEYPTFIQDLRNELAK 27
              |:| | ::| |  || : ||||
Db        816 FSLSEEFKYVTVRQDEKMELAK 837


RESULT 95
US-09-708-427-16942
; Sequence 16942, Application US/09708427
; GENERAL INFORMATION:
;  APPLICANT: N. ALEXANDROV et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES F
;  TITLE OF INVENTION:  THEREBY
;  FILE REFERENCE: 2750-1243P
;  CURRENT APPLICATION NUMBER: US/09/708,427
;  CURRENT FILING DATE:  2000-11-09
;  NUMBER OF SEQ ID NOS: 85364
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16942
;   LENGTH: 2049
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1..2049
;   OTHER INFORMATION: Xaa is any amino acid
;   NAME/KEY: misc_feature
;   LOCATION: 1..2049
;   OTHER INFORMATION: Ceres Seq. ID 1831486
US-09-708-427-16942

  Query Match             31.9%;  Score 51;  DB 27;  Length 2049;
  Best Local Similarity   50.0%;  Pred. No. 2.7e+03;
  Matches   11;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 FNLGEAYEYPTFIQDLRNELAK 27
              |:| | ::| |  || : ||||
Db        920 FSLSEEFKYVTVRQDEKMELAK 941


RESULT 96
US-09-708-427-16941
; Sequence 16941, Application US/09708427
; GENERAL INFORMATION:
;  APPLICANT: N. ALEXANDROV et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES F
;  TITLE OF INVENTION:  THEREBY
;  FILE REFERENCE: 2750-1243P
;  CURRENT APPLICATION NUMBER: US/09/708,427
;  CURRENT FILING DATE:  2000-11-09
;  NUMBER OF SEQ ID NOS: 85364
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16941
;   LENGTH: 2172
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1..2172
;   OTHER INFORMATION: Xaa is any amino acid
;   NAME/KEY: misc_feature
;   LOCATION: 1..2172
;   OTHER INFORMATION: Ceres Seq. ID 1831485
US-09-708-427-16941

  Query Match             31.9%;  Score 51;  DB 27;  Length 2172;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+03;
  Matches   11;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 FNLGEAYEYPTFIQDLRNELAK 27
              |:| | ::| |  || : ||||
Db       1043 FSLSEEFKYVTVRQDEKMELAK 1064


RESULT 97
PCT-US05-11532-1717
; Sequence 1717, Application PC/TUS0511532
; GENERAL INFORMATION:
;  APPLICANT: Porter, Mark
;  APPLICANT:  Higgs, Brandon
```

```
;  APPLICANT:  Mendrick, Donna
;  APPLICANT:  Elashoff, Michael
;  TITLE OF INVENTION: HEPATOTOXICITY MOLECULAR MODELS
;  FILE REFERENCE: 044921-5134-WO
;  CURRENT APPLICATION NUMBER: PCT/US05/11532
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: US 60/559,949
;  PRIOR FILING DATE: 2004-04-07
;  NUMBER OF SEQ ID NOS: 2005
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1717
;   LENGTH: 291
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US05-11532-1717

  Query Match             31.6%;  Score 50.5;  DB 1;  Length 291;
  Best Local Similarity   45.8%;  Pred. No. 6.6e+02;
  Matches   11;  Conservative    4;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   | || | : |
Db        133 NVGMSYEYPEYFLEIPDLDNTIKK 156


RESULT 98
US-09-791-537-91812
; Sequence 91812, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91812
;   LENGTH: 291
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-791-537-91812

  Query Match             31.6%;  Score 50.5;  DB 27;  Length 291;
  Best Local Similarity   45.8%;  Pred. No. 6.6e+02;
  Matches   11;  Conservative    4;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   | || | : |
Db        133 NVGMSYEYPEYFLEIPDLDNTIKK 156


RESULT 99
US-10-219-051B-8973
; Sequence 8973, Application US/10219051B
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
; SEQ ID NO 8973
;   LENGTH: 291
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: SWISS-Prot / AAD00504
;   DATABASE ENTRY DATE: 2002-10-01
US-10-219-051B-8973

  Query Match             31.6%;  Score 50.5;  DB 32;  Length 291;
  Best Local Similarity   45.8%;  Pred. No. 6.6e+02;
  Matches   11;  Conservative    4;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   | || | : |
Db        133 NVGMSYEYPEYFLEIPDLDNTIKK 156


RESULT 100
US-10-219-051B-8977
; Sequence 8977, Application US/10219051B
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
; SEQ ID NO 8977
;   LENGTH: 291
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: SWISS-Prot / AAD00504
;   DATABASE ENTRY DATE: 2002-10-01
US-10-219-051B-8977

  Query Match             31.6%;  Score 50.5;  DB 32;  Length 291;
  Best Local Similarity   45.8%;  Pred. No. 6.6e+02;
  Matches   11;  Conservative    4;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   | || | : |
Db        133 NVGMSYEYPEYFLEIPDLDNTIKK 156


Search completed: September 18, 2006, 19:30:05
Job time : 149.307 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:15:47 ; Search time 10.3911 Seconds
(without alignments)
303.155 Million cell updates/sec

Title: US-10-758-902-1
Perfect score: 160
Sequence: 1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 428092 seqs, 105003536 residues

Total number of hits satisfying chosen parameters: 428092

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending_Patents_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54.5	34.1	608	8	US-60-838-415-27473	Sequence 27473, A
2	50.5	31.6	312	1	PCT-US06-11960-620	Sequence 620, App
3	50.5	31.6	1211	7	US-11-434-137-2492	Sequence 2492, Ap
4	50.5	31.6	1211	7	US-11-434-184-2492	Sequence 2492, Ap
5	50.5	31.6	1211	7	US-11-434-203-2492	Sequence 2492, Ap
6	50.5	31.6	1211	7	US-11-434-127-2492	Sequence 2492, Ap
7	50.5	31.6	1211	7	US-11-434-199-2492	Sequence 2492, Ap
8	50	31.2	531	8	US-60-838-415-21012	Sequence 21012, A
9	49.5	30.9	1610	6	US-10-805-394A-6666	Sequence 6666, Ap
10	49.5	30.9	1610	7	US-11-507-094-14	Sequence 14, Appl
11	49.5	30.9	1610	7	US-11-507-094-56	Sequence 56, Appl
12	49	30.6	234	8	US-60-838-415-21535	Sequence 21535, A
13	49	30.6	355	1	PCT-US06-18535-31556	Sequence 31556, A
14	49	30.6	355	7	US-11-431-855-31556	Sequence 31556, A
15	49	30.6	355	8	US-60-838-415-11133	Sequence 11133, A
16	49	30.6	1852	6	US-10-534-657-19	Sequence 19, Appl
17	49	30.6	2150	7	US-11-437-729-404	Sequence 404, App
18	49	30.6	2150	7	US-11-475-062-3524	Sequence 3524, Ap
19	49	30.6	2155	7	US-11-437-729-409	Sequence 409, App
20	49	30.6	2155	7	US-11-475-062-3528	Sequence 3528, Ap
21	49	30.6	2155	8	US-60-836-986-3274	Sequence 3274, Ap
22	49	30.6	2278	7	US-11-437-729-401	Sequence 401, App
23	49	30.6	2278	7	US-11-437-729-403	Sequence 403, App
24	49	30.6	2278	7	US-11-475-062-3521	Sequence 3521, Ap
25	49	30.6	2278	7	US-11-475-062-3523	Sequence 3523, Ap
26	49	30.6	2364	7	US-11-437-729-402	Sequence 402, App
27	49	30.6	2364	7	US-11-437-729-405	Sequence 405, App
28	49	30.6	2364	7	US-11-437-729-407	Sequence 407, App
29	49	30.6	2364	7	US-11-437-729-408	Sequence 408, App
30	49	30.6	2364	7	US-11-475-062-3522	Sequence 3522, Ap
31	49	30.6	2364	7	US-11-475-062-3525	Sequence 3525, Ap
32	49	30.6	2364	7	US-11-475-062-3526	Sequence 3526, Ap
33	49	30.6	2364	7	US-11-475-062-3527	Sequence 3527, Ap
34	49	30.6	2364	8	US-60-836-986-3273	Sequence 3273, Ap
35	48.5	30.3	312	7	US-11-490-374-1083	Sequence 1083, Ap
36	48.5	30.3	312	7	US-11-490-374-1086	Sequence 1086, Ap
37	48.5	30.3	312	7	US-11-431-708-2029	Sequence 2029, Ap
38	48.5	30.3	312	7	US-11-431-708-2032	Sequence 2032, Ap
39	48.5	30.3	312	7	US-11-437-729-2659	Sequence 2659, Ap
40	48.5	30.3	312	7	US-11-437-729-2662	Sequence 2662, Ap
41	48.5	30.3	312	7	US-11-475-062-859	Sequence 859, App
42	48.5	30.3	312	7	US-11-475-062-860	Sequence 860, App
43	48.5	30.3	312	7	US-11-475-062-862	Sequence 862, App
44	48.5	30.3	312	7	US-11-475-062-863	Sequence 863, App
45	48.5	30.3	312	7	US-11-475-062-2591	Sequence 2591, Ap
46	48.5	30.3	312	7	US-11-475-062-2594	Sequence 2594, Ap
47	48.5	30.3	312	8	US-60-836-986-6134	Sequence 6134, Ap
48	48.5	30.3	352	7	US-11-490-374-1082	Sequence 1082, Ap
49	48.5	30.3	352	7	US-11-490-374-1085	Sequence 1085, Ap
50	48.5	30.3	352	7	US-11-431-708-2028	Sequence 2028, Ap
51	48.5	30.3	352	7	US-11-431-708-2031	Sequence 2031, Ap
52	48.5	30.3	352	7	US-11-437-729-2657	Sequence 2657, Ap
53	48.5	30.3	352	7	US-11-437-729-2661	Sequence 2661, Ap
54	48.5	30.3	352	7	US-11-475-062-2589	Sequence 2589, Ap
55	48.5	30.3	352	7	US-11-475-062-2593	Sequence 2593, Ap
56	48.5	30.3	395	1	PCT-US06-18535-17554	Sequence 17554, A
57	48.5	30.3	395	7	US-11-431-855-17554	Sequence 17554, A
58	48	30.0	260	7	US-11-482-150-41	Sequence 41, Appl
59	48	30.0	264	7	US-11-482-150-29	Sequence 29, Appl
60	47	29.4	429	1	PCT-US06-18535-12020	Sequence 12020, A
61	47	29.4	429	7	US-11-431-855-12020	Sequence 12020, A
62	47	29.4	431	1	PCT-US06-18535-12598	Sequence 12598, A
63	47	29.4	431	1	PCT-US06-18535-18634	Sequence 18634, A
64	47	29.4	431	1	PCT-US06-18535-24144	Sequence 24144, A
65	47	29.4	431	7	US-11-431-855-12598	Sequence 12598, A
66	47	29.4	431	7	US-11-431-855-18634	Sequence 18634, A
67	47	29.4	431	7	US-11-431-855-24144	Sequence 24144, A
68	47	29.4	785	6	US-10-309-407-348	Sequence 348, App
69	47	29.4	803	7	US-11-371-354-70011	Sequence 70011, A
70	47	29.4	803	8	US-60-836-986-2328	Sequence 2328, Ap
71	46	28.7	2388	1	PCT-US06-32336-800	Sequence 800, App
72	45.5	28.4	311	7	US-11-507-097-1904	Sequence 1904, Ap
73	45.5	28.4	315	6	US-10-805-394A-5497	Sequence 5497, Ap
74	45.5	28.4	697	8	US-60-838-415-6195	Sequence 6195, Ap
75	45.5	28.4	772	6	US-10-805-394A-6661	Sequence 6661, Ap
76	45.5	28.4	1149	8	US-60-838-415-27651	Sequence 27651, A
77	45	28.1	210	7	US-11-429-373-1150	Sequence 1150, Ap
78	45	28.1	210	7	US-11-429-374-1150	Sequence 1150, Ap
79	45	28.1	210	7	US-11-429-276-1150	Sequence 1150, Ap
80	45	28.1	259	6	US-10-805-394A-6680	Sequence 6680, Ap
81	45	28.1	261	5	US-09-674-546B-1546	Sequence 1546, Ap
82	45	28.1	372	1	PCT-US06-18535-25575	Sequence 25575, A
83	45	28.1	372	7	US-11-431-855-25575	Sequence 25575, A
84	45	28.1	551	7	US-11-371-354-56715	Sequence 56715, A
85	45	28.1	799	8	US-60-836-986-28515	Sequence 28515, A
86	45	28.1	816	7	US-11-027-891A-2733	Sequence 2733, Ap
87	45	28.1	816	7	US-11-027-879A-2733	Sequence 2733, Ap
88	45	28.1	816	7	US-11-027-892A-2733	Sequence 2733, Ap
89	44.5	27.8	397	7	US-11-416-490-135	Sequence 135, App
90	44.5	27.8	470	1	PCT-US06-18535-24526	Sequence 24526, A
91	44.5	27.8	470	7	US-11-431-855-24526	Sequence 24526, A
92	44.5	27.8	619	6	US-10-527-571A-143	Sequence 143, App
93	44.5	27.8	619	6	US-10-527-571B-143	Sequence 143, App
94	44	27.5	245	6	US-10-805-394A-5373	Sequence 5373, Ap
95	44	27.5	351	1	PCT-US06-18535-30230	Sequence 30230, A
96	44	27.5	351	7	US-11-431-855-30230	Sequence 30230, A
97	44	27.5	369	8	US-60-838-415-21148	Sequence 21148, A
98	44	27.5	440	8	US-60-838-415-14961	Sequence 14961, A

99	44	27.5	479	1	PCT-US06-30281-18413	Sequence 18413, A
100	44	27.5	479	1	PCT-US06-30281-18415	Sequence 18415, A

ALIGNMENTS

```
RESULT 1
US-60-838-415-27473
; Sequence 27473, Application US/60838415
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(54146)A
;  CURRENT APPLICATION NUMBER: US/60/838,415
;  CURRENT FILING DATE:  2006-08-17
;  NUMBER OF SEQ ID NOS: 30376
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27473
;   LENGTH: 608
;   TYPE: PRT
;   ORGANISM: Magnetospirillum magnetotacticum MS-1
US-60-838-415-27473

  Query Match             34.1%;  Score 54.5;  DB 8;  Length 608;
  Best Local Similarity   60.9%;  Pred. No. 6.5;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    5;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL 25
              |||:| || | ||    ||| ||
Db         66 TVSYN-GEIYNYP----DLRREL 83


RESULT 2
PCT-US06-11960-620
; Sequence 620, Application PC/TUS0611960
; GENERAL INFORMATION:
;  APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION,
;  TITLE OF INVENTION:  ASSESSMENT, PREVENTION, AND THERAPY OF NEUROLOGICAL
;  TITLE OF INVENTION:  DISEASES, DISORDERS AND CONDITIONS
;  FILE REFERENCE: DFS-060.25
;  CURRENT APPLICATION NUMBER: PCT/US06/11960
;  CURRENT FILING DATE:  2006-03-31
;  PRIOR APPLICATION NUMBER: 60/667,922
;  PRIOR FILING DATE: 2005-03-31
;  NUMBER OF SEQ ID NOS: 767
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 620
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Mus musculus
PCT-US06-11960-620

  Query Match             31.6%;  Score 50.5;  DB 1;  Length 312;
  Best Local Similarity   45.8%;  Pred. No. 12;
  Matches   11;  Conservative    4;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   | || | : |
Db        133 NVGMSYEYPEYFLEIPDLDNTIKK 156


RESULT 3
US-11-434-137-2492
; Sequence 2492, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2492
;   LENGTH: 1211
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-137-2492

  Query Match             31.6%;  Score 50.5;  DB 7;  Length 1211;
  Best Local Similarity   41.7%;  Pred. No. 63;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAK 27
              ::|:||   ||  |: |: |: ||
Db       1178 INFSLG-GNEYEAFVSDITNQQAK 1200


RESULT 4
US-11-434-184-2492
; Sequence 2492, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2492
;   LENGTH: 1211
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-184-2492

  Query Match             31.6%;  Score 50.5;  DB 7;  Length 1211;
  Best Local Similarity   41.7%;  Pred. No. 63;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAK 27
              ::|:||   ||  |: |: |: ||
Db       1178 INFSLG-GNEYEAFVSDITNQQAK 1200


RESULT 5
US-11-434-203-2492
; Sequence 2492, Application US/11434203
```

```
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2492
;   LENGTH: 1211
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-203-2492

  Query Match             31.6%;  Score 50.5;  DB 7;  Length 1211;
  Best Local Similarity   41.7%;  Pred. No. 63;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAK 27
              ::|:||   ||  |: |: |: ||
Db       1178 INFSLG-GNEYEAFVSDITNQQAK 1200


RESULT 6
US-11-434-127-2492
; Sequence 2492, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2492
;   LENGTH: 1211
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-127-2492

  Query Match             31.6%;  Score 50.5;  DB 7;  Length 1211;
  Best Local Similarity   41.7%;  Pred. No. 63;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAK 27
              ::|:||   ||  |: |: |: ||
Db       1178 INFSLG-GNEYEAFVSDITNQQAK 1200


RESULT 7
US-11-434-199-2492
; Sequence 2492, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 2492
;   LENGTH: 1211
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-199-2492

  Query Match             31.6%;  Score 50.5;  DB 7;  Length 1211;
  Best Local Similarity   41.7%;  Pred. No. 63;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAK 27
              ::|:||   ||  |: |: |: ||
Db       1178 INFSLG-GNEYEAFVSDITNQQAK 1200


RESULT 8
US-60-838-415-21012
; Sequence 21012, Application US/60838415
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(54146)A
;  CURRENT APPLICATION NUMBER: US/60/838,415
;  CURRENT FILING DATE:  2006-08-17
;  NUMBER OF SEQ ID NOS: 30376
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21012
;   LENGTH: 531
;   TYPE: PRT
;   ORGANISM: Coccidioides immitis RS
US-60-838-415-21012

  Query Match             31.2%;  Score 50;  DB 8;  Length 531;
  Best Local Similarity   43.5%;  Pred. No. 27;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL 25
              |:|| : |   :|  :| ||||:
Db        323 TLSFCIFELSRHPAVVQRLRNEI 345


RESULT 9
US-10-805-394A-6666
; Sequence 6666, Application US/10805394A
```

```
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/10/805,394A
;  CURRENT FILING DATE:  2004-03-22
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6666
;   LENGTH: 1610
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-805-394A-6666

  Query Match             30.9%;  Score 49.5;  DB 6;  Length 1610;
  Best Local Similarity   55.0%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         11 AYEYPTFIQDLRNELAKGTP 30
              |||||| |: |   | :| |
Db         71 AYEYPT-IRSLAQRLVEGEP 89


RESULT 10
US-11-507-094-14
; Sequence 14, Application US/11507094
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr?ger, Burkhard
;  APPLICANT:  Sch?der, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CP
;  CURRENT APPLICATION NUMBER: US/11/507,094
;  CURRENT FILING DATE:  2006-08-18
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932182.5
;  PRIOR FILING DATE: 1999-07-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 14
;   LENGTH: 1610
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-11-507-094-14

  Query Match             30.9%;  Score 49.5;  DB 7;  Length 1610;
  Best Local Similarity   55.0%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         11 AYEYPTFIQDLRNELAKGTP 30
              |||||| |: |   | :| |
Db         71 AYEYPT-IRSLAQRLVEGEP 89


RESULT 11
US-11-507-094-56
; Sequence 56, Application US/11507094
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr?ger, Burkhard
;  APPLICANT:  Sch?der, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CP
;  CURRENT APPLICATION NUMBER: US/11/507,094
;  CURRENT FILING DATE:  2006-08-18
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932182.5
;  PRIOR FILING DATE: 1999-07-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 56
;   LENGTH: 1610
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-11-507-094-56

  Query Match             30.9%;  Score 49.5;  DB 7;  Length 1610;
  Best Local Similarity   55.0%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         11 AYEYPTFIQDLRNELAKGTP 30
              |||||| |: |   | :| |
Db         71 AYEYPT-IRSLAQRLVEGEP 89


RESULT 12
US-60-838-415-21535
; Sequence 21535, Application US/60838415
; GENERAL INFORMATION:
```

```
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(54146)A
;  CURRENT APPLICATION NUMBER: US/60/838,415
;  CURRENT FILING DATE:  2006-08-17
;  NUMBER OF SEQ ID NOS: 30376
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21535
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Thiomicrospira crunogena XCL-2
US-60-838-415-21535

  Query Match             30.6%;  Score 49;  DB 8;  Length 234;
  Best Local Similarity   55.6%;  Pred. No. 14;
  Matches   10;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         10 EAYEYPTFIQDLRNELAK 27
              :|  | | || :|:||||
Db        216 DANRYDTVIQQMRDELAK 233


RESULT 13
PCT-US06-18535-31556
; Sequence 31556, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31556
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Verticillium dahliae
PCT-US06-18535-31556

  Query Match             30.6%;  Score 49;  DB 1;  Length 355;
  Best Local Similarity   44.4%;  Pred. No. 23;
  Matches   12;  Conservative    4;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAKGTP 30
              :|||: | |:    |||:  | | | |
Db         15 ISFNVSEQYD----IQDVVGEGAYGPP 37


RESULT 14
US-11-431-855-31556
; Sequence 31556, Application US/11431855
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31556
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Verticillium dahliae
US-11-431-855-31556

  Query Match             30.6%;  Score 49;  DB 7;  Length 355;
  Best Local Similarity   44.4%;  Pred. No. 23;
  Matches   12;  Conservative    4;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAKGTP 30
              :|||: | |:    |||:  | | | |
Db         15 ISFNVSEQYD----IQDVVGEGAYGPP 37


RESULT 15
US-60-838-415-11133
; Sequence 11133, Application US/60838415
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(54146)A
;  CURRENT APPLICATION NUMBER: US/60/838,415
;  CURRENT FILING DATE:  2006-08-17
;  NUMBER OF SEQ ID NOS: 30376
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11133
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Verticillium dahliae
US-60-838-415-11133

  Query Match             30.6%;  Score 49;  DB 8;  Length 355;
  Best Local Similarity   44.4%;  Pred. No. 23;
  Matches   12;  Conservative    4;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAKGTP 30
              :|||: | |:    |||:  | | | |
Db         15 ISFNVSEQYD----IQDVVGEGAYGPP 37


RESULT 16
US-10-534-657-19
; Sequence 19, Application US/10534657
; GENERAL INFORMATION:
;  APPLICANT: Ding, Jeak Ling
;  APPLICANT:  Lim, Eng Hwa
;  APPLICANT:  Lam, Toong Jin
;  APPLICANT:  National University of Singapore
;  TITLE OF INVENTION: Recombinant Vitellogenin Enriched Feed
;  FILE REFERENCE: 040184-000300US
;  CURRENT APPLICATION NUMBER: US/10/534,657
;  CURRENT FILING DATE:  2006-01-27
;  PRIOR APPLICATION NUMBER: US 60/425,263
;  PRIOR FILING DATE: 2002-11-12
;  PRIOR APPLICATION NUMBER: WO PCT/SG03/00266
;  PRIOR FILING DATE: 2003-11-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 1852
;   TYPE: PRT
;   ORGANISM: Gallus gallus
;   FEATURE:
;   OTHER INFORMATION: chicken vitellogenin
US-10-534-657-19

  Query Match             30.6%;  Score 49;  DB 6;  Length 1852;
  Best Local Similarity   38.5%;  Pred. No. 1.8e+02;
  Matches   10;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ::| || ||  :  ::  | |||
Db        192 VQKSIGMAYIYPCPVDVMKERLTKGT 217


RESULT 17
US-11-437-729-404
; Sequence 404, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 404
;   LENGTH: 2150
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-404

  Query Match             30.6%;  Score 49;  DB 7;  Length 2150;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 18
US-11-475-062-3524
; Sequence 3524, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3524
;   LENGTH: 2150
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-3524

  Query Match             30.6%;  Score 49;  DB 7;  Length 2150;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 19
US-11-437-729-409
; Sequence 409, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 409
;   LENGTH: 2155
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-409

  Query Match             30.6%;  Score 49;  DB 7;  Length 2155;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1710 SHELGQDYEHVTMLQERFREFARDT 1734


RESULT 20
US-11-475-062-3528
; Sequence 3528, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3528
;   LENGTH: 2155
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-3528

  Query Match             30.6%;  Score 49;  DB 7;  Length 2155;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1710 SHELGQDYEHVTMLQERFREFARDT 1734


RESULT 21
US-60-836-986-3274
; Sequence 3274, Application US/60836986
; GENERAL INFORMATION:
;  APPLICANT: Hood, Leroy
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Johnson, Richard
;  APPLICANT:  Marelli, Marcello
;  APPLICANT:  Li, Xiaojun
;  TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 460092.405P1
;  CURRENT APPLICATION NUMBER: US/60/836,986
;  CURRENT FILING DATE:  2006-08-09
;  NUMBER OF SEQ ID NOS: 32934
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3274
;   LENGTH: 2155
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-836-986-3274

  Query Match             30.6%;  Score 49;  DB 8;  Length 2155;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1710 SHELGQDYEHVTMLQERFREFARDT 1734


RESULT 22
US-11-437-729-401
; Sequence 401, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 401
;   LENGTH: 2278
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-401

  Query Match             30.6%;  Score 49;  DB 7;  Length 2278;
  Best Local Similarity   40.0%;  Pred. No. 2.4e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
```

```
              |  ||: ||: | :|:   | |: |
Db       1637 SHELGQDYEHVTMLQERFREFARDT 1661


RESULT 23
US-11-437-729-403
; Sequence 403, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 403
;   LENGTH: 2278
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-403

  Query Match             30.6%;  Score 49;  DB 7;  Length 2278;
  Best Local Similarity   40.0%;  Pred. No. 2.4e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1637 SHELGQDYEHVTMLQERFREFARDT 1661


RESULT 24
US-11-475-062-3521
; Sequence 3521, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3521
;   LENGTH: 2278
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-3521

  Query Match             30.6%;  Score 49;  DB 7;  Length 2278;
  Best Local Similarity   40.0%;  Pred. No. 2.4e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1637 SHELGQDYEHVTMLQERFREFARDT 1661


RESULT 25
US-11-475-062-3523
; Sequence 3523, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3523
;   LENGTH: 2278
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-3523

  Query Match             30.6%;  Score 49;  DB 7;  Length 2278;
  Best Local Similarity   40.0%;  Pred. No. 2.4e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1637 SHELGQDYEHVTMLQERFREFARDT 1661


RESULT 26
US-11-437-729-402
; Sequence 402, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 402
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-402

  Query Match             30.6%;  Score 49;  DB 7;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 27
US-11-437-729-405
; Sequence 405, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 405
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-405

  Query Match             30.6%;  Score 49;  DB 7;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 28
US-11-437-729-407
; Sequence 407, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 407
```

```
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-407

  Query Match             30.6%;  Score 49;  DB 7;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 29
US-11-437-729-408
; Sequence 408, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 408
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-408

  Query Match             30.6%;  Score 49;  DB 7;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 30
US-11-475-062-3522
; Sequence 3522, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3522
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-3522

  Query Match             30.6%;  Score 49;  DB 7;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 31
US-11-475-062-3525
; Sequence 3525, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3525
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-3525

  Query Match             30.6%;  Score 49;  DB 7;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 32
US-11-475-062-3526
; Sequence 3526, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3526
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-3526

  Query Match             30.6%;  Score 49;  DB 7;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 33
US-11-475-062-3527
; Sequence 3527, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3527
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-3527

  Query Match             30.6%;  Score 49;  DB 7;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 34
US-60-836-986-3273
```

```
; Sequence 3273, Application US/60836986
; GENERAL INFORMATION:
;  APPLICANT: Hood, Leroy
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Johnson, Richard
;  APPLICANT:  Marelli, Marcello
;  APPLICANT:  Li, Xiaojun
;  TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 460092.405P1
;  CURRENT APPLICATION NUMBER: US/60/836,986
;  CURRENT FILING DATE:  2006-08-09
;  NUMBER OF SEQ ID NOS: 32934
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3273
;   LENGTH: 2364
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-836-986-3273

  Query Match             30.6%;  Score 49;  DB 8;  Length 2364;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+02;
  Matches   10;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | :|:   | |: |
Db       1723 SHELGQDYEHVTMLQERFREFARDT 1747


RESULT 35
US-11-490-374-1083
; Sequence 1083, Application US/11490374
; GENERAL INFORMATION:
;  APPLICANT: KIM, Yeounjin
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001615ORD
;  CURRENT APPLICATION NUMBER: US/11/490,374
;  CURRENT FILING DATE:  2006-07-21
;  NUMBER OF SEQ ID NOS: 2638
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1083
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-490-374-1083

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 36
US-11-490-374-1086
; Sequence 1086, Application US/11490374
; GENERAL INFORMATION:
;  APPLICANT: KIM, Yeounjin
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001615ORD
;  CURRENT APPLICATION NUMBER: US/11/490,374
;  CURRENT FILING DATE:  2006-07-21
;  NUMBER OF SEQ ID NOS: 2638
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1086
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-490-374-1086

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 37
US-11-431-708-2029
; Sequence 2029, Application US/11431708
; GENERAL INFORMATION:
;  APPLICANT: RUBEN, Steven
;  TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001599-ORD
;  CURRENT APPLICATION NUMBER: US/11/431,708
;  CURRENT FILING DATE:  2006-05-11
;  NUMBER OF SEQ ID NOS: 8544
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2029
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-431-708-2029

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 38
US-11-431-708-2032
; Sequence 2032, Application US/11431708
; GENERAL INFORMATION:
;  APPLICANT: RUBEN, Steven
;  TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001599-ORD
;  CURRENT APPLICATION NUMBER: US/11/431,708
;  CURRENT FILING DATE:  2006-05-11
;  NUMBER OF SEQ ID NOS: 8544
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2032
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-431-708-2032

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 39
US-11-437-729-2659
; Sequence 2659, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2659
;   LENGTH: 312
```

```
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-2659

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 40
US-11-437-729-2662
; Sequence 2662, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2662
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-2662

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 41
US-11-475-062-859
; Sequence 859, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 859
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-859

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 42
US-11-475-062-860
; Sequence 860, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 860
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-860

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 43
US-11-475-062-862
; Sequence 862, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 862
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-862

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 44
US-11-475-062-863
; Sequence 863, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 863
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-863

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 45
US-11-475-062-2591
; Sequence 2591, Application US/11475062
```

```
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2591
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-2591

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 46
US-11-475-062-2594
; Sequence 2594, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2594
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-2594

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 47
US-60-836-986-6134
; Sequence 6134, Application US/60836986
; GENERAL INFORMATION:
;  APPLICANT: Hood, Leroy
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Johnson, Richard
;  APPLICANT:  Marelli, Marcello
;  APPLICANT:  Li, Xiaojun
;  TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 460092.405P1
;  CURRENT APPLICATION NUMBER: US/60/836,986
;  CURRENT FILING DATE:  2006-08-09
;  NUMBER OF SEQ ID NOS: 32934
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6134
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-836-986-6134

  Query Match             30.3%;  Score 48.5;  DB 8;  Length 312;
  Best Local Similarity   41.7%;  Pred. No. 23;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        133 NVGMSYEYPEYFLDVPDLDNVIKK 156


RESULT 48
US-11-490-374-1082
; Sequence 1082, Application US/11490374
; GENERAL INFORMATION:
;  APPLICANT: KIM, Yeounjin
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001615ORD
;  CURRENT APPLICATION NUMBER: US/11/490,374
;  CURRENT FILING DATE:  2006-07-21
;  NUMBER OF SEQ ID NOS: 2638
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1082
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-490-374-1082

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 352;
  Best Local Similarity   41.7%;  Pred. No. 27;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        173 NVGMSYEYPEYFLDVPDLDNVIKK 196


RESULT 49
US-11-490-374-1085
; Sequence 1085, Application US/11490374
; GENERAL INFORMATION:
;  APPLICANT: KIM, Yeounjin
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001615ORD
;  CURRENT APPLICATION NUMBER: US/11/490,374
;  CURRENT FILING DATE:  2006-07-21
;  NUMBER OF SEQ ID NOS: 2638
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1085
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-490-374-1085

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 352;
  Best Local Similarity   41.7%;  Pred. No. 27;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        173 NVGMSYEYPEYFLDVPDLDNVIKK 196


RESULT 50
US-11-431-708-2028
; Sequence 2028, Application US/11431708
; GENERAL INFORMATION:
;  APPLICANT: RUBEN, Steven
;  TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001599-ORD
;  CURRENT APPLICATION NUMBER: US/11/431,708
;  CURRENT FILING DATE:  2006-05-11
;  NUMBER OF SEQ ID NOS: 8544
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2028
;   LENGTH: 352
;   TYPE: PRT
```

```
;   ORGANISM: Homo sapiens
US-11-431-708-2028

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 352;
  Best Local Similarity   41.7%;  Pred. No. 27;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        173 NVGMSYEYPEYFLDVPDLDNVIKK 196


RESULT 51
US-11-431-708-2031
; Sequence 2031, Application US/11431708
; GENERAL INFORMATION:
;  APPLICANT: RUBEN, Steven
;  TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001599-ORD
;  CURRENT APPLICATION NUMBER: US/11/431,708
;  CURRENT FILING DATE:  2006-05-11
;  NUMBER OF SEQ ID NOS: 8544
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2031
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-431-708-2031

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 352;
  Best Local Similarity   41.7%;  Pred. No. 27;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        173 NVGMSYEYPEYFLDVPDLDNVIKK 196


RESULT 52
US-11-437-729-2657
; Sequence 2657, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2657
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-2657

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 352;
  Best Local Similarity   41.7%;  Pred. No. 27;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        173 NVGMSYEYPEYFLDVPDLDNVIKK 196


RESULT 53
US-11-437-729-2661
; Sequence 2661, Application US/11437729
; GENERAL INFORMATION:
;  APPLICANT: JOSELOFF, Elizabeth et al.
;  TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001606
;  CURRENT APPLICATION NUMBER: US/11/437,729
;  CURRENT FILING DATE:  2006-05-22
;  NUMBER OF SEQ ID NOS: 6151
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2661
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-437-729-2661

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 352;
  Best Local Similarity   41.7%;  Pred. No. 27;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        173 NVGMSYEYPEYFLDVPDLDNVIKK 196


RESULT 54
US-11-475-062-2589
; Sequence 2589, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2589
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-2589

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 352;
  Best Local Similarity   41.7%;  Pred. No. 27;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        173 NVGMSYEYPEYFLDVPDLDNVIKK 196


RESULT 55
US-11-475-062-2593
; Sequence 2593, Application US/11475062
; GENERAL INFORMATION:
;  APPLICANT: BIRSE, Charles et al.
;  TITLE OF INVENTION: CANCER TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001706
;  CURRENT APPLICATION NUMBER: US/11/475,062
;  CURRENT FILING DATE:  2006-06-27
;  NUMBER OF SEQ ID NOS: 16099
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2593
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-475-062-2593

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 352;
  Best Local Similarity   41.7%;  Pred. No. 27;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          7 NLGEAYEYPTF---IQDLRNELAK 27
              |:| :|||| :   : || | : |
Db        173 NVGMSYEYPEYFLDVPDLDNVIKK 196


RESULT 56
PCT-US06-18535-17554
; Sequence 17554, Application PC/TUS0618535
; GENERAL INFORMATION:
```

```
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17554
;   LENGTH: 395
;   TYPE: PRT
;   ORGANISM: Corynebacterium efficiens YS-314
PCT-US06-18535-17554

  Query Match             30.3%;  Score 48.5;  DB 1;  Length 395;
  Best Local Similarity   43.3%;  Pred. No. 31;
  Matches   13;  Conservative    5;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          4 VSFN---LGEAYEYPTFIQDLRNELAKGTP 30
              |||:   || |   ||  : :: :|| |||
Db        302 VSFSELALGGAISVPTLDKPVKLKLAPGTP 331


RESULT 57
US-11-431-855-17554
; Sequence 17554, Application US/11431855
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17554
;   LENGTH: 395
;   TYPE: PRT
;   ORGANISM: Corynebacterium efficiens YS-314
US-11-431-855-17554

  Query Match             30.3%;  Score 48.5;  DB 7;  Length 395;
  Best Local Similarity   43.3%;  Pred. No. 31;
  Matches   13;  Conservative    5;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          4 VSFN---LGEAYEYPTFIQDLRNELAKGTP 30
              |||:   || |   ||  : :: :|| |||
Db        302 VSFSELALGGAISVPTLDKPVKLKLAPGTP 331


RESULT 58
US-11-482-150-41
; Sequence 41, Application US/11482150
; GENERAL INFORMATION:
;  APPLICANT: The Regents of the University of California
;  APPLICANT:  Dandekar, Abhaya
;  APPLICANT:  Muir, Ryann M.
;  TITLE OF INVENTION: ORGANISMS WITH ELEVATED LEVELS OF GALLIC
;  TITLE OF INVENTION:  ACID/POLYPHENOL OXIDASE AND METHODS OF GENERATING SUCH
;  TITLE OF INVENTION:  ORGANISMS
;  FILE REFERENCE: 514112001120
;  CURRENT APPLICATION NUMBER: US/11/482,150
;  CURRENT FILING DATE:  2006-07-05
;  PRIOR APPLICATION NUMBER: WO PCT/US2004/043738
;  PRIOR FILING DATE: 2004-12-22
;  PRIOR APPLICATION NUMBER: US 60/534,424
;  PRIOR FILING DATE: 2004-01-05
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 260
;   TYPE: PRT
;   ORGANISM: Aquifex aeolicus
US-11-482-150-41

  Query Match             30.0%;  Score 48;  DB 7;  Length 260;
  Best Local Similarity   42.3%;  Pred. No. 22;
  Matches   11;  Conservative    5;  Mismatches    6;  Indels    4;  Gaps    1;

Qy          2 NTVSFNLGEAYEYPT----FIQDLRN 23
              ||| |  |:|| | |    |:: |::
Db         88 NTVKFENGKAYGYNTDWIGFLKSLKS 113


RESULT 59
US-11-482-150-29
; Sequence 29, Application US/11482150
; GENERAL INFORMATION:
;  APPLICANT: The Regents of the University of California
;  APPLICANT:  Dandekar, Abhaya
;  APPLICANT:  Muir, Ryann M.
;  TITLE OF INVENTION: ORGANISMS WITH ELEVATED LEVELS OF GALLIC
;  TITLE OF INVENTION:  ACID/POLYPHENOL OXIDASE AND METHODS OF GENERATING SUCH
;  TITLE OF INVENTION:  ORGANISMS
;  FILE REFERENCE: 514112001120
;  CURRENT APPLICATION NUMBER: US/11/482,150
;  CURRENT FILING DATE:  2006-07-05
;  PRIOR APPLICATION NUMBER: WO PCT/US2004/043738
;  PRIOR FILING DATE: 2004-12-22
;  PRIOR APPLICATION NUMBER: US 60/534,424
;  PRIOR FILING DATE: 2004-01-05
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 264
;   TYPE: PRT
;   ORGANISM: Aquifex aeolicus
US-11-482-150-29

  Query Match             30.0%;  Score 48;  DB 7;  Length 264;
  Best Local Similarity   42.3%;  Pred. No. 23;
  Matches   11;  Conservative    5;  Mismatches    6;  Indels    4;  Gaps    1;

Qy          2 NTVSFNLGEAYEYPT----FIQDLRN 23
              ||| |  |:|| | |    |:: |::
Db         86 NTVKFENGKAYGYNTDWIGFLKSLKS 111


RESULT 60
PCT-US06-18535-12020
; Sequence 12020, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12020
;   LENGTH: 429
;   TYPE: PRT
;   ORGANISM: Rickettsia prowazekii str. Madrid E
PCT-US06-18535-12020

  Query Match             29.4%;  Score 47;  DB 1;  Length 429;
  Best Local Similarity   60.0%;  Pred. No. 59;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GEAYEYPTFIQDLRN 23
              |  |  |||::||||
Db        260 GVIYWAPTFLKDLRN 274


RESULT 61
US-11-431-855-12020
; Sequence 12020, Application US/11431855
; GENERAL INFORMATION:
```

```
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12020
;   LENGTH: 429
;   TYPE: PRT
;   ORGANISM: Rickettsia prowazekii str. Madrid E
US-11-431-855-12020

  Query Match             29.4%;  Score 47;  DB 7;  Length 429;
  Best Local Similarity   60.0%;  Pred. No. 59;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GEAYEYPTFIQDLRN 23
              |  |  |||::||||
Db        260 GVIYWAPTFLKDLRN 274


RESULT 62
PCT-US06-18535-12598
; Sequence 12598, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12598
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Rickettsia conorii str. Malish 7
PCT-US06-18535-12598

  Query Match             29.4%;  Score 47;  DB 1;  Length 431;
  Best Local Similarity   60.0%;  Pred. No. 59;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GEAYEYPTFIQDLRN 23
              |  |  |||::||||
Db        260 GVIYWAPTFLKDLRN 274


RESULT 63
PCT-US06-18535-18634
; Sequence 18634, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18634
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Rickettsia sibirica 246
PCT-US06-18535-18634

  Query Match             29.4%;  Score 47;  DB 1;  Length 431;
  Best Local Similarity   60.0%;  Pred. No. 59;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GEAYEYPTFIQDLRN 23
              |  |  |||::||||
Db        260 GVIYWAPTFLKDLRN 274


RESULT 64
PCT-US06-18535-24144
; Sequence 24144, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24144
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Rickettsia rickettsii
PCT-US06-18535-24144

  Query Match             29.4%;  Score 47;  DB 1;  Length 431;
  Best Local Similarity   60.0%;  Pred. No. 59;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GEAYEYPTFIQDLRN 23
              |  |  |||::||||
Db        260 GVIYWAPTFLKDLRN 274


RESULT 65
US-11-431-855-12598
; Sequence 12598, Application US/11431855
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12598
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Rickettsia conorii str. Malish 7
US-11-431-855-12598

  Query Match             29.4%;  Score 47;  DB 7;  Length 431;
  Best Local Similarity   60.0%;  Pred. No. 59;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GEAYEYPTFIQDLRN 23
              |  |  |||::||||
Db        260 GVIYWAPTFLKDLRN 274


RESULT 66
US-11-431-855-18634
; Sequence 18634, Application US/11431855
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18634
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Rickettsia sibirica 246
US-11-431-855-18634

  Query Match             29.4%;  Score 47;  DB 7;  Length 431;
  Best Local Similarity   60.0%;  Pred. No. 59;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          9 GEAYEYPTFIQDLRN 23
              |  |  |||::||||
Db        260 GVIYWAPTFLKDLRN 274
```

RESULT 67
US-11-431-855-24144
; Sequence 24144, Application US/11431855
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et. al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53708)C
; CURRENT APPLICATION NUMBER: US/11/431,855
; CURRENT FILING DATE: 2006-05-10
; NUMBER OF SEQ ID NOS: 33637
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24144
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Rickettsia rickettsii
US-11-431-855-24144

Query Match 29.4%; Score 47; DB 7; Length 431;
Best Local Similarity 60.0%; Pred. No. 59;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          9 GEAYEYPTFIQDLRN 23
              |  |  |||::||||
Db        260 GVIYWAPTFLKDLRN 274
```

RESULT 68
US-10-309-407-348
; Sequence 348, Application US/10309407
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Douglas
; APPLICANT: Madden, Kevin T.
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd G.
; APPLICANT: Norman, Thea
; APPLICANT: Royer, John C.
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric F.
; APPLICANT: Zhang, Lixin
; APPLICANT: Mayorga, Maria
; APPLICANT: Feibelman, Toby
; APPLICANT: Doten, Reed
; TITLE OF INVENTION: METHODS FOR IMPROVING SECONDARY
; TITLE OF INVENTION: METABOLITE PRODUCTION OF FUNGI
; FILE REFERENCE: 14184-023001
; CURRENT APPLICATION NUMBER: US/10/309,407
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US 09/691,499
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 496
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-309-407-348

Query Match 29.4%; Score 47; DB 6; Length 785;
Best Local Similarity 42.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```
Qy         12 YEYPTFIQDLRNELAKGTP 30
              | || ||:|::: | :  |
Db        504 YLYPLFIRDIQSVLKQNNP 522
```

RESULT 69
US-11-371-354-70011
; Sequence 70011, Application US/11371354
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70011
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-70011

Query Match 29.4%; Score 47; DB 7; Length 803;
Best Local Similarity 39.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 4; Indels 8; Gaps 1;

```
Qy          2 NTVSFNL--------GEAYEYPTFIQDL 21
              ||:||:|        ||: |:  | :||
Db        243 NTISFSLEEEEELEGGESAEFTCFSEDL 270
```

RESULT 70
US-60-836-986-2328
; Sequence 2328, Application US/60836986
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Johnson, Richard
; APPLICANT: Marelli, Marcello
; APPLICANT: Li, Xiaojun
; TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 460092.405P1
; CURRENT APPLICATION NUMBER: US/60/836,986
; CURRENT FILING DATE: 2006-08-09
; NUMBER OF SEQ ID NOS: 32934
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2328
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-836-986-2328

Query Match 29.4%; Score 47; DB 8; Length 803;
Best Local Similarity 39.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 4; Indels 8; Gaps 1;

```
Qy          2 NTVSFNL--------GEAYEYPTFIQDL 21
              ||:||:|        ||: |:  | :||
Db        243 NTISFSLEEEEELEGGESAEFTCFSEDL 270


RESULT 71
PCT-US06-32336-800
; Sequence 800, Application PC/TUS0632336
; GENERAL INFORMATION:
;  APPLICANT: Gene Logic, Inc.
;  TITLE OF INVENTION: MOLECULAR TOXICITY MODELS FROM ISOLATED HEPATOCYTES
;  FILE REFERENCE: GENE-126/01WO
;  CURRENT APPLICATION NUMBER: PCT/US06/32336
;  CURRENT FILING DATE:  2006-08-24
;  PRIOR APPLICATION NUMBER: US 60/708,754
;  PRIOR FILING DATE: 2005-08-17
;  NUMBER OF SEQ ID NOS: 1252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 800
;   LENGTH: 2388
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
PCT-US06-32336-800

  Query Match             28.7%;  Score 46;  DB 1;  Length 2388;
  Best Local Similarity   36.0%;  Pred. No. 7.2e+02;
  Matches    9;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGT 29
              |  ||: ||: | ::|   | :: |
Db       1719 SHELGQDYEHVTMLRDKFREFSRDT 1743


RESULT 72
US-11-507-097-1904
; Sequence 1904, Application US/11507097
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: BGI-129CP
;  CURRENT APPLICATION NUMBER: US/11/507,097
;  CURRENT FILING DATE:  2006-08-17
;  PRIOR APPLICATION NUMBER: 60/142,764
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: 60/152,318
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1904
;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-11-507-097-1904

  Query Match             28.4%;  Score 45.5;  DB 7;  Length 311;
  Best Local Similarity   43.3%;  Pred. No. 67;
  Matches   13;  Conservative    4;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          2 NTVSFNLGEA-YEYPTFIQDLRNELAKGTP 30
              |   |:|||  |    || : :|| | :|
Db        236 NPEKFDLGEARAEAEESIQSIADELKKESP 265


RESULT 73
US-10-805-394A-5497
; Sequence 5497, Application US/10805394A
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/10/805,394A
;  CURRENT FILING DATE:  2004-03-22
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5497
;   LENGTH: 315
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-805-394A-5497

  Query Match             28.4%;  Score 45.5;  DB 6;  Length 315;
  Best Local Similarity   43.3%;  Pred. No. 68;
  Matches   13;  Conservative    4;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          2 NTVSFNLGEA-YEYPTFIQDLRNELAKGTP 30
              |   |:|||  |    || : :|| | :|
Db        240 NPEKFDLGEARAEAEESIQSIADELKKESP 269


RESULT 74
US-60-838-415-6195
; Sequence 6195, Application US/60838415
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(54146)A
;  CURRENT APPLICATION NUMBER: US/60/838,415
;  CURRENT FILING DATE:  2006-08-17
;  NUMBER OF SEQ ID NOS: 30376
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6195
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough
US-60-838-415-6195

  Query Match             28.4%;  Score 45.5;  DB 8;  Length 697;
  Best Local Similarity   52.2%;  Pred. No. 1.8e+02;
  Matches   12;  Conservative    2;  Mismatches    4;  Indels    5;  Gaps    2;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL 25
              |: || || | ||    ||| :|
Db         76 TLVFN-GEIYNYP----DLRRDL 93


RESULT 75
US-10-805-394A-6661
; Sequence 6661, Application US/10805394A
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
```

```
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/10/805,394A
;  CURRENT FILING DATE:  2004-03-22
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6661
;   LENGTH: 772
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-805-394A-6661

  Query Match             28.4%;  Score 45.5;  DB 6;  Length 772;
  Best Local Similarity   45.8%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    3;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          8 LGEAYEYPTF-IQDLRNELAKGTP 30
              || | :|  | :   | |: ||||
Db        248 LGLAIDYGLFMVSRFREEMDKGTP 271


RESULT 76
US-60-838-415-27651
; Sequence 27651, Application US/60838415
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(54146)A
;  CURRENT APPLICATION NUMBER: US/60/838,415
;  CURRENT FILING DATE:  2006-08-17
;  NUMBER OF SEQ ID NOS: 30376
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27651
;   LENGTH: 1149
;   TYPE: PRT
;   ORGANISM: Cryptococcus neoformans var. neoformans JEC21
US-60-838-415-27651

  Query Match             28.4%;  Score 45.5;  DB 8;  Length 1149;
  Best Local Similarity   45.5%;  Pred. No. 3.4e+02;
  Matches   10;  Conservative    3;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          9 GEAYEYPTFIQDLRNELAKGTP 30
              |: |||   | ||   : :|||
Db        357 GQTYEYAKTIVDL---MTRGTP 375


RESULT 77
US-11-429-373-1150
; Sequence 1150, Application US/11429373
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564
;  CURRENT APPLICATION NUMBER: US/11/429,373
;  CURRENT FILING DATE:  2006-05-08
;  PRIOR APPLICATION NUMBER: 10/775,204
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: PCT/US02/40891
;  PRIOR FILING DATE: 2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1150
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Salmo salar
US-11-429-373-1150

  Query Match             28.1%;  Score 45;  DB 7;  Length 210;
  Best Local Similarity   40.9%;  Pred. No. 49;
  Matches    9;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNEL 25
              :|| | |::|||:    : | |
Db         96 ISFRLIESWEYPSQTLTISNSL 117


RESULT 78
US-11-429-374-1150
; Sequence 1150, Application US/11429374
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564
;  CURRENT APPLICATION NUMBER: US/11/429,374
;  CURRENT FILING DATE:  2006-05-08
;  PRIOR APPLICATION NUMBER: 10/775,204
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: PCT/US02/40891
;  PRIOR FILING DATE: 2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1150
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Salmo salar
US-11-429-374-1150

  Query Match             28.1%;  Score 45;  DB 7;  Length 210;
  Best Local Similarity   40.9%;  Pred. No. 49;
  Matches    9;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNEL 25
```

```
              :|| | |::|||:    : | |
Db          96 ISFRLIESWEYPSQTLTISNSL 117


RESULT 79
US-11-429-276-1150
; Sequence 1150, Application US/11429276
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF564
;  CURRENT APPLICATION NUMBER: US/11/429,276
;  CURRENT FILING DATE:  2006-05-08
;  PRIOR APPLICATION NUMBER: 10/775,204
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: PCT/US02/40891
;  PRIOR FILING DATE: 2002-12-23
;  PRIOR APPLICATION NUMBER: 60/341,811
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/360,000
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/378,950
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/398,008
;  PRIOR FILING DATE: 2002-07-24
;  PRIOR APPLICATION NUMBER: 60/411,355
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/414,984
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/417,611
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/420,246
;  PRIOR FILING DATE: 2002-10-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2222
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1150
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Salmo salar
US-11-429-276-1150

  Query Match             28.1%;  Score 45;  DB 7;  Length 210;
  Best Local Similarity   40.9%;  Pred. No. 49;
  Matches    9;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 VSFNLGEAYEYPTFIQDLRNEL 25
              :|| | |::|||:    : | |
Db         96 ISFRLIESWEYPSQTLTISNSL 117


RESULT 80
US-10-805-394A-6680
; Sequence 6680, Application US/10805394A
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/10/805,394A
;  CURRENT FILING DATE:  2004-03-22
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6680
;   LENGTH: 259
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-805-394A-6680

  Query Match             28.1%;  Score 45;  DB 6;  Length 259;
  Best Local Similarity   75.0%;  Pred. No. 63;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 TFIQDLRNELAK 27
              || :|| |||||
Db         16 TFCEDLSNELAK 27


RESULT 81
US-09-674-546B-1546
; Sequence 1546, Application US/09674546B
; GENERAL INFORMATION:
;  APPLICANT: Institute for Genomic Research
;  APPLICANT:  Chiron Corporation
;  TITLE OF INVENTION: Neisseria Meningitidis Antigens and Compositions
;  FILE REFERENCE: CHIR-0334
;  CURRENT APPLICATION NUMBER: US/09/674,546B
;  CURRENT FILING DATE:  2002-11-04
;  NUMBER OF SEQ ID NOS: 3265
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1546
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Neisseria meningitidis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (251)..(251)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-674-546B-1546

  Query Match             28.1%;  Score 45;  DB 5;  Length 261;
  Best Local Similarity   53.3%;  Pred. No. 64;
  Matches    8;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDL 21
              |:   |||||:| :|
Db         41 NVFVGYEYPTYISNL 55


RESULT 82
PCT-US06-18535-25575
; Sequence 25575, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25575
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Ustilago maydis 521
PCT-US06-18535-25575

  Query Match             28.1%;  Score 45;  DB 1;  Length 372;
  Best Local Similarity   33.3%;  Pred. No. 1e+02;
  Matches    7;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         10 EAYEYPTFIQDLRNELAKGTP 30
              | :  | : |:|:: : :|||
```

```
Db        302 EIHSNPEYPQELKDHIPRGTP 322


RESULT 83
US-11-431-855-25575
; Sequence 25575, Application US/11431855
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25575
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Ustilago maydis 521
US-11-431-855-25575

  Query Match             28.1%;  Score 45;  DB 7;  Length 372;
  Best Local Similarity   33.3%;  Pred. No. 1e+02;
  Matches    7;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         10 EAYEYPTFIQDLRNELAKGTP 30
              | :  | : |:|:: : :|||
Db        302 EIHSNPEYPQELKDHIPRGTP 322


RESULT 84
US-11-371-354-56715
; Sequence 56715, Application US/11371354
; GENERAL INFORMATION:
;  APPLICANT: CARRINO, JOHN
;  APPLICANT:  LIANG, FENG
;  TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFYING MATCHED REAGENTS
;  FILE REFERENCE: INV-1005-UT2
;  CURRENT APPLICATION NUMBER: US/11/371,354
;  CURRENT FILING DATE:  2006-03-07
;  PRIOR APPLICATION NUMBER: 60/673,045
;  PRIOR FILING DATE: 2005-04-19
;  PRIOR APPLICATION NUMBER: 60/665,199
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/665,200
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/659,493
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/659,492
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/953,586
;  PRIOR FILING DATE: 2005-02-15
;  PRIOR APPLICATION NUMBER: 60/651,390
;  PRIOR FILING DATE: 2005-02-08
;  NUMBER OF SEQ ID NOS: 78682
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56715
;   LENGTH: 551
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-371-354-56715

  Query Match             28.1%;  Score 45;  DB 7;  Length 551;
  Best Local Similarity   36.4%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    3;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLR 22
              |  :   |   | | :| :|||
Db        438 YKCLQIELSRGYNYDSFHEDLR 459


RESULT 85
US-60-836-986-28515
; Sequence 28515, Application US/60836986
; GENERAL INFORMATION:
;  APPLICANT: Hood, Leroy
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Johnson, Richard
;  APPLICANT:  Marelli, Marcello
;  APPLICANT:  Li, Xiaojun
;  TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 460092.405P1
;  CURRENT APPLICATION NUMBER: US/60/836,986
;  CURRENT FILING DATE:  2006-08-09
;  NUMBER OF SEQ ID NOS: 32934
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28515
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-836-986-28515

  Query Match             28.1%;  Score 45;  DB 8;  Length 799;
  Best Local Similarity   45.5%;  Pred. No. 2.6e+02;
  Matches   10;  Conservative    2;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLR 22
              ||| | :|   |  | || : |
Db         76 YNTASDDLELLYHIPEFIPEAR 97


RESULT 86
US-11-027-891A-2733
; Sequence 2733, Application US/11027891A
; GENERAL INFORMATION:
;  APPLICANT: Doucette-Stamm, Lynn
;  APPLICANT:  Bush, David
;  APPLICANT:  Zeng, Qiandong
;  APPLICANT:  Opperman, Timothy
;  APPLICANT:  Houseweart, Chad Eric
;  TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE: 3687.1000-025
;  CURRENT APPLICATION NUMBER: US/11/027,891A
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: US 10/640,833
;  PRIOR FILING DATE: 2003-08-14
;  PRIOR APPLICATION NUMBER: US 09/583,110
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/107,433
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/085,131
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: US 60/051,553
;  PRIOR FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 5324
; SEQ ID NO 2733
;   LENGTH: 816
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-11-027-891A-2733

  Query Match             28.1%;  Score 45;  DB 7;  Length 816;
  Best Local Similarity   41.2%;  Pred. No. 2.7e+02;
  Matches    7;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 LGEAYEYPTFIQDLRNE 24
              :|: | |  |: |||::
Db        372 IGQLYRYQHFLADLRHD 388


RESULT 87
US-11-027-879A-2733
; Sequence 2733, Application US/11027879A
; GENERAL INFORMATION:
```

```
;  APPLICANT: Doucette-Stamm, Lynn
;  APPLICANT:  Bush, David
;  APPLICANT:  Zeng, Qiandong
;  APPLICANT:  Opperman, Timothy
;  APPLICANT:  Houseweart, Chad Eric
;  TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE: 3687.1000-021
;  CURRENT APPLICATION NUMBER: US/11/027,879A
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: US 10/640,833
;  PRIOR FILING DATE: 2003-08-14
;  PRIOR APPLICATION NUMBER: US 09/583,110
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/107,433
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/085,131
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: US 60/051,553
;  PRIOR FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 5324
; SEQ ID NO 2733
;   LENGTH: 816
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-11-027-879A-2733

  Query Match             28.1%;  Score 45;  DB 7;  Length 816;
  Best Local Similarity   41.2%;  Pred. No. 2.7e+02;
  Matches    7;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 LGEAYEYPTFIQDLRNE 24
              :|: | |   |: |||::
Db        372 IGQLYRYQHFLADLRHD 388


RESULT 88
US-11-027-892A-2733
; Sequence 2733, Application US/11027892A
; GENERAL INFORMATION:
;  APPLICANT: Doucette-Stamm, Lynn
;  APPLICANT:  Bush, David
;  APPLICANT:  Zeng, Qiandong
;  APPLICANT:  Opperman, Timothy
;  APPLICANT:  Houseweart, Chad Eric
;  TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE: 3687.1000-009
;  CURRENT APPLICATION NUMBER: US/11/027,892A
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: US 10/640,833
;  PRIOR FILING DATE: 2003-08-14
;  PRIOR APPLICATION NUMBER: US 09/583,110
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/107,433
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/085,131
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: US 60/051,553
;  PRIOR FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 5324
; SEQ ID NO 2733
;   LENGTH: 816
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-11-027-892A-2733

  Query Match             28.1%;  Score 45;  DB 7;  Length 816;
  Best Local Similarity   41.2%;  Pred. No. 2.7e+02;
  Matches    7;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 LGEAYEYPTFIQDLRNE 24
              :|: | |   |: |||::
Db        372 IGQLYRYQHFLADLRHD 388


RESULT 89
US-11-416-490-135
; Sequence 135, Application US/11416490
; GENERAL INFORMATION:
;  APPLICANT: ChromaGenics B.V.
;  APPLICANT:  Otte, Arie P.
;  APPLICANT:  Kwaks, Theodorus H.J.
;  APPLICANT:  Sewalt, Richard G.A.B.
;  APPLICANT:  van Blokland, Rik
;  TITLE OF INVENTION: Selection of host cells expressing protein at high levels
;  FILE REFERENCE: 0117 B US P00 CIP
;  CURRENT APPLICATION NUMBER: US/11/416,490
;  CURRENT FILING DATE:  2006-05-02
;  PRIOR APPLICATION NUMBER: US 11/269,525
;  PRIOR FILING DATE: 2005-11-07
;  PRIOR APPLICATION NUMBER: US 11/359,953
;  PRIOR FILING DATE: 2006-02-21
;  PRIOR APPLICATION NUMBER: US 60/626,301
;  PRIOR FILING DATE: 2004-11-08
;  PRIOR APPLICATION NUMBER: US 60/696,610
;  PRIOR FILING DATE: 2005-07-05
;  PRIOR APPLICATION NUMBER: EP 04105593.0
;  PRIOR FILING DATE: 2004-11-08
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 135
;   LENGTH: 397
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-11-416-490-135

  Query Match             27.8%;  Score 44.5;  DB 7;  Length 397;
  Best Local Similarity   28.1%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    8;  Mismatches   12;  Indels    3;  Gaps    1;

Qy          1 YNTVSFNLGEA---YEYPTFIQDLRNELAKGT 29
              | |  : || |   : ||| ::: :  : : |
Db        181 YETAHYMLGTAAGPHPYPTIVREFQRMIGEET 212


RESULT 90
PCT-US06-18535-24526
; Sequence 24526, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24526
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Gibberella zeae PH-1
PCT-US06-18535-24526

  Query Match             27.8%;  Score 44.5;  DB 1;  Length 470;
  Best Local Similarity   45.8%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    4;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          2 NTVSFNLGEAYEYPTFIQDLRNEL 25
              : | |  |  | || |:||| ::|
Db        296 DAVIFCTGFLYSYP-FLQDLDHKL 318


RESULT 91
US-11-431-855-24526
; Sequence 24526, Application US/11431855
; GENERAL INFORMATION:
```

```
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24526
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Gibberella zeae PH-1
US-11-431-855-24526

  Query Match             27.8%;  Score 44.5;  DB 7;  Length 470;
  Best Local Similarity   45.8%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    4;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          2 NTVSFNLGEAYEYPTFIQDLRNEL 25
              : | |  |  | || |:||| ::|
Db        296 DAVIFCTGFLYSYP-FLQDLDHKL 318


RESULT 92
US-10-527-571A-143
; Sequence 143, Application US/10527571A
; GENERAL INFORMATION:
;  APPLICANT: Syngenta Participations AG
;  APPLICANT:  Stam, Lynn
;  APPLICANT:  Kamdar, Kim
;  APPLICANT:  Spana, Eric
;  APPLICANT:  Bachmann, Jane
;  TITLE OF INVENTION: Nucleic Acid Sequences from Drosophila Melanogaster that Encode P
;  TITLE OF INVENTION:  Essential for Viability and Uses Thereof
;  FILE REFERENCE: 70131USPCT
;  CURRENT APPLICATION NUMBER: US/10/527,571A
;  CURRENT FILING DATE:  2005-03-14
;  PRIOR APPLICATION NUMBER: 60/422,377
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
;   LENGTH: 619
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-10-527-571A-143

  Query Match             27.8%;  Score 44.5;  DB 6;  Length 619;
  Best Local Similarity   41.7%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    3;  Mismatches    9;  Indels    9;  Gaps    3;

Qy          4 VSFNLG---EAYEYPTF-----IQDLRNE-LAKGTP 30
              | || |   :|||| :     |:|| |   | | |
Db        365 VGFNAGNGTQAYEYNPYSQNMVIRDLANRGWANGFP 400


RESULT 93
US-10-527-571B-143
; Sequence 143, Application US/10527571B
; GENERAL INFORMATION:
;  APPLICANT: Syngenta Participations AG
;  APPLICANT:  Stam, Lynn
;  APPLICANT:  Kamdar, Kim
;  APPLICANT:  Spana, Eric
;  APPLICANT:  Bachmann, Jane
;  TITLE OF INVENTION: Nucleic Acid Sequences from Drosophila Melanogaster that Encode P
;  TITLE OF INVENTION:  Essential for Viability and Uses Thereof
;  FILE REFERENCE: 70131WOPCT
;  CURRENT APPLICATION NUMBER: US/10/527,571B
;  CURRENT FILING DATE:  2005-03-14
;  PRIOR APPLICATION NUMBER: 60/422,377
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
;   LENGTH: 619
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-10-527-571B-143

  Query Match             27.8%;  Score 44.5;  DB 6;  Length 619;
  Best Local Similarity   41.7%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    3;  Mismatches    9;  Indels    9;  Gaps    3;

Qy          4 VSFNLG---EAYEYPTF-----IQDLRNE-LAKGTP 30
              | || |   :|||| :     |:|| |   | | |
Db        365 VGFNAGNGTQAYEYNPYSQNMVIRDLANRGWANGFP 400


RESULT 94
US-10-805-394A-5373
; Sequence 5373, Application US/10805394A
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/10/805,394A
;  CURRENT FILING DATE:  2004-03-22
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5373
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-805-394A-5373

  Query Match             27.5%;  Score 44;  DB 6;  Length 245;
  Best Local Similarity   47.1%;  Pred. No. 84;
  Matches    8;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         13 EYPTFIQDLRNELAKGT 29
              ::|  |:|  ||  |||
Db         88 KHPVDIEDFENEQGKGT 104


RESULT 95
PCT-US06-18535-30230
; Sequence 30230, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30230
;   LENGTH: 351
;   TYPE: PRT
;   ORGANISM: Chloroflexus aurantiacus
PCT-US06-18535-30230
```

```
  Query Match             27.5%;  Score 44;  DB 1;  Length 351;
  Best Local Similarity   50.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 TVSFNLGEAYEYPTFI 18
              ||| :  |||| ::
Db        223 TVSLHADPAYEYPYYL 238


RESULT 96
US-11-431-855-30230
; Sequence 30230, Application US/11431855
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30230
;   LENGTH: 351
;   TYPE: PRT
;   ORGANISM: Chloroflexus aurantiacus
US-11-431-855-30230

  Query Match             27.5%;  Score 44;  DB 7;  Length 351;
  Best Local Similarity   50.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 TVSFNLGEAYEYPTFI 18
              ||| :  |||| ::
Db        223 TVSLHADPAYEYPYYL 238


RESULT 97
US-60-838-415-21148
; Sequence 21148, Application US/60838415
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(54146)A
;  CURRENT APPLICATION NUMBER: US/60/838,415
;  CURRENT FILING DATE:  2006-08-17
;  NUMBER OF SEQ ID NOS: 30376
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21148
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Oenococcus oeni PSU-1
US-60-838-415-21148

  Query Match             27.5%;  Score 44;  DB 8;  Length 369;
  Best Local Similarity   40.7%;  Pred. No. 1.4e+02;
  Matches   11;  Conservative    4;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          4 VSFNLGEAYEYPTFIQDLRNELAKGTP 30
              | |:||  |:  :| |    :| |||
Db        225 VLFDLGTVYK--GYISDASRTVALGTP 249


RESULT 98
US-60-838-415-14961
; Sequence 14961, Application US/60838415
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(54146)A
;  CURRENT APPLICATION NUMBER: US/60/838,415
;  CURRENT FILING DATE:  2006-08-17
;  NUMBER OF SEQ ID NOS: 30376
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14961
;   LENGTH: 440
;   TYPE: PRT
;   ORGANISM: Methanosarcina mazei Go1
US-60-838-415-14961

  Query Match             27.5%;  Score 44;  DB 8;  Length 440;
  Best Local Similarity   36.0%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    3;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNEL 25
              |    |: | |  |  || |: |:
Db        189 YGMPFMNIDEPYGIPKIIQHLKKEI 213


RESULT 99
PCT-US06-30281-18413
; Sequence 18413, Application PC/TUS0630281
; GENERAL INFORMATION:
;  APPLICANT: Genizon BioSciences
;  TITLE OF INVENTION: GeneMap of the human genes associated with psoriasis
;  FILE REFERENCE: Abdelmajid Belouchi, John Verner Raelson, Walter Edward Bradley, Brunc
;    Paquin,
;    Quynh Nguyen-Huu, Pascal Croteau, Rene Allard, Randall David Little, Sophie
;    Debrus, Johanne Cousineau,
;    Tim Keith, Natali Henderson, Daniel Dubois, Paul Van Eerdewegh and Jonathan
;    Segal.
;  CURRENT APPLICATION NUMBER: PCT/US06/30281
;  CURRENT FILING DATE:  2006-08-11
;  NUMBER OF SEQ ID NOS: 40189
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18413
;   LENGTH: 479
;   TYPE: PRT
;   ORGANISM: Homosapiens
PCT-US06-30281-18413

  Query Match             27.5%;  Score 44;  DB 1;  Length 479;
  Best Local Similarity   31.8%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKG 28
              :||| |:: : :   ||  ::|
Db          8 SLGETYDFDSIMHYARNTFSRG 29


RESULT 100
PCT-US06-30281-18415
; Sequence 18415, Application PC/TUS0630281
; GENERAL INFORMATION:
;  APPLICANT: Genizon BioSciences
;  TITLE OF INVENTION: GeneMap of the human genes associated with psoriasis
;  FILE REFERENCE: Abdelmajid Belouchi, John Verner Raelson, Walter Edward Bradley, Brunc
;    Paquin,
;    Quynh Nguyen-Huu, Pascal Croteau, Rene Allard, Randall David Little, Sophie
;    Debrus, Johanne Cousineau,
;    Tim Keith, Natali Henderson, Daniel Dubois, Paul Van Eerdewegh and Jonathan
;    Segal.
;  CURRENT APPLICATION NUMBER: PCT/US06/30281
;  CURRENT FILING DATE:  2006-08-11
;  NUMBER OF SEQ ID NOS: 40189
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18415
;   LENGTH: 479
;   TYPE: PRT
;   ORGANISM: Homosapiens
PCT-US06-30281-18415

  Query Match             27.5%;  Score 44;  DB 1;  Length 479;
  Best Local Similarity   31.8%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 NLGEAYEYPTFIQDLRNELAKG 28
              :||| |:: : :   ||  ::|
```

Db 8 SLGETYDFDSIMHYARNTFSRG 29

Search completed: September 18, 2006, 19:31:11
Job time : 12.3911 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 17:38:01 ; Search time 235.57 Seconds
(without alignments)
1775.239 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_18092006_162712_11663/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss05h -USER=US10758902_@CGN_1_1_252_@runat_18092006_162712_11663
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	609	79.3	363	3	US-09-445-160B-8	Sequence 8, Appli
2	221.5	28.8	756	2	US-07-854-845B-1	Sequence 1, Appli
3	220.5	28.7	913	2	US-07-901-707-13	Sequence 13, Appl
4	220.5	28.7	913	2	US-07-988-430-13	Sequence 13, Appl
5	220.5	28.7	913	2	US-08-425-336-13	Sequence 13, Appl
6	220.5	28.7	913	2	US-08-488-113B-13	Sequence 13, Appl
7	220.5	28.7	913	2	US-08-477-484B-13	Sequence 13, Appl
8	220.5	28.7	913	2	US-08-646-360-13	Sequence 13, Appl
9	220.5	28.7	913	3	US-08-839-765-13	Sequence 13, Appl
10	220.5	28.7	913	3	US-09-136-389-13	Sequence 13, Appl
11	220.5	28.7	913	3	US-09-610-838-13	Sequence 13, Appl
12	220.5	28.7	913	3	US-09-711-485-13	Sequence 13, Appl
13	220.5	28.7	913	7	PCT-US92-09487-13	Sequence 13, Appl
14	211.5	27.5	762	2	US-07-854-845B-9	Sequence 9, Appli
15	190.5	24.8	962	2	US-08-324-301-14	Sequence 14, Appl
16	183.5	23.9	886	2	US-07-923-692C-3	Sequence 3, Appli
17	183.5	23.9	886	2	US-08-184-237-3	Sequence 3, Appli
18	183.5	23.9	886	2	US-08-482-920-3	Sequence 3, Appli
19	183.5	23.9	886	3	US-08-484-341-3	Sequence 3, Appli
20	183.5	23.9	886	3	US-08-483-502-3	Sequence 3, Appli
21	183.5	23.9	886	3	US-09-726-651A-3	Sequence 3, Appli
22	179.5	23.4	758	3	US-08-902-486-6	Sequence 6, Appli
23	179.5	23.4	762	3	US-09-601-667C-16	Sequence 16, Appl
24	179.5	23.4	762	3	US-09-601-667C-19	Sequence 19, Appl
25	179.5	23.4	768	3	US-09-601-667C-17	Sequence 17, Appl
26	179.5	23.4	768	3	US-09-601-667C-20	Sequence 20, Appl
27	179.5	23.4	1094	2	US-08-245-754A-1	Sequence 1, Appli
28	179.5	23.4	1094	2	US-08-597-731-1	Sequence 1, Appli
29	179.5	23.4	1499	3	US-08-902-486-14	Sequence 14, Appl
30	176.5	23.0	774	3	US-08-776-059-30	Sequence 30, Appl
31	176.5	23.0	1596	3	US-09-601-667C-15	Sequence 15, Appl
32	176.5	23.0	1596	3	US-09-601-667C-18	Sequence 18, Appl
33	176.5	23.0	1923	3	US-08-776-059-34	Sequence 34, Appl
34	174.5	22.7	837	3	US-09-627-165E-15	Sequence 15, Appl
35	171.5	22.3	762	3	US-09-627-165E-3	Sequence 3, Appli
36	169.5	22.1	705	3	US-08-776-059-38	Sequence 38, Appl
37	169	22.0	807	2	US-08-356-786-7	Sequence 7, Appli
38	169	22.0	1140	2	US-08-218-303-15	Sequence 15, Appl
39	169	22.0	1140	2	US-08-338-793D-60	Sequence 60, Appl
40	169	22.0	1605	2	US-08-356-786-9	Sequence 9, Appli
41	169	22.0	1731	3	US-09-785-921A-2	Sequence 2, Appli
42	169	22.0	1731	3	US-09-785-921A-3	Sequence 3, Appli
43	169	22.0	1731	5	US-10-618-560-2	Sequence 2, Appli
44	169	22.0	1731	5	US-10-618-560-3	Sequence 3, Appli
45	169	22.0	1805	3	US-09-785-921A-10	Sequence 10, Appl
46	169	22.0	1805	5	US-10-618-560-10	Sequence 10, Appl
47	168.5	21.9	762	3	US-09-627-165E-1	Sequence 1, Appli
48	168.5	21.9	852	2	US-09-069-330-1	Sequence 1, Appli
49	167	21.7	1698	3	US-09-785-921A-1	Sequence 1, Appli
50	167	21.7	1698	5	US-10-618-560-1	Sequence 1, Appli
51	167	21.7	1855	3	US-09-147-208-33	Sequence 33, Appl
52	167	21.7	1855	3	US-09-147-208-40	Sequence 40, Appl
53	167	21.7	1855	3	US-09-147-208-47	Sequence 47, Appl
54	167	21.7	1855	3	US-09-147-208-54	Sequence 54, Appl
55	167	21.7	1855	3	US-09-550-117A-33	Sequence 33, Appl
56	167	21.7	1855	3	US-09-550-117A-40	Sequence 40, Appl
57	167	21.7	1855	3	US-09-550-117A-47	Sequence 47, Appl
58	167	21.7	1855	3	US-09-550-117A-54	Sequence 54, Appl
59	167	21.7	1855	3	US-09-403-752A-3	Sequence 3, Appli
60	167	21.7	1855	3	US-09-403-752A-5	Sequence 5, Appli
61	167	21.7	1855	3	US-09-403-752A-7	Sequence 7, Appli
62	167	21.7	1855	3	US-09-403-752A-9	Sequence 9, Appli
63	167	21.7	1855	3	US-09-403-752A-13	Sequence 13, Appl
64	167	21.7	1855	3	US-09-403-752A-15	Sequence 15, Appl
65	167	21.7	1855	3	US-09-403-752A-17	Sequence 17, Appl
66	167	21.7	1855	3	US-09-403-752A-19	Sequence 19, Appl
67	167	21.7	1855	3	US-09-403-752A-21	Sequence 21, Appl
68	167	21.7	1855	3	US-09-403-752A-23	Sequence 23, Appl
69	167	21.7	1855	3	US-09-403-752A-25	Sequence 25, Appl
70	167	21.7	1855	3	US-09-403-752A-27	Sequence 27, Appl
71	167	21.7	1855	3	US-09-403-752A-29	Sequence 29, Appl
72	167	21.7	1855	3	US-09-403-752A-31	Sequence 31, Appl
73	167	21.7	1855	3	US-09-403-752A-33	Sequence 33, Appl
74	167	21.7	1855	3	US-09-403-752A-35	Sequence 35, Appl
75	167	21.7	1855	3	US-09-403-752A-37	Sequence 37, Appl
76	167	21.7	1855	3	US-09-403-752A-39	Sequence 39, Appl
77	167	21.7	1855	3	US-09-403-752A-48	Sequence 48, Appl
78	167	21.7	1855	3	US-09-403-752A-50	Sequence 50, Appl
79	167	21.7	1855	3	US-09-403-752A-52	Sequence 52, Appl
80	167	21.7	1855	3	US-09-403-752A-54	Sequence 54, Appl
81	167	21.7	1855	3	US-09-403-752A-74	Sequence 74, Appl

82	167	21.7	1855	3	US-09-403-752A-77	Sequence 77, Appl
83	167	21.7	1855	3	US-09-403-752A-80	Sequence 80, Appl
84	167	21.7	1855	3	US-09-403-752A-83	Sequence 83, Appl
85	167	21.7	1855	3	US-09-403-752A-86	Sequence 86, Appl
86	167	21.7	1855	3	US-09-403-752A-89	Sequence 89, Appl
87	167	21.7	1855	3	US-09-403-752A-92	Sequence 92, Appl
88	167	21.7	1855	3	US-09-403-752A-95	Sequence 95, Appl
89	167	21.7	1855	3	US-09-403-752A-98	Sequence 98, Appl
90	167	21.7	1855	3	US-09-403-752A-101	Sequence 101, App
91	167	21.7	1855	3	US-09-403-752A-104	Sequence 104, App
92	167	21.7	1855	3	US-09-403-752A-110	Sequence 110, App
93	167	21.7	1855	3	US-09-403-752A-113	Sequence 113, App
94	167	21.7	1855	3	US-09-403-752A-116	Sequence 116, App
95	167	21.7	1855	3	US-09-403-752A-119	Sequence 119, App
96	167	21.7	1855	3	US-09-403-752A-122	Sequence 122, App
97	167	21.7	1855	3	US-09-403-752A-125	Sequence 125, App
98	167	21.7	1855	3	US-09-551-151A-3	Sequence 3, Appli
99	167	21.7	1855	3	US-09-551-151A-5	Sequence 5, Appli
100	167	21.7	1855	3	US-09-551-151A-7	Sequence 7, Appli

ALIGNMENTS

```
RESULT 1
US-09-445-160B-8
; Sequence 8, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenza
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
;  FILE REFERENCE: Stirpe
;  CURRENT APPLICATION NUMBER: US/09/445,160B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/NL98/00336
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 8
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;  PUBLICATION INFORMATION:
US-09-445-160B-8

Alignment Scores:
Pred. No.:              2.33e-73        Length:         363
Score:                  609.00          Matches:        120
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            79.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-758-902-9 (1-149) x US-09-445-160B-8 (1-363)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361

RESULT 2
US-07-854-845B-1
; Sequence 1, Application US/07854845B
; Patent No. 5340732
;  GENERAL INFORMATION:
;    APPLICANT:  HABUKA, No. 5340732iyuki
;    APPLICANT:  MIYANO, Masashi
;    APPLICANT:  MATSUMOTO, Takashi
;    APPLICANT:  NOMA, Masana
;    TITLE OF INVENTION:  ANTIVIRAL PROTEIN
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH, & BIRCH
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22042
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/854,845B
;      FILING DATE:  20-MAR-1992
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy Jr., Gerald M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  42-194P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-205-8000
;      TELEFAX:  703-205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Mirabilis jalapa
US-07-854-845B-1

Alignment Scores:
Pred. No.:              1.94e-20        Length:         756
Score:                  221.50          Matches:        54
Percent Similarity:     55.9%           Conservative:   27
Best Local Similarity:  37.2%           Mismatches:     55
Query Match:            28.8%           Indels:         9
DB:                     2               Gaps:           4

US-10-758-902-9 (1-149) x US-07-854-845B-1 (1-756)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||           |||   :::||||||   ::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 84
```

```
Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||      |||      |||            |||:::|||   |||:::
Db         85 GTCGCAGACAAAACCGAACAGTGT-----------ACCATCCAGAAAATCTCTAAAACC 132

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                 :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||||:::   |||:::||||||:::||||||   |||      :::   |||
Db        193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
              ||||||   |||          |||                ::      |||||||||
Db        253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||      |||
Db        313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                 :::   |||||||||      ||||||:::::::::||||||   ||||||
Db        373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429

Qy        141 AlaIleTrpGlyLys 145
                 |||:::||||||
Db        430 AACATTTATGGCAAA 444

RESULT 3
US-07-901-707-13
; Sequence 13, Application US/07901707
; Patent No. 5376546
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Composition and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/901,707
;      FILING DATE:  19920619
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5376546and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27129/30910
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-5750
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-901-707-13

Alignment Scores:
Pred. No.:                3.46e-20        Length:          913
Score:                    220.50          Matches:         52
Percent Similarity:       59.9%           Conservative:    33
Best Local Similarity:    36.6%           Mismatches:      50
Query Match:              28.7%           Indels:          7
DB:                       2               Gaps:            3

US-10-758-902-9 (1-149) x US-07-901-707-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||              |||      |||      |||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||   |||          |||      :::|||:::            ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::            :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
              |||   :::   |||      :::   |||.    |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::::||||||:::   |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
                 ::::::
Db        487 TTGTTT 492

RESULT 4
US-07-988-430-13
; Sequence 13, Application US/07988430
; Patent No. 5416202
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/988,430
;       FILING DATE:  19921209
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  No. 5416202and, Greta E.
;       REGISTRATION NUMBER:  35302
;       REFERENCE/DOCKET NUMBER:  31133
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 346-5750
;       TELEFAX:  (312) 984-9740
;       TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  913 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-07-988-430-13

Alignment Scores:
Pred. No.:              3.46e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-07-988-430-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||            |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 5
US-08-425-336-13
```

```
; Sequence 13, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-425-336-13

Alignment Scores:
Pred. No.:              3.46e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-08-425-336-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||            |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
```

```
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101

Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121

Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141

Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143

Db        487 TTGTTT 492
```

RESULT 6
US-08-488-113B-13
; Sequence 13, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-488-113B-13

Alignment Scores:

Pred. No.:	3.46e-20	Length:	913
Score:	220.50	Matches:	52
Percent Similarity:	59.9%	Conservative:	33
Best Local Similarity:	36.6%	Mismatches:	50
Query Match:	28.7%	Indels:	7
DB:	2	Gaps:	3

US-10-758-902-9 (1-149) x US-08-488-113B-13 (1-913)

```
Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21

Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41

Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61

Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81

Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101

Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121

Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141

Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143

Db        487 TTGTTT 492
```

RESULT 7
US-08-477-484B-13
; Sequence 13, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995

```
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-477-484B-13

Alignment Scores:
Pred. No.:              3.46e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-08-477-484B-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||        |||     |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||              |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||::::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
```

```
Db         487 TTGTTT 492

RESULT 8
US-08-646-360-13
; Sequence 13, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-646-360-13

Alignment Scores:
Pred. No.:              3.46e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-08-646-360-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||        |||     |||      ||||||:::|||
```

```
Db        82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy        22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
             |||       |||                 |||       :::|||:::          ||||||
Db       142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy        42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
             :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db       202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy        62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
             ||||||||||||||||||:::||||||||||||   |||:::                 :::
Db       262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy        82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
             |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db       310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy       102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
               |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db       370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy       122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                 |||:::::::::::::||||||:::       |||       :::|||
Db       427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy       142 IleTrp 143
             ::::::
Db       487 TTGTTT 492

RESULT 9
US-08-839-765-13
; Sequence 13, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-839-765-13

Alignment Scores:
Pred. No.:                3.46e-20        Length:          913
Score:                    220.50          Matches:         52
Percent Similarity:       59.9%           Conservative:    33
Best Local Similarity:    36.6%           Mismatches:      50
Query Match:              28.7%           Indels:          7
DB:                       3               Gaps:            3

US-10-758-902-9 (1-149) x US-08-839-765-13 (1-913)

Qy         4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
             |||:::|||:::|||         |||       |||       ||||||:::|||
Db        82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy        22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
             |||       |||                 |||       :::|||:::          ||||||
Db       142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy        42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
             :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db       202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy        62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
             ||||||||||||||||||:::||||||||||||   |||:::                 :::
Db       262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy        82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
             |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db       310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy       102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
               |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db       370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy       122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                 |||:::::::::::::||||||:::       |||       :::|||
Db       427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy       142 IleTrp 143
             ::::::
Db       487 TTGTTT 492

RESULT 10
US-09-136-389-13
; Sequence 13, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
```

```
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60661
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/136,389
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/646,360
;       FILING DATE:  13-MAY-1996
;       APPLICATION NUMBER:  PCT/US94/05348
;       FILING DATE:  12-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  200-70.P4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  913 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-136-389-13

Alignment Scores:
Pred. No.:              3.46e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     3               Gaps:           3

US-10-758-902-9 (1-149) x US-09-136-389-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||             |||       |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||                |||       :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::                :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
              |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                      |||:::::::::::::||||||:::       |||       :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 11
US-09-610-838-13
; Sequence 13, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/610,838
;      FILING DATE:  06-JUL-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:  18-AUG-1998
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
```

```
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-610-838-13

Alignment Scores:
Pred. No.:              3.46e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     3               Gaps:           3

US-10-758-902-9 (1-149) x US-09-610-838-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||           |||     |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::               :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 12
US-09-711-485-13
; Sequence 13, Application US/09711485
; Patent No. 6649742
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/711,485
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/839,765
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-711-485-13

Alignment Scores:
Pred. No.:              3.46e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     3               Gaps:           3

US-10-758-902-9 (1-149) x US-09-711-485-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||           |||     |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||               |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::               :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
```

```
Db        487 TTGTTT 492

RESULT 13
PCT-US92-09487-13
; Sequence 13, Application PC/TUS9209487
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/09487
;      FILING DATE:  19921104
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US92-09487-13

Alignment Scores:
Pred. No.:              3.46e-20        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     7               Gaps:           3

US-10-758-902-9 (1-149) x PCT-US92-09487-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||::|||:::|||             |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||          |||     :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::               :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||     :::   |||       |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                      |||::::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 14
US-07-854-845B-9
; Sequence 9, Application US/07854845B
; Patent No. 5340732
;  GENERAL INFORMATION:
;    APPLICANT:  HABUKA, No. 5340732iyuki
;    APPLICANT:  MIYANO, Masashi
;    APPLICANT:  MATSUMOTO, Takashi
;    APPLICANT:  NOMA, Masana
;    TITLE OF INVENTION:  ANTIVIRAL PROTEIN
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH, & BIRCH
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22042
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/854,845B
;      FILING DATE:  20-MAR-1992
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy Jr., Gerald M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  42-194P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-205-8000
;      TELEFAX:  703-205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  762 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Mirabilis jalapa
US-07-854-845B-9

Alignment Scores:
```

```
Pred. No.:              4.44e-19        Length:         762
Score:                  211.50          Matches:        53
Percent Similarity:     55.2%           Conservative:   27
Best Local Similarity:  36.6%           Mismatches:     56
Query Match:            27.5%           Indels:         9
DB:                     2               Gaps:           4

US-10-758-902-9 (1-149) x US-07-854-845B-9 (1-762)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||   :::|||                |||   :::||||||   :::::::|||   :::
Db         25 TCTCTGGACCTGAACAACCCGACCACCTACCTGTCTTTCATAACGAATATCCGTACGAAA 84

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp--- 43
              :::|||      |||                     |||:::|||   |||:::
Db         85 GTCGCAGACAAAACCGAA----------CAGTCGACCATCCAGAAAATCTCTAAAACC 132

Qy         44 ---AspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
                 :::|||:::      :::|||:::      :::|||   :::   :::   :::
Db        133 TTCACCCAGCGTTACTCTTACATAGACTTGATCGTGAGCTCGACGCAGAAAATCACCCTA 192

Qy         63 AlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAsp 82
              |||||||||:::   |||:::||||||:::||||||   |||      :::   |||
Db        193 GCTATCGACATGGCTGACCTGTACGTTCTGGGTTACTCTGACATCGCTAATAACAAGGGT 252

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              ||||||   |||         |||                 :::      ||||||||
Db        253 CGTGCTTTCTTCTTCAAAGACGTGACTGAGGCTGTTGCGAACAATTTCTTCCCGGGAGCT 312

Qy        103 ------ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                   |||||||||:::   |||||||||   |||||||||      |||
Db        313 ACAGGTACTAATCGTATCAAATTAACCTTTACAGGTTCTTATGGCGATCTCGAGAAAAAC 372

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                 :::   |||||||||      ||||||:::::::::||||||   ||||||
Db        373 GGCGGACTA---CGTAAGGACAATCCCCTAGGTATCTTCCGTCTGGAAAACTCGATAGTT 429

Qy        141 AlaIleTrpGlyLys 145
                |||:::||||||
Db        430 AACATTTATGGCAAA 444

RESULT 15
US-08-324-301-14
; Sequence 14, Application US/08324301
; Patent No. 5597569
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    APPLICANT:  Gawlak, Susan L.
;    APPLICANT:  Marquardt, Hans
;    TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;    TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONICA DIOICA
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,301
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/141,891
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0109A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-728-4800
;      TELEFAX:  206-727-3601
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  962 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
;      TISSUE TYPE:  leaf
US-08-324-301-14

Alignment Scores:
Pred. No.:              4.29e-16        Length:         962
Score:                  190.50          Matches:        50
Percent Similarity:     57.8%           Conservative:   24
Best Local Similarity:  39.1%           Mismatches:     47
Query Match:            24.8%           Indels:         7
DB:                     2               Gaps:           4

US-10-758-902-9 (1-149) x US-08-324-301-14 (1-962)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro---ValCys 32
              |||   |||||||||:::::|||||   :::|||      |||||||||   |||
Db        133 TACAAAACTTTTATAAGGAATCTGCGCACCAAACTCACGGTTGGAACTCCAAGGGTGTAC 192

Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
                 :::||||||                |||          ||||||   ||||||   :::
Db        193 GATATACCTGTCCTGAGAAACGCAGCAGCCGGGCTCGCGCGCTTTCAATTAGTTACCCTC 252

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
              |||      :::   ::::::|||   ||||||:::||||||   :::||||||||||||
Db        253 ACAAATTACAATGGCGAATCTGTCACTGTGGCTTTAGATGTAGTGAACGTGTACGTTGTT 312

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
              |||:::                  :::   |||   ||||||          |||
Db        313 GCATATCGA------------GCTGGAAACACTGCTTACTTTCTCGCAGATGCATCAACA 360

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||   |||:::   |||   |||   |||   :::   |||
Db        361 GAAGCCAACAATGTGTTGTTTGCAGGCATC---AATCATGTAAGACTTCCTTATGGAGGG 417

Qy        113 SerTyrGlnLysLeuValAsnAlaAla---LysValAspArgLysAspLeuGluLeuGly 131
              :::|||      |||      ||||||   ::::::   |||:::::::::|||||||||
Db        418 AATTACGATGGCCTTGAGACAGCTGCAGGCAGAATTTCGAGGGAAAATATTGAACTTGGA 477

Qy        132 ValTyrLysLeuGluPheSerIle 139
                  ::::::      :::|||
Db        478 TTTTCCGAAATAAGTAGTGCCATT 501

RESULT 16
US-07-923-692C-3
; Sequence 3, Application US/07923692C
; Patent No. 5316931
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Limbach & Limbach
```

```
;      STREET:  2001 Ferry Building
;      CITY:  San Francisco
;      STATE:  CAL
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent in Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,692C
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  BIOG-20121
;      REFERENCE/DOCKET NUMBER:  USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-433-4150
;      TELEFAX:  415-433-8716
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  886 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chinese cucumber
;    IMMEDIATE SOURCE:
;      CLONE:  alpha-trichosanthin
;    FEATURE:
;      NAME/KEY:  CDS (B) LOCATION: 8. .877
;      LOCATION:  8. .877
US-07-923-692C-3

Alignment Scores:
Pred. No.:              3.39e-15        Length:         886
Score:                  183.50          Matches:        44
Percent Similarity:     53.5%           Conservative:   32
Best Local Similarity:  31.0%           Mismatches:     61
Query Match:            23.9%           Indels:         5
DB:                     2               Gaps:           2

US-10-758-902-9 (1-149) x US-07-923-692C-3 (1-886)
```

```
Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||     |||          |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||                 :::       :::|||:::          ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||       :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::           |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                       |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::|||||||||   :::   |||:::|||:::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496

RESULT 17
US-08-184-237-3
; Sequence 3, Application US/08184237
; Patent No. 5589367
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Limbach & Limbach
;      STREET:  2001 Ferry Building
;      CITY:  San Francisco
;      STATE:  CAL
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent in Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,237
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 923,692
;      FILING DATE:  31-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  BIOG-20121  USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-433-4150
;      TELEFAX:  415-433-8716
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  886 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chinese cucumber
;    IMMEDIATE SOURCE:
;      CLONE:  alpha-trichosanthin
;    FEATURE:
;      NAME/KEY:  CDS (B) LOCATION: 8. .877
;      LOCATION:  8. .877
US-08-184-237-3

Alignment Scores:
Pred. No.:              3.39e-15      Length:          886
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     2             Gaps:            2

US-10-758-902-9 (1-149) x US-08-184-237-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||                :::      :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::::||||||:::            |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::          |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::||||||||||   :::   |||:::|||::::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                        |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                 ::::::
Db        491 TTGTTT 496

RESULT 18
US-08-482-920-3
; Sequence 3, Application US/08482920
; Patent No. 5866785
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent in Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,920
;      FILING DATE:  07-JUNE-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 184,237
;      FILING DATE:  19-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  8129-112
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  886 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chinese cucumber
;    IMMEDIATE SOURCE:
;      CLONE:  alpha-trichosanthin
;    FEATURE:
;      NAME/KEY:  CDS (B) LOCATION: 8. .877
;      LOCATION:  8. .877
US-08-482-920-3

Alignment Scores:
Pred. No.:              3.39e-15        Length:         886
Score:                  183.50          Matches:        44
Percent Similarity:     53.5%           Conservative:   32
Best Local Similarity:  31.0%           Mismatches:     61
Query Match:            23.9%           Indels:         5
DB:                     2               Gaps:           2

US-10-758-902-9 (1-149) x US-08-482-920-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||              :::      :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::  :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::::||||||:::           |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::          |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496

RESULT 19
US-08-484-341-3
; Sequence 3, Application US/08484341
;   GENERAL INFORMATION:
;        APPLICANT: Donson, Jon
;                   Dawson, William O.
;                   Grantham, George L.
;                   Turpen, Thomas H.
;                   Turpen, Ann Myers
;                   Garger, Stephen J.
;                   Grill, Laurence K.
;        TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Limbach & Limbach
;             STREET: 2001 Ferry Building
;             CITY: San Francisco
;             STATE: CAL
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Patent in Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/484,341
;             FILING DATE: 07-Jun-1995
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/184,237
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 600,244
;             FILING DATE: 22-OCT-1990
;             APPLICATION NUMBER: US 641,617
;             FILING DATE: 16-JAN-1991
;             APPLICATION NUMBER: US 310,881
;             FILING DATE: 17-FEB-1989
;             APPLICATION NUMBER: US 160,766
;             FILING DATE: 26-FEB-1988
;             APPLICATION NUMBER: US 160,771
;             FILING DATE: 26-FEB-1988
;             APPLICATION NUMBER: US 347,637
;             FILING DATE: 05-MAY-1989
;             APPLICATION NUMBER: US 363,138
;             FILING DATE: 08-JUN-1989
;             APPLICATION NUMBER: US 219,279
;             FILING DATE: 15-JUL-1988
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Halluin, Albert P.
;             REGISTRATION NUMBER: 28,957
;             REFERENCE/DOCKET NUMBER: BIOG-20121  USA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-433-4150
;             TELEFAX: 415-433-8716
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 886 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Chinese cucumber
;        IMMEDIATE SOURCE:
;             CLONE: alpha-trichosanthin
;        FEATURE:
;             NAME/KEY:  CDS (B) LOCATION: 8. .877
;             LOCATION:  8. .877
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-484-341-3

Alignment Scores:
Pred. No.:              3.39e-15        Length:         886
Score:                  183.50          Matches:        44
Percent Similarity:     53.5%           Conservative:   32
Best Local Similarity:  31.0%           Mismatches:     61
Query Match:            23.9%           Indels:         5
DB:                     3               Gaps:           2

US-10-758-902-9 (1-149) x US-08-484-341-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
```

```
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61

Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81

Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101

Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121

Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141

Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143

Db        491 TTGTTT 496
```

RESULT 20
US-08-483-502-3
; Sequence 3, Application US/08483502
; Patent No. 6284492
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William O.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/739,143
; FILING DATE:
; APPLICATION NUMBER: US 600,244
; FILING DATE: 22-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 641,617
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 310,881
; FILING DATE: 17-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,766
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,771
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 347,637
; FILING DATE: 05-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 363,138
; FILING DATE: 08-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 219,279
; FILING DATE: 15-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 18604-090574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Chinese cucumber
; IMMEDIATE SOURCE:
; CLONE: alpha-trichosanthin
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 8..877
US-08-483-502-3

Alignment Scores:

Pred. No.:	3.39e-15	Length:	886
Score:	183.50	Matches:	44
Percent Similarity:	53.5%	Conservative:	32
Best Local Similarity:	31.0%	Mismatches:	61
Query Match:	23.9%	Indels:	5
DB:	3	Gaps:	2

US-10-758-902-9 (1-149) x US-08-483-502-3 (1-886)

```
Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21

Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41

Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61

Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81

Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101

Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121

Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141

Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490
```

```
Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496

RESULT 21
US-09-726-651A-3
; Sequence 3, Application US/09726651A
; Patent No. 6448046
; GENERAL INFORMATION:
;  APPLICANT: Donson, Jon
;  APPLICANT:  DAWSON, William O.
;  APPLICANT:  GRANTHAM, GEORGE L.
;  APPLICANT:  TURPEN, Thomas H.
;  APPLICANT:  TURPEN, Ann M.
;  APPLICANT:  GARGER, Stephen J.
;  APPLICANT:  GRILL, Laurence K.
;  TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
;  FILE REFERENCE: 008010023CNUS01
;  CURRENT APPLICATION NUMBER: US/09/726,651A
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: 08/483,502
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/184,237
;  PRIOR FILING DATE: 1994-01-19
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 886
;   TYPE: DNA
;   ORGANISM: Chinese Cucumber
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (8)...(877)
;   OTHER INFORMATION: Clone:alpha-trichosanthin
US-09-726-651A-3

Alignment Scores:
Pred. No.:              3.39e-15      Length:          886
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     3             Gaps:            2

US-10-758-902-9 (1-149) x US-09-726-651A-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              :::     :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||::::::||||||:::          |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProProGly 101
                    |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||::::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496

RESULT 22
US-08-902-486-6
; Sequence 6, Application US/08902486
; Patent No. 6140075
;  GENERAL INFORMATION:
;    APPLICANT:  Russel, David R.
;    APPLICANT:  Fuller, James T.
;    TITLE OF INVENTION:  METHOD FOR PRODUCING ANTIBODIES AND
;    TITLE OF INVENTION:  PROTEIN TOXINS IN PLANT CELLS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/902,486
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  670513.90261
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  758 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..748
US-08-902-486-6

Alignment Scores:
Pred. No.:              9.5e-15       Length:          758
Score:                  179.50        Matches:         44
Percent Similarity:     54.5%         Conservative:    34
Best Local Similarity:  30.8%         Mismatches:      58
Query Match:            23.4%         Indels:          7
DB:                     3             Gaps:            3

US-10-758-902-9 (1-149) x US-08-902-486-6 (1-758)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||:::::|||
Db          9 GTGAGCTTTCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 68

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
```

```
Db         69 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 128

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61

Db        129 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 188

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81

Db        189 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 236

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100

Db        237 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 296

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120

Db        297 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 356

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140

Db        357 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 416

Qy        141 AlaIleTrp 143

Db        417 ACTTTGTAT 425
```

RESULT 23
US-09-601-667C-16
; Sequence 16, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667C
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 16
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin A1
US-09-601-667C-16

Alignment Scores:

Pred. No.:	9.57e-15	Length:	762
Score:	179.50	Matches:	50
Percent Similarity:	57.1%	Conservative:	26
Best Local Similarity:	37.6%	Mismatches:	48
Query Match:	23.4%	Indels:	9
DB:	3	Gaps:	4

US-10-758-902-9 (1-149) x US-09-601-667C-16 (1-762)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32

Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49

Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69

Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGGTTACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89

Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109

Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129

Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142

Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426
```

RESULT 24
US-09-601-667C-19
; Sequence 19, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667C
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 19
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin A1
US-09-601-667C-19

Alignment Scores:

Pred. No.:	9.57e-15	Length:	762
Score:	179.50	Matches:	50
Percent Similarity:	57.1%	Conservative:	26
Best Local Similarity:	37.6%	Mismatches:	48
Query Match:	23.4%	Indels:	9
DB:	3	Gaps:	4

US-10-758-902-9 (1-149) x US-09-601-667C-19 (1-762)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32

Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49

Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69

Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTGTTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89

Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109

Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330
```

```
Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 25
US-09-601-667C-17
; Sequence 17, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 17
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-09-601-667C-17

Alignment Scores:
Pred. No.:              9.67e-15      Length:          768
Score:                  179.50        Matches:         49
Percent Similarity:     56.7%         Conservative:    27
Best Local Similarity:  36.6%         Mismatches:      49
Query Match:            23.4%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-601-667C-17 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||          :::   ::::::      |||||||||||||||:::
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGATCACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThr---AsnArgValThrLeu 108
              |||      |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGCACCACCCGAGATAGATCCTCTCTC 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||      |||          |||          |||      :::
Db        334 CCATTCACTGGAAGCTACACCGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATC 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCTCTCGGTATAGAGCAACTCATTCAATCCGTCTCTGCGCTT 432
```

```
RESULT 26
US-09-601-667C-20
; Sequence 20, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 20
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-09-601-667C-20

Alignment Scores:
Pred. No.:              9.67e-15      Length:          768
Score:                  179.50        Matches:         49
Percent Similarity:     56.7%         Conservative:    27
Best Local Similarity:  36.6%         Mismatches:      49
Query Match:            23.4%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-601-667C-20 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||          :::   ::::::      |||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTATTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG------------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThr---AsnArgValThrLeu 108
              |||      |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGTACAACACGGGATAGAAGTTCTTTG 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||      |||          |||          |||      :::
Db        334 CCTTTTACTGGTTCTTATACAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATT 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCATTGGGAATTGAGCAGTTGATCCAGAGTGTTTCTGCTTTG 432

RESULT 27
US-08-245-754A-1
; Sequence 1, Application US/08245754A
; Patent No. 5541110
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    TITLE OF INVENTION:  Cloning and Expression of a Gene
;    TITLE OF INVENTION:  Encoding Bryodin 1 From Bryonia dioica
;    NUMBER OF SEQUENCES:  16
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Aveune
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/245,754A
;      FILING DATE:  06-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0124
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 728-4800
;      TELEFAX:  (206) 727-3601
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1094 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
US-08-245-754A-1

Alignment Scores:
Pred. No.:              1.59e-14        Length:         1094
Score:                  179.50          Matches:        44
Percent Similarity:     54.5%           Conservative:   34
Best Local Similarity:  30.8%           Mismatches:     58
Query Match:            23.4%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-08-245-754A-1 (1-1094)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||  |||      |||             |||      ||||||:::::|||
Db        116 GTTAGCTTCCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 175

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                 |||      :::|||:::         :::|||
Db        176 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 235

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::        |||:::   |||:::   :::|||      :::   :::|||:::
Db        236 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 295

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||:::::||||||
Db        296 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 343

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||  :::   |||  ::::::          :::|||  :::|||
Db        344 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 403

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                     :::||||||||||   :::   |||:::|||:::::|||      |||
Db        404 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 463

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||          |||:::::::::   ||||||:::     |||:::   :::|||
Db        464 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 523

Qy        141 AlaIleTrp 143
                 ::::::
Db        524 ACTTTGTAT 532

RESULT 28
US-08-597-731-1
; Sequence 1, Application US/08597731
; Patent No. 5932447
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    TITLE OF INVENTION:  Cloning and Expression of a Gene
;    TITLE OF INVENTION:  Encoding Bryodin 1 From Bryonia dioica
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Aveune
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/597,731
;      FILING DATE:  07-FEB-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/245,754
;      FILING DATE:  06-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0124
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 728-4800
;      TELEFAX:  (206) 727-3601
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1094 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
US-08-597-731-1

Alignment Scores:
Pred. No.:              1.59e-14        Length:         1094
Score:                  179.50          Matches:        44
Percent Similarity:     54.5%           Conservative:   34
Best Local Similarity:  30.8%           Mismatches:     58
Query Match:            23.4%           Indels:         7
DB:                     2               Gaps:           3

US-10-758-902-9 (1-149) x US-08-597-731-1 (1-1094)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||  |||      |||             |||      ||||||:::::|||
Db        116 GTTAGCTTCCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 175

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                 |||      :::|||:::         :::|||
Db        176 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 235

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::        |||:::   |||:::   :::|||      :::   :::|||:::
Db        236 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 295
```

```
Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||:::::||:||||
Db        296 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 343

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||   :::   |||   ::::::                   :::|||   :::|||
Db        344 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 403

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                  :::|||||||||   :::   |||:::|||:::::|||      |||
Db        404 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 463

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||         |||:::::::::   ||||||:::      |||:::   :::|||
Db        464 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 523

Qy        141 AlaIleTrp 143
                 ::::::
Db        524 ACTTTGTAT 532

RESULT 29
US-08-902-486-14
; Sequence 14, Application US/08902486
; Patent No. 6140075
;  GENERAL INFORMATION:
;    APPLICANT:  Russel, David R.
;    APPLICANT:  Fuller, James T.
;    TITLE OF INVENTION:  METHOD FOR PRODUCING ANTIBODIES AND
;    TITLE OF INVENTION:  PROTEIN TOXINS IN PLANT CELLS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/902,486
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  670513.90261
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1499 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..1493
US-08-902-486-14

Alignment Scores:
Pred. No.:              2.47e-14        Length:         1499
Score:                  179.50          Matches:        44
Percent Similarity:     54.5%           Conservative:   34
Best Local Similarity:  30.8%           Mismatches:     58
Query Match:            23.4%           Indels:         7
DB:                     3               Gaps:           3

US-10-758-902-9 (1-149) x US-08-902-486-14 (1-1499)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||          |||      ||||||::::::|||
Db          9 GTGAGCTTTCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 68

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              |||      :::|||:::         :::|||
Db         69 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 128

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::        |||:::   |||:::   :::|||      :::   :::|||:::
Db        129 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 188

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||:::::||||||
Db        189 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 236

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||   :::   |||   ::::::                   :::|||   :::|||
Db        237 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 296

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                  :::|||||||||   :::   |||:::|||:::::|||      |||
Db        297 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 356

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||         |||:::::::::   ||||||:::      |||:::   :::|||
Db        357 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 416

Qy        141 AlaIleTrp 143
                 ::::::
Db        417 ACTTTGTAT 425

RESULT 30
US-08-776-059-30
; Sequence 30, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
;  APPLICANT: LENTZEN, Hans
;  APPLICANT: ECK, Jurgen
;  APPLICANT: BAUR, Axel
;  APPLICANT: ZINKE, Holger
;  TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
;  FILE REFERENCE: 674503-2003
;  CURRENT APPLICATION NUMBER: US/08/776,059B
;  CURRENT FILING DATE: 1999-06-19
;  EARLIER APPLICATION NUMBER: PCT/EP96/02273
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 95109949.8
;  EARLIER FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Viscum album
US-08-776-059-30

Alignment Scores:
Pred. No.:              2.49e-14        Length:         774
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     3               Gaps:           4

US-10-758-902-9 (1-149) x US-08-776-059-30 (1-774)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111
```

```
Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::     |||||||||||||||::::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||  ||||||           |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||  |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||       :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 31
US-09-601-667C-15
; Sequence 15, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 15
;   LENGTH: 1596
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MLA-I
US-09-601-667C-15

Alignment Scores:
Pred. No.:              6.86e-14      Length:          1596
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-601-667C-15 (1-1596)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::     |||||||||||||||::::::
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||  ||||||           |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||  |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||       :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 32
US-09-601-667C-18
; Sequence 18, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 18
;   LENGTH: 1596
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MLI (matched)
US-09-601-667C-18

Alignment Scores:
Pred. No.:              6.86e-14      Length:          1596
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-601-667C-18 (1-1596)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::     |||||||||||||||::::::
Db        166 GTTGAATTGACTAACCAAGGAGGTGATAGTATTACTGCTGCTATTGATGTGACTAACCTT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||  ||||||           |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||  |||   |||   |||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||       :::
```

```
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 33
US-08-776-059-34
; Sequence 34, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
;  APPLICANT: LENTZEN, Hans
;  APPLICANT: ECK, Jurgen
;  APPLICANT: BAUR, Axel
;  APPLICANT: ZINKE, Holger
;  TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
;  FILE REFERENCE: 674503-2003
;  CURRENT APPLICATION NUMBER: US/08/776,059B
;  CURRENT FILING DATE: 1999-06-19
;  EARLIER APPLICATION NUMBER: PCT/EP96/02273
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 95109949.8
;  EARLIER FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
;   LENGTH: 1923
;   TYPE: DNA
;   ORGANISM: Viscum album
US-08-776-059-34

Alignment Scores:
Pred. No.:              8.9e-14       Length:          1923
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-08-776-059-34 (1-1923)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db        199 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 258

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        259 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 318

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||               ::::::      |||||||||||||||::::::
Db        319 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 378

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        379 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 426

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        427 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 483

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        484 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 540

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        541 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 579

RESULT 34
US-09-627-165E-15
; Sequence 15, Application US/09627165E
; Patent No. 6846913
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jong-Bae
;  TITLE OF INVENTION: CRUDE EXTRACT FROM Viscum album coloratum, AND PROTEINS
;  TITLE OF INVENTION:  AND LECTINS ISOLATED THEREFROM
;  FILE REFERENCE: Korean Mistletoe Lectin
;  CURRENT APPLICATION NUMBER: US/09/627,165E
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 15
;   LENGTH: 837
;   TYPE: DNA
;   ORGANISM: Viscum album coloratum
US-09-627-165E-15

Alignment Scores:
Pred. No.:              5.19e-14      Length:          837
Score:                  174.50        Matches:         49
Percent Similarity:     55.6%         Conservative:    25
Best Local Similarity:  36.8%         Mismatches:      50
Query Match:            22.7%         Indels:          9
DB:                     3             Gaps:            4

US-10-758-902-9 (1-149) x US-09-627-165E-15 (1-837)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         19 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 78

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db         79 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCGGATGCGCAAAGATTTGTGTTG 138

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||               ::::::      |||||||||||||||::::::
Db        139 GTGGAACTCACCAATCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 198

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        199 TACGTGGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 246

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        247 GCACCAGACGGCGCGGAAAGGCATCTCTTCACCGGC---ACCACCAGATCCTCTCTCCCA 303

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||   |||||||||      |||         |||         |||      :::
Db        304 TTCACCGGAAGCTACACAGATCTGGAGCGATACGCCGGT---CATAGGGACCAGATCCCT 360

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        361 CTGGGTATAGAGGAACTCATTCAATCCGTCTCGGCGCTT 399

RESULT 35
US-09-627-165E-3
; Sequence 3, Application US/09627165E
; Patent No. 6846913
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jong-Bae
;  TITLE OF INVENTION: CRUDE EXTRACT FROM Viscum album coloratum, AND PROTEINS
;  TITLE OF INVENTION:  AND LECTINS ISOLATED THEREFROM
;  FILE REFERENCE: Korean Mistletoe Lectin
;  CURRENT APPLICATION NUMBER: US/09/627,165E
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 3
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Viscum album coloratum
;   FEATURE:
US-09-627-165E-3

Alignment Scores:
Pred. No.:              1.16e-13      Length:          762
```

```
Score:                  171.50          Matches:        47
Percent Similarity:     57.1%           Conservative:   29
Best Local Similarity:  35.3%           Mismatches:     48
Query Match:            22.3%           Indels:         9
DB:                     3               Gaps:           4

US-10-758-902-9 (1-149) x US-09-627-165E-3 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              :::|||      ||||||      ||||||:::   ::::::   |||:::
Db         46 CAATATTTCAAGTTCATCACGCTTCTCCGAGATCATGTCTCAAGCGGAAGCTTGTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              |||:::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 CAAATACCACTCTTGCGGCAGTCTACTGTCCCCGTCTCGGATACGCAGAGATTTGTGTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||:::::::::                 ::::::      |||||||||||||||:::::
Db        166 GTGGAACTCAGCAATCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  :::::::::   ||||||
Db        226 TACGTGGTGGCTTACCAA------------GCAGGCAACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCTCGCGGCGCGGAAACGTATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||       |||           |||           |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCTCGGCCCTT 426

RESULT 36
US-08-776-059-38
; Sequence 38, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
;  APPLICANT: LENTZEN, Hans
;  APPLICANT: ECK, Jurgen
;  APPLICANT: BAUR, Axel
;  APPLICANT: ZINKE, Holger
;  TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
;  FILE REFERENCE: 674503-2003
;  CURRENT APPLICATION NUMBER: US/08/776,059B
;  CURRENT FILING DATE: 1999-06-19
;  EARLIER APPLICATION NUMBER: PCT/EP96/02273
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 95109949.8
;  EARLIER FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
;   LENGTH: 705
;   TYPE: DNA
;   ORGANISM: Viscum album
US-08-776-059-38

Alignment Scores:
Pred. No.:              1.94e-13        Length:         705
Score:                  169.50          Matches:        47
Percent Similarity:     57.4%           Conservative:   27
Best Local Similarity:  36.4%           Mismatches:     46
Query Match:            22.1%           Indels:         9
DB:                     3               Gaps:           4

US-10-758-902-9 (1-149) x US-08-776-059-38 (1-705)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||      ||||||:::   ::::::   |||:::         ::::::|||:::

Db          7 TTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAATGAGATACCACTC 66

Qy         37 ThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeuValAspIleThr 53
                    |||:::         ::::::|||   :::|||||||||||||||:::::|||
Db         67 TTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTGGTGGAGCTCACC 126

Qy         54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73
                              ::::::      |||||||||||||||:::::|||||||||
Db        127 AACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTGTACGTCGTGGCT 186

Qy         74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93
              ||||||                  |||::::::   ||||||          |||
Db        187 TACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGACGCACCACGCGGC 234

Qy         94 AlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
              |||   :::   ||||||   |||   |||   |||   :::|||   |||:::||||||
Db        235 GCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCATTCAACGGAAGC 291

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
              |||      |||         |||         |||      :::   ||||||:::
Db        292 TACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCTCTCGGTATAGAC 348

Qy        134 LysLeuGluPheSerIleGluAlaIle 142
              :::|||      |||:::   |||:::
Db        349 CAACTCATTCAATCCGTCACGGCGCTT 375

RESULT 37
US-08-356-786-7
; Sequence 7, Application US/08356786
; Patent No. 5877305
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Protein for Cancer
;    TITLE OF INVENTION:  Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,786
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/831,967
;      FILING DATE:  06-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  807 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
```

```
;      LOCATION:  1..807
;      OTHER INFORMATION:  /note= "product = "Ricin-A chain"
US-08-356-786-7

Alignment Scores:
Pred. No.:              2.74e-13        Length:         807
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     2               Gaps:           6

US-10-758-902-9 (1-149) x US-08-356-786-7 (1-807)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db         19 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 78

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||     ::::::||||||
Db         79 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 138

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        139 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 198

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        199 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 258

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        259 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 306

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||     |||   ||||||   |||     |||   |||
Db        307 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 366

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        367 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 426

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::          |||   ||||||
Db        427 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 483

RESULT 38
US-08-218-303-15
; Sequence 15, Application US/08218303
; Patent No. 5547867
;  GENERAL INFORMATION:
;    APPLICANT:  Kara, Bhuphendra V.
;    APPLICANT:  Hockney, Robert C.
;    APPLICANT:  Fitton, John E.
;    TITLE OF INVENTION:  FERMENTATION PROCESS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1615 L Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20036-5601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/218,303
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/841,533
;      FILING DATE:  26-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  PNK/3893/94908/MJW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1140 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  143..943
US-08-218-303-15

Alignment Scores:
Pred. No.:              4.44e-13        Length:         1140
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     2               Gaps:           6

US-10-758-902-9 (1-149) x US-08-218-303-15 (1-1140)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        158 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 217

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||     ::::::||||||
Db        218 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 277

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        278 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 337

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        338 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 397

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        398 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 445

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||     |||   ||||||   |||     |||   |||
Db        446 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 505

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        506 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 565

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::          |||   ||||||
Db        566 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 622

RESULT 39
US-08-338-793D-60
; Sequence 60, Application US/08338793D
; Patent No. 5840521
;  GENERAL INFORMATION:
;    APPLICANT:  Barth, Peter Thomas
;    TITLE OF INVENTION:  VECTOR
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  CUSHMAN DARBY CUSHMAN
;      ADDRESSEE:  INTELLECTUAL PROPERTY GROUP OF
;      ADDRESSEE:  PILLSBURY MADISON & SUTRO, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
;      COMPUTER:  IBM PC/XT/AT Compatibles
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word or ASCII editors
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/338,793D
;      FILING DATE:  08-No. 5840521-94
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842,081
;      FILING DATE:  26-Feb-92
;      CLASSIFICATION:  435
;      APPLICATION NUMBER:  9104017.0
;      FILING DATE:  26-Feb-91
;      APPLICATION NUMBER:  9109188.4
;      FILING DATE:  29-Apr-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  DJB/9901/215431/TGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1140
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-338-793D-60

Alignment Scores:
Pred. No.:              4.44e-13      Length:         1140
Score:                  169.00        Matches:        51
Percent Similarity:     52.2%         Conservative:   32
Best Local Similarity:  32.1%         Mismatches:     60
Query Match:            22.0%         Indels:         16
DB:                     2             Gaps:           6

US-10-758-902-9 (1-149) x US-08-338-793D-60 (1-1140)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        158 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 217

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                :::   :::|||      |||      |||      |||      ::::::||||||
Db        218 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 277

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||::::::::
Db        278 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 337

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        338 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 397

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        398 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 445

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
```

```
Db        446 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 505

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
                  :::|||   :::|||          |||          |||:::::::::||||||||
Db        506 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 565

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        566 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 622

RESULT 40
US-08-356-786-9
; Sequence 9, Application US/08356786
; Patent No. 5877305
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Protein for Cancer
;    TITLE OF INVENTION:  Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,786
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/831,967
;      FILING DATE:  06-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1605 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1605
;      OTHER INFORMATION:  /note= "product = "G-FIT""
US-08-356-786-9

Alignment Scores:
Pred. No.:              7.17e-13      Length:         1605
Score:                  169.00        Matches:        51
Percent Similarity:     52.2%         Conservative:   32
Best Local Similarity:  32.1%         Mismatches:     60
Query Match:            22.0%         Indels:         16
DB:                     2             Gaps:           6

US-10-758-902-9 (1-149) x US-08-356-786-9 (1-1605)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
```

```
Db         25 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 84

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db         85 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 144

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        145 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 204

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        205 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 264

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||         ::::::
Db        265 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 312

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        313 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 372

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        373 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 432

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        433 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 489

RESULT 41
US-09-785-921A-2
; Sequence 2, Application US/09785921A
; Patent No. 6627197
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 2
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-2

Alignment Scores:
Pred. No.:              7.97e-13       Length:          1731
Score:                  169.00         Matches:         51
Percent Similarity:     52.2%          Conservative:    32
Best Local Similarity:  32.1%          Mismatches:      60
Query Match:            22.0%          Indels:          16
DB:                     3              Gaps:            6

US-10-758-902-9 (1-149) x US-09-785-921A-2 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||         ::::::
Db        361 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGAGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 42
US-09-785-921A-3
; Sequence 3, Application US/09785921A
; Patent No. 6627197
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 3
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-3

Alignment Scores:
Pred. No.:              7.97e-13       Length:          1731
Score:                  169.00         Matches:         51
Percent Similarity:     52.2%          Conservative:    32
Best Local Similarity:  32.1%          Mismatches:      60
Query Match:            22.0%          Indels:          16
DB:                     3              Gaps:            6

US-10-758-902-9 (1-149) x US-09-785-921A-3 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||         ::::::
Db        361 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
```

```
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 43
US-10-618-560-2
; Sequence 2, Application US/10618560
; Patent No. 7018633
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 2
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-2

Alignment Scores:
Pred. No.:              7.97e-13        Length:         1731
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     5               Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-2 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::|||||:::||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        361 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGAGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 44
US-10-618-560-3
; Sequence 3, Application US/10618560
; Patent No. 7018633
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 3
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-3

Alignment Scores:
Pred. No.:              7.97e-13        Length:         1731
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     5               Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-3 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::|||||:::||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        361 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 45
US-09-785-921A-10
; Sequence 10, Application US/09785921A
; Patent No. 6627197
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 10
```

```
;   LENGTH: 1805
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-10

Alignment Scores:
Pred. No.:              8.45e-13        Length:         1805
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-785-921A-10 (1-1805)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||           |||      ||||||
Db        129 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 188

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||       |||      |||       |||      ::::::||||||
Db        189 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 248

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        249 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 308

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        309 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 368

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        369 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 416

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        417 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 476

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||       |||       |||:::::::::|||||||||
Db        477 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 536

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::              |||   ||||||
Db        537 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 593

RESULT 46
US-10-618-560-10
; Sequence 10, Application US/10618560
; Patent No. 7018633
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 10
;   LENGTH: 1805
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-10

Alignment Scores:
Pred. No.:              8.45e-13        Length:         1805
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     5               Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-10 (1-1805)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||           |||      ||||||
Db        129 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 188

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||       |||      |||       |||      ::::::||||||
Db        189 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 248

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        249 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 308

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        309 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 368

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        369 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 416

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        417 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 476

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||       |||       |||:::::::::|||||||||
Db        477 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 536

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::              |||   ||||||
Db        537 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 593

RESULT 47
US-09-627-165E-1
; Sequence 1, Application US/09627165E
; Patent No. 6846913
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jong-Bae
;  TITLE OF INVENTION: CRUDE EXTRACT FROM Viscum album coloratum, AND PROTEINS
;  TITLE OF INVENTION:  AND LECTINS ISOLATED THEREFROM
;  FILE REFERENCE: Korean Mistletoe Lectin
;  CURRENT APPLICATION NUMBER: US/09/627,165E
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 1
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Viscum album coloratum
;   FEATURE:
;   NAME/KEY: misc_feature
US-09-627-165E-1

Alignment Scores:
Pred. No.:              2.95e-13        Length:         762
Score:                  168.50          Matches:        49
Percent Similarity:     54.9%           Conservative:   24
Best Local Similarity:  36.8%           Mismatches:     51
Query Match:            21.9%           Indels:         9
DB:                     3               Gaps:           4

US-10-758-902-9 (1-149) x US-09-627-165E-1 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
```

```
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCGGATGCGCAAAGATTTGTGTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69

Db        166 GTGGAACTCACCAATCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACTAACCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89

Db        226 TACGTGGTGGCTTACCAA----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109

Db        274 GCACCAGACGGCGCGGAAAGGCATCTCTTCACCGGC---ACCACCAGATCCTCCCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129

Db        331 TTCACCGGAAGCTACACAGATCTGGAGCGATTCGCCGGT---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142

Db        388 CTGGGTAGAGAGGAACTCATTCAATCCGTCTCGGCCCTT 426
```

RESULT 48
US-09-069-330-1
; Sequence 1, Application US/09069330
; Patent No. 5977335
; GENERAL INFORMATION:
; APPLICANT: Kim, Yong Sig
; APPLICANT: Park, Sun Chung
; APPLICANT: Oh, Soo Kyung
; APPLICANT: Cho, Jeong Woo
; APPLICANT: Chung, Chang. H.
; TITLE OF INVENTION: DNA Encoding Amarandin-S, Ribosome Inactivating Protein,
; TITLE OF INVENTION: of Amaranthus Viridis
; FILE REFERENCE: 1942/25
; CURRENT APPLICATION NUMBER: US/09/069,330
; CURRENT FILING DATE: 1998-04-29
; EARLIER APPLICATION NUMBER: US 08/916,444
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: WordPerfect 6.1 for Windows
; SEQ ID NO 1
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Amaranthus Viridis
US-09-069-330-1

Alignment Scores:

Pred. No.:	3.45e-13	Length:	852
Score:	168.50	Matches:	42
Percent Similarity:	50.0%	Conservative:	35
Best Local Similarity:	27.3%	Mismatches:	68
Query Match:	21.9%	Indels:	9
DB:	2	Gaps:	3

US-10-758-902-9 (1-149) x US-09-069-330-1 (1-852)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGlu---------TyrProThrPhe 17

Db        100 TATCGTACGGTGGGATTCGAATTACATAAAGAGAATTCACCAAATGGGTACGCAAATTTC 159

Qy         18 IleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr 37

Db        160 TTGAGAAGGTTGCGCAGTGCAGTCTCAGGTCCCACAAGAGCATGTAATTTAAACATTACA 219

Qy         38 LeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLys 57

Db        220 CAAAGTAATCCACCAATAGACAGAGAATATGTCTACATAAGGCTACAATTTAGCGACACA 279

Qy         58 LysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLys 77

Db        280 CAATGGGTAGTACTAGGAATGGCTGCCAAAGATATGTATATTTGGGGTTATGTTGACAAT 339

Qy         78 TrpAspGly----------LysAspArgAlaValPheLeuAspLysValProThr 92

Db        340 AGGCCAGGCTTCGGACCAGGCCAACCACCTGAGTCAAACTTCCTAATGGATTCTCCGCCA 399

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        400 GAAGCACGACAACGTCTTTTCCCAGGTTCTAACAGAAGAATAACA---GATTACGGAGGA 456

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        457 AATTACAACAGTCTTCAACAAAGAGCACAAAGGAATCGAGATAATGTTCCATTGGGACTG 516

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrpGlyLysThr 146

Db        517 ACAAGCCTAGACGGCGCACTTAAAAGCGTGTATGGAAAATCA 558
```

RESULT 49
US-09-785-921A-1
; Sequence 1, Application US/09785921A
; Patent No. 6627197
; GENERAL INFORMATION:
; APPLICANT: Keener, William K.
; APPLICANT: Ward, Thomas E.
; TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: LIT-PI-529
; CURRENT APPLICATION NUMBER: US/09/785,921A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Ricinus communis
US-09-785-921A-1

Alignment Scores:

Pred. No.:	1.45e-12	Length:	1698
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-785-921A-1 (1-1698)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db         88 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 147

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        148 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 207

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        208 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 267

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        268 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 327

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        328 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 375

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        376 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 435

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        436 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 495
```

```
Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||:::::            |||   ||||||
Db        496 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 552

RESULT 50
US-10-618-560-1
; Sequence 1, Application US/10618560
; Patent No. 7018633
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
;   LENGTH: 1698
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-1

Alignment Scores:
Pred. No.:              1.45e-12        Length:         1698
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     5               Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-1 (1-1698)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db         88 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 147

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        148 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 207

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
              :::           ::::::||||||:::||||||:::::::::
Db        208 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 267

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        268 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 327

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                      :::   |||   |||            ::::::
Db        328 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 375

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        376 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 435

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||  .      |||          |||:::::::::|||||||||
Db        436 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 495

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        496 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 552

RESULT 51
US-09-147-208-33
; Sequence 33, Application US/09147208
; Patent No. 6333303
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Antiviral Ricin-Like Proteins
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BERESKIN & PARR
;      STREET:  40 King Street West
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5H 3Y2
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/147,208
;      FILING DATE:  02-MAR-1999
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rudolph, John R.
;      REGISTRATION NUMBER:  38,003
;      REFERENCE/DOCKET NUMBER:  7841-76
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 364-7311
;      TELEFAX:  (416) 361-1398
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1855 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-147-208-33

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-147-208-33 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
              :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                      :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
```

```
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 52
US-09-147-208-40
; Sequence 40, Application US/09147208
; Patent No. 6333303
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Antiviral Ricin-Like Proteins
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BERESKIN & PARR
;      STREET:  40 King Street West
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5H 3Y2
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/147,208
;      FILING DATE:  02-MAR-1999
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rudolph, John R.
;      REGISTRATION NUMBER:  38,003
;      REFERENCE/DOCKET NUMBER:  7841-76
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 364-7311
;      TELEFAX:  (416) 361-1398
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1855 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-147-208-40

Alignment Scores:
Pred. No.:          1.64e-12        Length:         1855
Score:              167.00          Matches:        51
Percent Similarity: 51.6%           Conservative:   31
Best Local Similarity: 32.1%        Mismatches:     61
Query Match:        21.7%           Indels:         16
DB:                 3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-147-208-40 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||       |||       |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
                 :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 53
US-09-147-208-47
; Sequence 47, Application US/09147208
; Patent No. 6333303
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Antiviral Ricin-Like Proteins
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BERESKIN & PARR
;      STREET:  40 King Street West
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5H 3Y2
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/147,208
;      FILING DATE:  02-MAR-1999
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rudolph, John R.
;      REGISTRATION NUMBER:  38,003
;      REFERENCE/DOCKET NUMBER:  7841-76
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 364-7311
;      TELEFAX:  (416) 361-1398
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1855 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-147-208-47

Alignment Scores:
Pred. No.:          1.64e-12        Length:         1855
Score:              167.00          Matches:        51
Percent Similarity: 51.6%           Conservative:   31
Best Local Similarity: 32.1%        Mismatches:     61
Query Match:        21.7%           Indels:         16
DB:                 3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-147-208-47 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||       |||       |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306
```

```
Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||              ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||          |||          |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 54
US-09-147-208-54
; Sequence 54, Application US/09147208
; Patent No. 6333303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,208
; FILING DATE: 02-MAR-1999
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rudolph, John R.
; REGISTRATION NUMBER: 38,003
; REFERENCE/DOCKET NUMBER: 7841-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1855 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-147-208-54

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-147-208-54 (1-1855)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
                 |||      ::::::|||           |||           |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||       |||       |||       |||         :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||              ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||          |||          |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 55
US-09-550-117A-33
; Sequence 33, Application US/09550117A
; Patent No. 6531125
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; FILE REFERENCE: 10447-10
; CURRENT APPLICATION NUMBER: US/09/550,117A
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/147,208
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-206 insert
US-09-550-117A-33

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-550-117A-33 (1-1855)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
                 |||      ::::::|||           |||           |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||       |||       |||       |||         :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306
```

```
Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db         367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||   |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::             |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 56
US-09-550-117A-40
; Sequence 40, Application US/09550117A
; Patent No. 6531125
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Antiviral Ricin-Like Proteins
;  FILE REFERENCE: 10447-10
;  CURRENT APPLICATION NUMBER: US/09/550,117A
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/147,208
;  PRIOR FILING DATE: 1999-03-02
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-208 insert
US-09-550-117A-40

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-550-117A-40 (1-1855)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||       ::::::|||             |||             |||       ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||       |||       |||       |||          :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::             ::::::|||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db         367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414
```

```
Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||   |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::             |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 57
US-09-550-117A-47
; Sequence 47, Application US/09550117A
; Patent No. 6531125
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Antiviral Ricin-Like Proteins
;  FILE REFERENCE: 10447-10
;  CURRENT APPLICATION NUMBER: US/09/550,117A
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/147,208
;  PRIOR FILING DATE: 1999-03-02
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-209 insert
US-09-550-117A-47

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-550-117A-47 (1-1855)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||       ::::::|||             |||             |||       ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||       |||       |||       |||          :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::             ::::::|||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db         367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||   |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
```

```
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 58
US-09-550-117A-54
; Sequence 54, Application US/09550117A
; Patent No. 6531125
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; FILE REFERENCE: 10447-10
; CURRENT APPLICATION NUMBER: US/09/550,117A
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/147,208
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-212 insert
US-09-550-117A-54

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-550-117A-54 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::         ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                     :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||   |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 59
US-09-403-752A-3
; Sequence 3, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
; TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
; FILE REFERENCE: 10447-005
; CURRENT APPLICATION NUMBER: US/09/403,752A
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: U.S. 60/045,148
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: U.S. 60/063,715
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Cathepsin B linker regions of pAP-214
US-09-403-752A-3

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-403-752A-3 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::         ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                     :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||   |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 60
US-09-403-752A-5
; Sequence 5, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
; TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
; FILE REFERENCE: 10447-005
; CURRENT APPLICATION NUMBER: US/09/403,752A
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: U.S. 60/045,148
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: U.S. 60/063,715

```
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-216 insert
US-09-403-752A-5

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-403-752A-5 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||              |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::  :::|||  :::|||:::|||||||||:::  |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::  |||  |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||  :::  ||||||      |||  ||||||  |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||  :::|||          |||        |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||  :::|||  |||::::::          |||  ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 61
US-09-403-752A-7
; Sequence 7, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-218 insert
US-09-403-752A-7

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-403-752A-7 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||              |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::  :::|||  :::|||:::|||||||||:::  |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::  |||  |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||  :::  ||||||      |||  ||||||  |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||  :::|||          |||        |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||  :::|||  |||::::::          |||  ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 62
US-09-403-752A-9
; Sequence 9, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-220 insert
US-09-403-752A-9

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6
```

```
US-10-758-902-9 (1-149) x US-09-403-752A-9 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||  ||||||  |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 63
US-09-403-752A-13
; Sequence 13, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-224 insert
US-09-403-752A-13

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-13 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||  ||||||  |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 64
US-09-403-752A-15
; Sequence 15, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-226 insert
US-09-403-752A-15

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-15 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
```

```
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||  |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
                 :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 65
US-09-403-752A-17
; Sequence 17, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-228 insert
US-09-403-752A-17

Alignment Scores:
Pred. No.:                1.64e-12        Length:          1855
Score:                    167.00          Matches:         51
Percent Similarity:       51.6%           Conservative:    31
Best Local Similarity:    32.1%           Mismatches:      61
Query Match:              21.7%           Indels:          16
DB:                       3               Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-17 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                 :::   :::|||      |||      |||      |||          :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||  |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
```

```
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
                 :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 66
US-09-403-752A-19
; Sequence 19, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-230 insert
US-09-403-752A-19

Alignment Scores:
Pred. No.:                1.64e-12        Length:          1855
Score:                    167.00          Matches:         51
Percent Similarity:       51.6%           Conservative:    31
Best Local Similarity:    32.1%           Mismatches:      61
Query Match:              21.7%           Indels:          16
DB:                       3               Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-19 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                 :::   :::|||      |||      |||      |||          :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||  |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
                 :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
```

```
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 67
US-09-403-752A-21
; Sequence 21, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-232 insert
US-09-403-752A-21

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-21 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||          :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||                 ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 68
US-09-403-752A-23
; Sequence 23, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-234 insert
US-09-403-752A-23

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-23 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||          :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||                 ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 69
US-09-403-752A-25
; Sequence 25, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
```

```
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-236 insert
US-09-403-752A-25

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-403-752A-25 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::|||          |||           |||       ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||        |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 70
US-09-403-752A-27
; Sequence 27, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-238 insert
US-09-403-752A-27

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-403-752A-27 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::|||          |||           |||       ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||        |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 71
US-09-403-752A-29
; Sequence 29, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 29
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-240 insert
US-09-403-752A-29

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
```

```
DB:                    3              Gaps:          6

US-10-758-902-9 (1-149) x US-09-403-752A-29 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                 ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 72
US-09-403-752A-31
; Sequence 31, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-242 insert
US-09-403-752A-31

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-31 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                 ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 73
US-09-403-752A-33
; Sequence 33, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-244 insert
US-09-403-752A-33

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-33 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306
```

```
Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||           ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                  |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||           |||           |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::            |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 74
US-09-403-752A-35
; Sequence 35, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
; TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
; FILE REFERENCE: 10447-005
; CURRENT APPLICATION NUMBER: US/09/403,752A
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: U.S. 60/045,148
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: U.S. 60/063,715
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: pAP-246 insert
US-09-403-752A-35

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-403-752A-35 (1-1855)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||          |||          |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||         :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::          ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||           ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414
```

```
Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                  |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||           |||           |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::            |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 75
US-09-403-752A-37
; Sequence 37, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
; TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
; FILE REFERENCE: 10447-005
; CURRENT APPLICATION NUMBER: US/09/403,752A
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: U.S. 60/045,148
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: U.S. 60/063,715
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: pPA-248 insert
US-09-403-752A-37

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-403-752A-37 (1-1855)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||          |||          |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||         :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::          ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||           ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                  |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||           |||           |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534
```

```
Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||:::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 76
US-09-403-752A-39
; Sequence 39, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-250 insert
US-09-403-752A-39

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-39 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||:::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 77
US-09-403-752A-48
; Sequence 48, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 48
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-254 insert
US-09-403-752A-48

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-48 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||:::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 78
US-09-403-752A-50
; Sequence 50, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
```

```
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 50
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-258 insert
US-09-403-752A-50

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-403-752A-50 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                ::   :::|||      |||      |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 79
US-09-403-752A-52
; Sequence 52, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 52
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-256 insert
US-09-403-752A-52

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-403-752A-52 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                ::   :::|||      |||      |||       |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 80
US-09-403-752A-54
; Sequence 54, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 54
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-260 insert
US-09-403-752A-54

Alignment Scores:
Pred. No.:              1.64e-12        Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
```

```
Query Match:            21.7%       Indels:        16
DB:                     3           Gaps:          6

US-10-758-902-9 (1-149) x US-09-403-752A-54 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||          ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||          :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 81
US-09-403-752A-74
; Sequence 74, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 74
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-262 insert
US-09-403-752A-74

Alignment Scores:
Pred. No.:              1.64e-12    Length:        1855
Score:                  167.00      Matches:       51
Percent Similarity:     51.6%       Conservative:  31
Best Local Similarity:  32.1%       Mismatches:    61
Query Match:            21.7%       Indels:        16
DB:                     3           Gaps:          6

US-10-758-902-9 (1-149) x US-09-403-752A-74 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||          ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186
```

```
Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||          :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 82
US-09-403-752A-77
; Sequence 77, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 77
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-264 insert
US-09-403-752A-77

Alignment Scores:
Pred. No.:              1.64e-12    Length:        1855
Score:                  167.00      Matches:       51
Percent Similarity:     51.6%       Conservative:  31
Best Local Similarity:  32.1%       Mismatches:    61
Query Match:            21.7%       Indels:        16
DB:                     3           Gaps:          6

US-10-758-902-9 (1-149) x US-09-403-752A-77 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||          ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||          :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306
```

```
Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 83
US-09-403-752A-80
; Sequence 80, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
; TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
; FILE REFERENCE: 10447-005
; CURRENT APPLICATION NUMBER: US/09/403,752A
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: U.S. 60/045,148
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: U.S. 60/063,715
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: pAP-266 insert
US-09-403-752A-80

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-403-752A-80 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 84
US-09-403-752A-83
; Sequence 83, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
; TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
; FILE REFERENCE: 10447-005
; CURRENT APPLICATION NUMBER: US/09/403,752A
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: U.S. 60/045,148
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: U.S. 60/063,715
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: pAP-268 insert
US-09-403-752A-83

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-403-752A-83 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534
```

```
Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 85
US-09-403-752A-86
; Sequence 86, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 86
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-270 insert
US-09-403-752A-86

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-86 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||         |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||  :::   ||||||      |||  ||||||  |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 86
US-09-403-752A-89
; Sequence 89, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 89
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-272 insert
US-09-403-752A-89

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-89 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||         |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||  :::   ||||||      |||  ||||||  |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 87
US-09-403-752A-92
; Sequence 92, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
```

```
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 92
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-274 insert
US-09-403-752A-92

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-92 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||           ::::::
Db        367 ----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||  :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 88
US-09-403-752A-95
; Sequence 95, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 95
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-276 insert
US-09-403-752A-95

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-95 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||           ::::::
Db        367 ----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||  :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 89
US-09-403-752A-98
; Sequence 98, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 98
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-278 insert
US-09-403-752A-98

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
```

```
Best Local Similarity:  32.1%          Mismatches:    61
Query Match:            21.7%          Indels:        16
DB:                     3              Gaps:          6

US-10-758-902-9 (1-149) x US-09-403-752A-98 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 90
US-09-403-752A-101
; Sequence 101, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 101
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-280 insert
US-09-403-752A-101

Alignment Scores:
Pred. No.:              1.64e-12       Length:        1855
Score:                  167.00         Matches:       51
Percent Similarity:     51.6%          Conservative:  31
Best Local Similarity:  32.1%          Mismatches:    61
Query Match:            21.7%          Indels:        16
DB:                     3              Gaps:          6

US-10-758-902-9 (1-149) x US-09-403-752A-101 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 91
US-09-403-752A-104
; Sequence 104, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 104
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-282 insert
US-09-403-752A-104

Alignment Scores:
Pred. No.:              1.64e-12       Length:        1855
Score:                  167.00         Matches:       51
Percent Similarity:     51.6%          Conservative:  31
Best Local Similarity:  32.1%          Mismatches:    61
Query Match:            21.7%          Indels:        16
DB:                     3              Gaps:          6

US-10-758-902-9 (1-149) x US-09-403-752A-104 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::          ::::::||||||:::||||||:::::::::
```

```
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 92
US-09-403-752A-110
; Sequence 110, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
; TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
; FILE REFERENCE: 10447-005
; CURRENT APPLICATION NUMBER: US/09/403,752A
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: U.S. 60/045,148
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: U.S. 60/063,715
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: pAP-286 insert
US-09-403-752A-110

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-403-752A-110 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||             ::::::
```

```
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 93
US-09-403-752A-113
; Sequence 113, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
; TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
; FILE REFERENCE: 10447-005
; CURRENT APPLICATION NUMBER: US/09/403,752A
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: U.S. 60/045,148
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: U.S. 60/063,715
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: pAP-288 insert
US-09-403-752A-113

Alignment Scores:

Pred. No.:	1.64e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	3	Gaps:	6

US-10-758-902-9 (1-149) x US-09-403-752A-113 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
```

```
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 94
US-09-403-752A-116
; Sequence 116, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 116
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-290 insert
US-09-403-752A-116

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-116 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                 :::   :::|||       |||       |||       |||          :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 95
US-09-403-752A-119
```

```
; Sequence 119, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 119
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-292 insert
US-09-403-752A-119

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-119 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                 :::   :::|||       |||       |||       |||          :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 96
US-09-403-752A-122
; Sequence 122, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
```

```
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 122
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-294 insert
US-09-403-752A-122

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-122 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 97
US-09-403-752A-125
; Sequence 125, Application US/09403752A
; Patent No. 6593132
; GENERAL INFORMATION:
;  APPLICANT:  Borgford, Thor
;  TITLE OF INVENTION:  RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
;  TITLE OF INVENTION:  VIRAL OR PARASITIC INFECTIONS
;  FILE REFERENCE:  10447-005
;  CURRENT APPLICATION NUMBER: US/09/403,752A
;  CURRENT FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  U.S. 60/045,148
;  PRIOR FILING DATE:  1997-04-30
;  PRIOR APPLICATION NUMBER:  U.S. 60/063,715
;  PRIOR FILING DATE:  1997-10-29
;  NUMBER OF SEQ ID NOS:  142
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 125
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: pAP-296 insert
US-09-403-752A-125

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-403-752A-125 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 98
US-09-551-151A-3
; Sequence 3, Application US/09551151A
; Patent No. 6803358
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-011
;  CURRENT APPLICATION NUMBER: US/09/551,151A
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Cathepsin B linker regions of pAP-214
US-09-551-151A-3

Alignment Scores:
Pred. No.:              1.64e-12      Length:          1855
Score:                  167.00        Matches:         51
```

```
Percent Similarity:     51.6%          Conservative:  31
Best Local Similarity:  32.1%          Mismatches:    61
Query Match:            21.7%          Indels:        16
DB:                     3              Gaps:          6

US-10-758-902-9 (1-149) x US-09-551-151A-3 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||      |||        :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 99
US-09-551-151A-5
; Sequence 5, Application US/09551151A
; Patent No. 6803358
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-011
;  CURRENT APPLICATION NUMBER: US/09/551,151A
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-216 insert
US-09-551-151A-5

Alignment Scores:
Pred. No.:              1.64e-12       Length:        1855
Score:                  167.00         Matches:       51
Percent Similarity:     51.6%          Conservative:  31
Best Local Similarity:  32.1%          Mismatches:    61
Query Match:            21.7%          Indels:        16
DB:                     3              Gaps:          6

US-10-758-902-9 (1-149) x US-09-551-151A-5 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||      |||        :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::             ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||          ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 100
US-09-551-151A-7
; Sequence 7, Application US/09551151A
; Patent No. 6803358
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-011
;  CURRENT APPLICATION NUMBER: US/09/551,151A
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-218 insert
US-09-551-151A-7

Alignment Scores:
Pred. No.:              1.64e-12       Length:        1855
Score:                  167.00         Matches:       51
Percent Similarity:     51.6%          Conservative:  31
Best Local Similarity:  32.1%          Mismatches:    61
Query Match:            21.7%          Indels:        16
DB:                     3              Gaps:          6

US-10-758-902-9 (1-149) x US-09-551-151A-7 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||      |||        :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
```

```
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

Search completed: September 18, 2006, 17:57:14
Job time : 256.57 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 19:05:31 ; Search time 1682.28 Seconds
(without alignments)
1632.474 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_18092006_162718_11769/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10758902_@CGN_1_1_2326_@runat_18092006_162718_11769 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	726	94.5	2404	13	US-11-084-080-15	Sequence 15, Appl
2	726	94.5	2404	13	US-11-084-080-19	Sequence 19, Appl
3	726	94.5	2404	13	US-11-084-080-21	Sequence 21, Appl
4	726	94.5	2404	13	US-11-084-080-23	Sequence 23, Appl
5	726	94.5	2431	13	US-11-084-080-27	Sequence 27, Appl
6	609	79.3	363	9	US-10-758-902-8	Sequence 8, Appli
7	220.5	28.7	913	7	US-10-127-890-13	Sequence 13, Appl
8	220.5	28.7	913	10	US-10-717-243-13	Sequence 13, Appl
9	183.5	23.9	870	4	US-09-905-247-2	Sequence 2, Appli
10	183.5	23.9	886	7	US-10-280-679B-3	Sequence 3, Appli
11	183.5	23.9	886	8	US-10-280-725B-3	Sequence 3, Appli
12	179.5	23.4	762	13	US-11-042-707-16	Sequence 16, Appl
13	179.5	23.4	762	13	US-11-042-707-19	Sequence 19, Appl
14	179.5	23.4	768	13	US-11-042-707-17	Sequence 17, Appl
15	179.5	23.4	768	13	US-11-042-707-20	Sequence 20, Appl
16	176.5	23.0	756	3	US-09-347-064-7	Sequence 7, Appli
17	176.5	23.0	762	3	US-09-347-064-1	Sequence 1, Appli
18	176.5	23.0	855	10	US-10-499-297-1	Sequence 1, Appli
19	176.5	23.0	1596	13	US-11-042-707-15	Sequence 15, Appl
20	176.5	23.0	1596	13	US-11-042-707-18	Sequence 18, Appl
21	176.5	23.0	1958	10	US-10-499-297-5	Sequence 5, Appli
22	173	22.5	2788	10	US-10-800-052-35	Sequence 35, Appl
23	173	22.5	2803	10	US-10-800-052-2	Sequence 2, Appli
24	173	22.5	2805	10	US-10-800-052-37	Sequence 37, Appl
25	173	22.5	2869	10	US-10-800-052-20	Sequence 20, Appl
26	173	22.5	2878	10	US-10-800-052-26	Sequence 26, Appl
27	169	22.0	807	16	US-11-010-795-23	Sequence 23, Appl
28	169	22.0	1623	10	US-10-893-584-273	Sequence 273, App
29	169	22.0	1731	3	US-09-785-921A-2	Sequence 2, Appli
30	169	22.0	1731	3	US-09-785-921A-3	Sequence 3, Appli
31	169	22.0	1731	8	US-10-618-560-2	Sequence 2, Appli
32	169	22.0	1731	8	US-10-618-560-3	Sequence 3, Appli
33	169	22.0	1805	3	US-09-785-921A-10	Sequence 10, Appl
34	169	22.0	1805	8	US-10-618-560-10	Sequence 10, Appl
35	169	22.0	1807	10	US-10-893-584-196	Sequence 196, App
36	169	22.0	1810	10	US-10-893-584-168	Sequence 168, App
37	169	22.0	1813	10	US-10-893-584-245	Sequence 245, App
38	169	22.0	1819	10	US-10-893-584-238	Sequence 238, App
39	169	22.0	1822	10	US-10-893-584-175	Sequence 175, App
40	169	22.0	1822	10	US-10-893-584-182	Sequence 182, App
41	169	22.0	1825	10	US-10-893-584-231	Sequence 231, App
42	169	22.0	1828	10	US-10-893-584-210	Sequence 210, App
43	169	22.0	1831	10	US-10-893-584-161	Sequence 161, App
44	169	22.0	1831	10	US-10-893-584-203	Sequence 203, App
45	169	22.0	1834	10	US-10-893-584-154	Sequence 154, App
46	169	22.0	1837	10	US-10-893-584-266	Sequence 266, App
47	169	22.0	1843	10	US-10-893-584-259	Sequence 259, App
48	169	22.0	1849	10	US-10-893-584-252	Sequence 252, App
49	169	22.0	1855	10	US-10-893-584-147	Sequence 147, App
50	169	22.0	1855	10	US-10-893-584-189	Sequence 189, App
51	169	22.0	1855	10	US-10-893-584-217	Sequence 217, App
52	169	22.0	1855	10	US-10-893-584-224	Sequence 224, App
53	168	21.9	7306	10	US-10-477-373A-2	Sequence 2, Appli
54	168	21.9	8155	10	US-10-477-373A-1	Sequence 1, Appli
55	167	21.7	1698	3	US-09-785-921A-1	Sequence 1, Appli
56	167	21.7	1698	8	US-10-618-560-1	Sequence 1, Appli
57	167	21.7	1855	7	US-10-394-511-3	Sequence 3, Appli
58	167	21.7	1855	7	US-10-394-511-5	Sequence 5, Appli
59	167	21.7	1855	7	US-10-394-511-7	Sequence 7, Appli
60	167	21.7	1855	7	US-10-394-511-9	Sequence 9, Appli
61	167	21.7	1855	7	US-10-394-511-13	Sequence 13, Appl
62	167	21.7	1855	7	US-10-394-511-15	Sequence 15, Appl
63	167	21.7	1855	7	US-10-394-511-17	Sequence 17, Appl
64	167	21.7	1855	7	US-10-394-511-19	Sequence 19, Appl
65	167	21.7	1855	7	US-10-394-511-21	Sequence 21, Appl
66	167	21.7	1855	7	US-10-394-511-23	Sequence 23, Appl
67	167	21.7	1855	7	US-10-394-511-25	Sequence 25, Appl
68	167	21.7	1855	7	US-10-394-511-27	Sequence 27, Appl
69	167	21.7	1855	7	US-10-394-511-29	Sequence 29, Appl
70	167	21.7	1855	7	US-10-394-511-31	Sequence 31, Appl
71	167	21.7	1855	7	US-10-394-511-33	Sequence 33, Appl
72	167	21.7	1855	7	US-10-394-511-35	Sequence 35, Appl
73	167	21.7	1855	7	US-10-394-511-37	Sequence 37, Appl
74	167	21.7	1855	7	US-10-394-511-39	Sequence 39, Appl

75	167	21.7	1855	7	US-10-394-511-48	Sequence 48, Appl
76	167	21.7	1855	7	US-10-394-511-50	Sequence 50, Appl
77	167	21.7	1855	7	US-10-394-511-52	Sequence 52, Appl
78	167	21.7	1855	7	US-10-394-511-54	Sequence 54, Appl
79	167	21.7	1855	7	US-10-394-511-74	Sequence 74, Appl
80	167	21.7	1855	7	US-10-394-511-77	Sequence 77, Appl
81	167	21.7	1855	7	US-10-394-511-80	Sequence 80, Appl
82	167	21.7	1855	7	US-10-394-511-83	Sequence 83, Appl
83	167	21.7	1855	7	US-10-394-511-86	Sequence 86, Appl
84	167	21.7	1855	7	US-10-394-511-89	Sequence 89, Appl
85	167	21.7	1855	7	US-10-394-511-92	Sequence 92, Appl
86	167	21.7	1855	7	US-10-394-511-95	Sequence 95, Appl
87	167	21.7	1855	7	US-10-394-511-98	Sequence 98, Appl
88	167	21.7	1855	7	US-10-394-511-101	Sequence 101, App
89	167	21.7	1855	7	US-10-394-511-104	Sequence 104, App
90	167	21.7	1855	7	US-10-394-511-110	Sequence 110, App
91	167	21.7	1855	7	US-10-394-511-113	Sequence 113, App
92	167	21.7	1855	7	US-10-394-511-116	Sequence 116, App
93	167	21.7	1855	7	US-10-394-511-119	Sequence 119, App
94	167	21.7	1855	7	US-10-394-511-122	Sequence 122, App
95	167	21.7	1855	7	US-10-394-511-125	Sequence 125, App
96	167	21.7	1855	10	US-10-893-584-3	Sequence 3, Appli
97	167	21.7	1855	10	US-10-893-584-5	Sequence 5, Appli
98	167	21.7	1855	10	US-10-893-584-7	Sequence 7, Appli
99	167	21.7	1855	10	US-10-893-584-9	Sequence 9, Appli
100	167	21.7	1855	10	US-10-893-584-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-11-084-080-15
; Sequence 15, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845
US-11-084-080-15

Alignment Scores:

Pred. No.:	2.21e-90	Length:	2404
Score:	726.00	Matches:	144
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	5
Query Match:	94.5%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-9 (1-149) x US-11-084-080-15 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20

                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 884

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 944

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1004

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1064

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1124

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1184

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                ||||||   |||||||||   ||||||||||||||   ||||||||||||||||||||
Db       1185 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 1244

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
                ||||||   |||||||||   ||||||
Db       1245 GCAATCCATGGTAAAACGATAAATGGT 1271
```

RESULT 2
US-11-084-080-19
; Sequence 19, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Alignment Scores:

Pred. No.:	2.21e-90	Length:	2404
Score:	726.00	Matches:	144
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	5
Query Match:	94.5%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-9 (1-149) x US-11-084-080-19 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1643 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1702

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1703 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 1762

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1763 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1822

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1823 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1882

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1883 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1942

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1943 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 2002

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||  |||||||||  ||||||||||||||  ||||||||||||||||||||||||||||
Db       2003 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 2062

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||  |||||||||  ||||||
Db       2063 GCAATCCATGGTAAAACGATAAATGGT 2089
```

RESULT 3
US-11-084-080-21
; Sequence 21, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-21

Alignment Scores:

Pred. No.:	2.21e-90	Length:	2404
Score:	726.00	Matches:	144
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	5
Query Match:	94.5%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-9 (1-149) x US-11-084-080-21 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 191

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 251

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 311

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 371

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 431

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 491

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||  |||||||||  ||||||||||||||  ||||||||||||||||||||||||||||
Db        492 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 551

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||  |||||||||  ||||||
Db        552 GCAATCCATGGTAAAACGATAAATGGT 578
```

RESULT 4
US-11-084-080-23
; Sequence 23, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Alignment Scores:

Pred. No.:	2.21e-90	Length:	2404
Score:	726.00	Matches:	144
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	5
Query Match:	94.5%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-9 (1-149) x US-11-084-080-23 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        950 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1009

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1010 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 1069

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1129

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1130 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1189

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1190 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1249

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1250 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1309

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||   |||||||||   ||||||||||||||||   ||||||||||||||||||||
Db       1310 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 1369

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||   |||||||||   ||||||
Db       1370 GCAATCCATGGTAAAACGATAAATGGT 1396
```

RESULT 5
US-11-084-080-27
; Sequence 27, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 2431
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-011
US-11-084-080-27

Alignment Scores:

Pred. No.:	2.25e-90	Length:	2431
Score:	726.00	Matches:	144
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	5
Query Match:	94.5%	Indels:	0
DB:	13	Gaps:	0

US-10-758-902-9 (1-149) x US-11-084-080-27 (1-2431)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 911

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        912 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 971

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1031

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1091

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1092 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1151

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1152 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1211

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              ||||||   |||||||||   ||||||||||||||||   ||||||||||||||||||||
Db       1212 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 1271

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149
              ||||||   |||||||||   ||||||
Db       1272 GCAATCCATGGTAAAACGATAAATGGT 1298
```

RESULT 6
US-10-758-902-8
; Sequence 8, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenzo
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
; FILE REFERENCE: PNJ-005CN
; CURRENT APPLICATION NUMBER: US/10/758,902
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 09/445160
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: PCT/NL98/0336
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Bougainvillaea Spectabilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(361)
US-10-758-902-8

Alignment Scores:

Pred. No.:	3.71e-75	Length:	363
Score:	609.00	Matches:	120
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	79.3%	Indels:	0
DB:	9	Gaps:	0

US-10-758-902-9 (1-149) x US-10-758-902-8 (1-363)

```
Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361

RESULT 7
US-10-127-890-13
; Sequence 13, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 913 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-127-890-13

Alignment Scores:
Pred. No.:                5.81e-20        Length:          913
Score:                    220.50          Matches:         52
Percent Similarity:       59.9%           Conservative:    33
Best Local Similarity:    36.6%           Mismatches:      50
Query Match:              28.7%           Indels:          7
DB:                       7               Gaps:            3

US-10-758-902-9 (1-149) x US-10-127-890-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||              |||       |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||             |||      :::|||:::            ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::              :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||       :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::|||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 8
US-10-717-243-13
; Sequence 13, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
;           SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/717,243
;           FILING DATE: 18-Nov-2003
;           CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/08/839,765
;           FILING DATE: 15-APR-1997
;           APPLICATION NUMBER: US 08/425,336
;           FILING DATE: 18-APR-1995
;           APPLICATION NUMBER: US 08/064,691
;           FILING DATE: 12-MAY-1993
;           APPLICATION NUMBER: US 07/988,430
;           FILING DATE: 09-DEC-1992
;           APPLICATION NUMBER: US 07/901,707
;           FILING DATE: 19-JUN-1992
;           APPLICATION NUMBER: US 07/787,567
;           FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;           NAME: McNicholas, Janet M.
;           REGISTRATION NUMBER: 32,918
;           REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 312/707-8889
;           TELEFAX: 312/707-9155
;           TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 913 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-717-243-13

Alignment Scores:
Pred. No.:                5.81e-20        Length:          913
Score:                    220.50          Matches:         52
Percent Similarity:       59.9%           Conservative:    33
Best Local Similarity:    36.6%           Mismatches:      50
Query Match:              28.7%           Indels:          7
DB:                       10              Gaps:            3

US-10-758-902-9 (1-149) x US-10-717-243-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||          |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::           :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 9
US-09-905-247-2
; Sequence 2, Application US/09905247
; Publication No. US20040197853A1
; GENERAL INFORMATION:
;  APPLICANT: KE, YI-BAO
;  APPLICANT:  NIE, HUI-LING
;  TITLE OF INVENTION: Mutant Trichosanthin
;  FILE REFERENCE: 04399/000J615-US0
;  CURRENT APPLICATION NUMBER: US/09/905,247
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: CN 00119553.0
;  PRIOR FILING DATE: 2000-08-02
;  PRIOR APPLICATION NUMBER: CN 01103102.6
;  PRIOR FILING DATE: 2001-01-18
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 870
;   TYPE: DNA
;   ORGANISM: Trichosanthes Kirilowii M.
US-09-905-247-2

Alignment Scores:
Pred. No.:                8.57e-15        Length:          870
Score:                    183.50          Matches:         44
Percent Similarity:       53.5%           Conservative:    32
Best Local Similarity:    31.0%           Mismatches:      61
Query Match:              23.9%           Indels:          5
DB:                       4               Gaps:            2

US-10-758-902-9 (1-149) x US-09-905-247-2 (1-870)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||          |||      ||||||   :::|||
Db         73 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 132

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                :::      :::|||:::         ||||||
Db        133 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCAGTCTT 192

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        193 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 252

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::           |||
Db        253 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 303

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                       |||   :::          |||   |||          :::|||
Db        304 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 363

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                       :::|||||||||   :::   |||:::|||::::::|||      ||||||
Db        364 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCA 423

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                        |||:::::::::   ||||||:::      |||:::   :::|||
Db        424 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCTGCTTTGGACAGTGCCATTACCACT 483

Qy        142 IleTrp 143
              ::::::
Db        484 TTGTTT 489

RESULT 10
US-10-280-679B-3
; Sequence 3, Application US/10280679B
```

```
; Publication No. US20030150019A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
;  FILE REFERENCE: LSBC-0109-US03
;  CURRENT APPLICATION NUMBER: US/10/280,679B
;  CURRENT FILING DATE:  2000-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 886
;   TYPE: DNA
;   ORGANISM: Chinese Cucumber
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (8)..(877)
;   OTHER INFORMATION:
US-10-280-679B-3

Alignment Scores:
Pred. No.:              8.81e-15      Length:          886
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     7             Gaps:            2

US-10-758-902-9 (1-149) x US-10-280-679B-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||          |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              :::     :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::::||||||:::           |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
                     |||   :::          |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                :::|||||||||   :::   |||:::|||::::::|||       ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                     |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                 ::::::
Db        491 TTGTTT 496

RESULT 11
US-10-280-725B-3
; Sequence 3, Application US/10280725B
; Publication No. US20040049025A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Recombinant Viral Nucleic Acids
;  FILE REFERENCE: LSBC-0109-US02
;  CURRENT APPLICATION NUMBER: US/10/280,725B
;  CURRENT FILING DATE:  2002-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 886
;   TYPE: DNA
;   ORGANISM: Chinese Cucumber
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (8)..(877)
;   OTHER INFORMATION:
US-10-280-725B-3

Alignment Scores:
Pred. No.:              8.81e-15      Length:          886
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     8             Gaps:            2

US-10-758-902-9 (1-149) x US-10-280-725B-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||          |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              :::     :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259
```

```
Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGly 101
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
Db        491 TTGTTT 496
```

RESULT 12
US-11-042-707-16
; Sequence 16, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/11/042,707
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 16
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mistletoe lectin A1
US-11-042-707-16

Alignment Scores:

Pred. No.:	2.57e-14	Length:	762
Score:	179.50	Matches:	50
Percent Similarity:	57.1%	Conservative:	26
Best Local Similarity:	37.6%	Mismatches:	48
Query Match:	23.4%	Indels:	9
DB:	13	Gaps:	4

US-10-758-902-9 (1-149) x US-11-042-707-16 (1-762)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGGTTACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
Db        226 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426
```

RESULT 13
US-11-042-707-19
; Sequence 19, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/11/042,707
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 19
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mistletoe lectin A1
US-11-042-707-19

Alignment Scores:

Pred. No.:	2.57e-14	Length:	762
Score:	179.50	Matches:	50
Percent Similarity:	57.1%	Conservative:	26
Best Local Similarity:	37.6%	Mismatches:	48
Query Match:	23.4%	Indels:	9
DB:	13	Gaps:	4

US-10-758-902-9 (1-149) x US-11-042-707-19 (1-762)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTGTTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
Db        226 TATGTTGTTGCATATCAG------------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
```

```
            ||||||:::   :::|||      |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 14
US-11-042-707-17
; Sequence 17, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 17
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-11-042-707-17

Alignment Scores:
Pred. No.:              2.6e-14       Length:          768
Score:                  179.50        Matches:         49
Percent Similarity:     56.7%         Conservative:    27
Best Local Similarity:  36.6%         Mismatches:      49
Query Match:            23.4%         Indels:          9
DB:                     13            Gaps:            4

US-10-758-902-9 (1-149) x US-11-042-707-17 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||:::::::|||         :::   ::::::      |||||||||||||||:::
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGATCACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThr---AsnArgValThrLeu 108
              |||      |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGCACCACCCGAGATAGATCCTCTCTC 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||      |||         |||         |||      :::
Db        334 CCATTCACTGGAAGCTACACCGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATC 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCTCTCGGTATAGAGCAACTCATTCAATCCGTCTCTGCGCTT 432

RESULT 15
US-11-042-707-20
; Sequence 20, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 20
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-11-042-707-20

Alignment Scores:
Pred. No.:              2.6e-14       Length:          768
Score:                  179.50        Matches:         49
Percent Similarity:     56.7%         Conservative:    27
Best Local Similarity:  36.6%         Mismatches:      49
Query Match:            23.4%         Indels:          9
DB:                     13            Gaps:            4

US-10-758-902-9 (1-149) x US-11-042-707-20 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||:::::::|||         :::   ::::::      |||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTATTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThr---AsnArgValThrLeu 108
              |||      |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGTACAACACGGGATAGAAGTTCTTTG 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||      |||         |||         |||      :::
Db        334 CCTTTTACTGGTTCTTATACAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATT 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCATTGGGAATTGAGCAGTTGATCCAGAGTGTTTCTGCTTTG 432

RESULT 16
US-09-347-064-7
; Sequence 7, Application US/09347064A
; Patent No. US20020045208A1
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
```

```
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064-7

Alignment Scores:
Pred. No.:              6.71e-14        Length:         756
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     3               Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064-7 (1-756)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||             ::::::      ||||||||||||||::::::
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 17
US-09-347-064-1
; Sequence 1, Application US/09347064A
; Patent No. US20020045208A1
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064-1

Alignment Scores:
Pred. No.:              6.79e-14        Length:         762
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     3               Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064-1 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||             ::::::      ||||||||||||||::::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 18
US-10-499-297-1
; Sequence 1, Application US/10499297
; Publication No. US20050221380A1
; GENERAL INFORMATION:
;  APPLICANT: Muthing, Johannes
;  APPLICANT:  Peter-Katalinic, Jasna
;  APPLICANT:  Langer, Martin
;  APPLICANT:  Mockel, Babette
;  APPLICANT:  Eck, Jurgen
;  TITLE OF INVENTION: METHOD FOR DETERMINATION OF THE
;  TITLE OF INVENTION:  RESPONSIVENESS OF AN INDIVIDUAL TO MISTLETOE LECTIN
;  FILE REFERENCE: VOSS-P01-010
;  CURRENT APPLICATION NUMBER: US/10/499,297
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: EP 01130745.1
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 855
;   TYPE: DNA
;   ORGANISM: Viscum album
US-10-499-297-1

Alignment Scores:
Pred. No.:              8.05e-14        Length:         855
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     10              Gaps:           4
```

US-10-758-902-9 (1-149) x US-10-499-297-1 (1-855)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db        145 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 204

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        205 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 264

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                 ::::::      |||||||||||||||::::::
Db        265 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 324

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                ||:::::   ||||||
Db        325 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 372

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||  |||  |||  |||   :::|||
Db        373 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 429

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::||||||||||      |||          |||          |||      :::
Db        430 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 486

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        487 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 525
```

RESULT 19
US-11-042-707-15
; Sequence 15, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/11/042,707
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 15
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MLA-I
US-11-042-707-15

Alignment Scores:

Pred. No.:	2.03e-13	Length:	1596
Score:	176.50	Matches:	49
Percent Similarity:	57.1%	Conservative:	27
Best Local Similarity:	36.8%	Mismatches:	48
Query Match:	23.0%	Indels:	9
DB:	13	Gaps:	4

US-10-758-902-9 (1-149) x US-11-042-707-15 (1-1596)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                 ::::::      |||||||||||||||::::::
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                ||:::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||  |||  |||  |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::||||||||||      |||          |||          |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426
```

RESULT 20
US-11-042-707-18
; Sequence 18, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/11/042,707
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 18
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MLI (matched)
US-11-042-707-18

Alignment Scores:

Pred. No.:	2.03e-13	Length:	1596
Score:	176.50	Matches:	49
Percent Similarity:	57.1%	Conservative:	27
Best Local Similarity:	36.8%	Mismatches:	48
Query Match:	23.0%	Indels:	9
DB:	13	Gaps:	4

US-10-758-902-9 (1-149) x US-11-042-707-18 (1-1596)

```
Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                 ::::::      |||||||||||||||::::::
Db        166 GTTGAATTGACTAACCAAGGAGGTGATAGTATTACTGCTGCTATTGATGTGACTAACCTT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                ||:::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273
```

```
Qy          90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
               |||      |||   :::   ||||||  |||   |||   |||   :::|||
Db         274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330

Qy         110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
               |||:::|||||||||      |||          |||          |||      :::
Db         331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy         130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
               ||||||:::   :::|||      |||:::   |||:::
Db         388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 21
US-10-499-297-5
; Sequence 5, Application US/10499297
; Publication No. US20050221380A1
; GENERAL INFORMATION:
;  APPLICANT: Muthing, Johannes
;  APPLICANT:  Peter-Katalinic, Jasna
;  APPLICANT:  Langer, Martin
;  APPLICANT:  Mockel, Babette
;  APPLICANT:  Eck, Jurgen
;  TITLE OF INVENTION: METHOD FOR DETERMINATION OF THE
;  TITLE OF INVENTION:  RESPONSIVENESS OF AN INDIVIDUAL TO MISTLETOE LECTIN
;  FILE REFERENCE: VOSS-P01-010
;  CURRENT APPLICATION NUMBER: US/10/499,297
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: EP 01130745.1
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1958
;   TYPE: DNA
;   ORGANISM: Viscum album
US-10-499-297-5

Alignment Scores:
Pred. No.:              2.75e-13        Length:         1958
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     10              Gaps:           4

US-10-758-902-9 (1-149) x US-10-499-297-5 (1-1958)

Qy          13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
               ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         199 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 258

Qy          33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
               ::::::|||:::      |||:::         :::::|||   :::|||||||||||
Db         259 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 318

Qy          50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
               |||:::::::|||           ::::::      ||||||||||||||||::::::
Db         319 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 378

Qy          70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
               |||||||||   ||||||                     |||::::::   ||||||
Db         379 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 426

Qy          90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
               |||      |||   :::   ||||||  |||   |||   |||   :::|||
Db         427 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 483

Qy         110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
               |||:::|||||||||      |||          |||          |||      :::
Db         484 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 540

Qy         130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
               ||||||:::   :::|||      |||:::   |||:::
Db         541 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 579

RESULT 22
US-10-800-052-35
; Sequence 35, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 2788
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: pWKK-21
US-10-800-052-35

Alignment Scores:
Pred. No.:              1.44e-12        Length:         2788
Score:                  173.00          Matches:        52
Percent Similarity:     52.2%           Conservative:   31
Best Local Similarity:  32.7%           Mismatches:     60
Query Match:            22.5%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-35 (1-2788)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||          |||          |||      ||||||
Db        1288 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1347

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db        1348 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1407

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::          ::::::||||||:::|||||||||:::::
Db        1408 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1467

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        1468 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1527

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        1528 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1575

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        1576 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1635

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||          |||          |||:::::::::|||||||||
Db        1636 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1695

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                     ||||||   :::|||   |||::::::           |||   ||||||
Db        1696 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1752

RESULT 23
US-10-800-052-2
; Sequence 2, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
```

```
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 2803
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Plasmid pWKK-500.
US-10-800-052-2

Alignment Scores:
Pred. No.:              1.46e-12        Length:         2803
Score:                  173.00          Matches:        52
Percent Similarity:     52.2%           Conservative:   31
Best Local Similarity:  32.7%           Mismatches:     60
Query Match:            22.5%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-2 (1-2803)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||     ::::::|||             |||           |||     ||||||
Db       1402 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1461

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db       1462 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1521

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::|||||||||::::::
Db       1522 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1581

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db       1582 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1641

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||            ::::::
Db       1642 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1689

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db       1690 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1749

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||.        |||         |||:::::::::|||||||||
Db       1750 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1809

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                ||||||   :::|||   |||::::::            |||   ||||||
Db       1810 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1866

RESULT 24
US-10-800-052-37
; Sequence 37, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 2805
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: pWKK-15
US-10-800-052-37

Alignment Scores:
Pred. No.:              1.46e-12        Length:         2805
Score:                  173.00          Matches:        52
Percent Similarity:     52.2%           Conservative:   31
Best Local Similarity:  32.7%           Mismatches:     60
Query Match:            22.5%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-37 (1-2805)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||     ::::::|||             |||           |||     ||||||
Db       1405 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1464

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db       1465 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1524

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::|||||||||::::::
Db       1525 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1584

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db       1585 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1644

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||            ::::::
Db       1645 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1692

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db       1693 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1752

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db       1753 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1812

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                ||||||   :::|||   |||::::::            |||   ||||||
Db       1813 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1869

RESULT 25
US-10-800-052-20
; Sequence 20, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2869
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Coding region of pWKK-700.
US-10-800-052-20

Alignment Scores:
Pred. No.:              1.51e-12        Length:         2869
Score:                  173.00          Matches:        52
Percent Similarity:     52.2%           Conservative:   31
Best Local Similarity:  32.7%           Mismatches:     60
Query Match:            22.5%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-20 (1-2869)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
```

```
Db       1486 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1545

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db       1546 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1605

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db       1606 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1665

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db       1666 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1725

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db       1726 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1773

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db       1774 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1833

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db       1834 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1893

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
Db       1894 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1950
```

RESULT 26
US-10-800-052-26
; Sequence 26, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
; APPLICANT: Keener, William K
; TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
; FILE REFERENCE: B-221
; CURRENT APPLICATION NUMBER: US/10/800,052
; CURRENT FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 2878
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pWKK-800
US-10-800-052-26

Alignment Scores:

Pred. No.:	1.51e-12	Length:	2878
Score:	173.00	Matches:	52
Percent Similarity:	52.2%	Conservative:	31
Best Local Similarity:	32.7%	Mismatches:	60
Query Match:	22.5%	Indels:	16
DB:	10	Gaps:	6

US-10-758-902-9 (1-149) x US-10-800-052-26 (1-2878)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db       1495 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1554

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db       1555 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1614

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db       1615 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1674

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db       1675 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1734

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db       1735 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1782

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db       1783 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1842

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db       1843 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1902

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
Db       1903 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1959
```

RESULT 27
US-11-010-795-23
; Sequence 23, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Ricinus communis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(804)
US-11-010-795-23

Alignment Scores:

Pred. No.:	8.37e-13	Length:	807
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	16	Gaps:	6

US-10-758-902-9 (1-149) x US-11-010-795-23 (1-807)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db         19 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 78

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db         79 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 138

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        139 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 198

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        199 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 258

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
```

```
Db        259 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 306

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db        307 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 366

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        367 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 426

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        427 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 483

RESULT 28
US-10-893-584-273
; Sequence 273, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 273
;   LENGTH: 1623
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Ricin-like toxin (TST10054)
US-10-893-584-273

Alignment Scores:
Pred. No.:              2.36e-12        Length:         1623
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-273 (1-1623)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db         16 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 75

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db         76 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 135

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        136 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 195

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        196 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 255

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||                  ::::::
Db        256 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 303

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db        304 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 363

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        364 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 423

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        424 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 480

RESULT 29
US-09-785-921A-2
; Sequence 2, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 2
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-2

Alignment Scores:
Pred. No.:              2.6e-12         Length:         1731
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-785-921A-2 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||                  ::::::
Db        361 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGAGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585
```

```
RESULT 30
US-09-785-921A-3
; Sequence 3, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 3
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-3

Alignment Scores:
Pred. No.:              2.6e-12       Length:          1731
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     3             Gaps:            6

US-10-758-902-9 (1-149) x US-09-785-921A-3 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::|||||||:::||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                         :::   |||   |||           ::::::
Db        361 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                ||||||   :::|||   |||::::::          |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 31
US-10-618-560-2
; Sequence 2, Application US/10618560
; Publication No. US20040048784A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 2
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-2

Alignment Scores:
Pred. No.:              2.6e-12       Length:          1731
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-10-618-560-2 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::|||||||:::||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                         :::   |||   |||           ::::::
Db        361 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGAGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                ||||||   :::|||   |||::::::          |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 32
US-10-618-560-3
; Sequence 3, Application US/10618560
; Publication No. US20040048784A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 3
;   LENGTH: 1731
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-3
```

```
Alignment Scores:
Pred. No.:              2.6e-12         Length:         1731
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-3 (1-1731)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        121 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 180

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        181 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 240

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::||||||:::|||||||:::::::::
Db        241 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 300

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::::::  :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        301 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 360

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||            ::::::
Db        361 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 408

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        409 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 468

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        469 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 528

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        529 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 585

RESULT 33
US-09-785-921A-10
; Sequence 10, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 10
;   LENGTH: 1805
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-10

Alignment Scores:
Pred. No.:              2.76e-12        Length:         1805
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-785-921A-10 (1-1805)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        129 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 188

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        189 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 248

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::||||||:::|||||||:::::::::
Db        249 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 308

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::::::  :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        309 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 368

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||            ::::::
Db        369 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 416

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        417 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 476

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        477 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 536

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        537 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 593

RESULT 34
US-10-618-560-10
; Sequence 10, Application US/10618560
; Publication No. US20040048784A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/10/618,560
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: US 09/785,921
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 10
;   LENGTH: 1805
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-10-618-560-10

Alignment Scores:
Pred. No.:              2.76e-12        Length:         1805
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-10-618-560-10 (1-1805)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        129 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 188

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        189 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 248

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::||||||:::|||||||:::::::::
Db        249 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 308
```

```
Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db         309 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 368

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db         369 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 416

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         417 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 476

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         477 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 536

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                     ||||||   :::|||   |||::::::             |||   ||||||
Db         537 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 593

RESULT 35
US-10-893-584-196
; Sequence 196, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
;   LENGTH: 1807
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-196

Alignment Scores:
Pred. No.:              2.77e-12        Length:         1807
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-196 (1-1807)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||     ::::::|||           |||           |||     ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db         367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                     ||||||   :::|||   |||::::::             |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 36
US-10-893-584-168
; Sequence 168, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 168
;   LENGTH: 1810
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-168

Alignment Scores:
Pred. No.:              2.77e-12        Length:         1810
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-168 (1-1810)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||     ::::::|||           |||           |||     ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                     :::           ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
```

```
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 37
US-10-893-584-245
; Sequence 245, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
;   LENGTH: 1813
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-245

Alignment Scores:
Pred. No.:              2.78e-12        Length:         1813
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-245 (1-1813)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 38
US-10-893-584-238
; Sequence 238, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
;   LENGTH: 1819
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-238

Alignment Scores:
Pred. No.:              2.8e-12         Length:         1819
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-238 (1-1819)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474
```

```
Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 39
US-10-893-584-175
; Sequence 175, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-175

Alignment Scores:
Pred. No.:              2.8e-12       Length:          1822
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     10            Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-175 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 40
US-10-893-584-182
; Sequence 182, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-182

Alignment Scores:
Pred. No.:              2.8e-12       Length:          1822
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     10            Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-182 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
```

```
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 41
US-10-893-584-231
; Sequence 231, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 231
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-231

Alignment Scores:

Pred. No.:	2.81e-12	Length:	1825
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	10	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-231 (1-1825)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 42

```
US-10-893-584-210
; Sequence 210, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; LENGTH: 1828
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-210
```

Alignment Scores:

Pred. No.:	2.82e-12	Length:	1828
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	10	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-210 (1-1828)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 43
US-10-893-584-161
; Sequence 161, Application US/10893584
; Publication No. US20050272048A1

```
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 161
;   LENGTH: 1831
;*  TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-161
```

Alignment Scores:			
Pred. No.:	2.82e-12	Length:	1831
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	10	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-161 (1-1831)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 44
US-10-893-584-203
; Sequence 203, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
;   LENGTH: 1831
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-203
```

Alignment Scores:			
Pred. No.:	2.82e-12	Length:	1831
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	10	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-203 (1-1831)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 45
US-10-893-584-154
; Sequence 154, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
```

```
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
;   LENGTH: 1834
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-154
```

Alignment Scores:

Pred. No.:	2.83e-12	Length:	1834
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	10	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-154 (1-1834)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||              |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 46
US-10-893-584-266
; Sequence 266, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-266
```

Alignment Scores:

Pred. No.:	2.84e-12	Length:	1837
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	10	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-266 (1-1837)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||              |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 47
US-10-893-584-259
; Sequence 259, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
```

```
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 259
;   LENGTH: 1843
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-259

Alignment Scores:
Pred. No.:                2.85e-12        Length:         1843
Score:                    169.00          Matches:        51
Percent Similarity:       52.2%           Conservative:   32
Best Local Similarity:    32.1%           Mismatches:     60
Query Match:              22.0%           Indels:         16
DB:                       10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-259 (1-1843)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||       ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 48
US-10-893-584-252
; Sequence 252, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 252
;   LENGTH: 1849
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-252

Alignment Scores:
Pred. No.:                2.86e-12        Length:         1849
Score:                    169.00          Matches:        51
Percent Similarity:       52.2%           Conservative:   32
Best Local Similarity:    32.1%           Mismatches:     60
Query Match:              22.0%           Indels:         16
DB:                       10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-252 (1-1849)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||       ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 49
US-10-893-584-147
; Sequence 147, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 147
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-147

Alignment Scores:
Pred. No.:              2.88e-12        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-147 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::|||||:::|||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 50
US-10-893-584-189
; Sequence 189, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-189

Alignment Scores:
Pred. No.:              2.88e-12        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-189 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::|||||:::|||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 51
US-10-893-584-217
; Sequence 217, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-217
```

```
Alignment Scores:
Pred. No.:              2.88e-12        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-217 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      :::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 52
US-10-893-584-224
; Sequence 224, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-224

Alignment Scores:
Pred. No.:              2.88e-12        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-224 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      :::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 53
US-10-477-373A-2
; Sequence 2, Application US/10477373A
; Publication No. US20050191626A1
; GENERAL INFORMATION:
;  APPLICANT: TAIRA Kazunari
;  APPLICANT:  FUJITA Satoshi
;  APPLICANT:  YOSHIZAKI Shinya
;  APPLICANT:  WARASHINA Masaki
;  TITLE OF INVENTION: METHODS FOR FORMING A STABLE COMPLEX BETWEEN THE TRANSCRIPT AND
;  TITLE OF INVENTION:  TRANSLATION PRODUCT OF A DNA ENCODING AN ARBITRARY POLYPEPTIDE, N
;  TITLE OF INVENTION:  CONSTRUCTS TO BE USED IN THESE METHODS, COMPLEXES FORMED BY THE N
;  TITLE OF INVENTION:  OF THESE METHODS TO SCREEN FOR FUNCTIONAL PROTEINS, AND mRNAs ANI
;  TITLE OF INVENTION:  ENCODING THESE PROTEINS
;  FILE REFERENCE: 6235-67303-01
;  CURRENT APPLICATION NUMBER: US/10/477,373A
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: PCT/JP02/04582
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: JP 2001-141594
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: JP 2002-62751
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 2
;   LENGTH: 7306
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant expression vector for streptavidin fused with the Rici
;   OTHER INFORMATION: communis Ricin-A chain (short spacer).
US-10-477-373A-2

Alignment Scores:
```

```
Pred. No.:              3.04e-11        Length:         7306
Score:                  168.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            21.9%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-477-373A-2 (1-7306)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db       5787 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 5846

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||      |||      ::::::||||||
Db       5847 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 5906

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::           ::::::|||||:::||||||:::::::::
Db       5907 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 5966

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db       5967 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 6026

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db       6027 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 6074

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db       6075 GAAGCAATCACTTATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 6134

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||::::::::|||||||||
Db       6135 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 6194

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db       6195 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 6251

RESULT 54
US-10-477-373A-1
; Sequence 1, Application US/10477373A
; Publication No. US20050191626A1
; GENERAL INFORMATION:
;  APPLICANT: TAIRA Kazunari
;  APPLICANT:  FUJITA Satoshi
;  APPLICANT:  YOSHIZAKI Shinya
;  APPLICANT:  WARASHINA Masaki
;  TITLE OF INVENTION: METHODS FOR FORMING A STABLE COMPLEX BETWEEN THE TRANSCRIPT AND
;  TITLE OF INVENTION:  TRANSLATION PRODUCT OF A DNA ENCODING AN ARBITRARY POLYPEPTIDE,
;  TITLE OF INVENTION:  CONSTRUCTS TO BE USED IN THESE METHODS, COMPLEXES FORMED BY THE
;  TITLE OF INVENTION:  OF THESE METHODS TO SCREEN FOR FUNCTIONAL PROTEINS, AND mRNAs AN
;  TITLE OF INVENTION:  ENCODING THESE PROTEINS
;  FILE REFERENCE: 6235-67303-01
;  CURRENT APPLICATION NUMBER: US/10/477,373A
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: PCT/JP02/04582
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: JP 2001-141594
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: JP 2002-62751
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 1
;   LENGTH: 8155
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant expression vector for streptavidin fused with the Ric
;   OTHER INFORMATION: communis Ricin-A chain (long spacer).
US-10-477-373A-1

Alignment Scores:
Pred. No.:              3.58e-11        Length:         8155
Score:                  168.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            21.9%           Indels:         16
DB:                     10              Gaps:           6

US-10-758-902-9 (1-149) x US-10-477-373A-1 (1-8155)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db       5787 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 5846

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||      |||      ::::::||||||
Db       5847 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 5906

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::           ::::::|||||:::||||||:::::::::
Db       5907 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 5966

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db       5967 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 6026

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db       6027 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 6074

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db       6075 GAAGCAATCACTTATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 6134

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||::::::::|||||||||
Db       6135 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 6194

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db       6195 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 6251

RESULT 55
US-09-785-921A-1
; Sequence 1, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K.
;  APPLICANT:  Ward, Thomas E.
;  TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: LIT-PI-529
;  CURRENT APPLICATION NUMBER: US/09/785,921A
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
;   LENGTH: 1698
;   TYPE: DNA
;   ORGANISM: Ricinus communis
US-09-785-921A-1

Alignment Scores:
Pred. No.:              4.82e-12        Length:         1698
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     3               Gaps:           6

US-10-758-902-9 (1-149) x US-09-785-921A-1 (1-1698)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
```

```
Db         88 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 147

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        148 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 207

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        208 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 267

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        268 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 327

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        328 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 375

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        376 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 435

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        436 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 495

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147

Db        496 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 552
```

RESULT 56
US-10-618-560-1
; Sequence 1, Application US/10618560
; Publication No. US20040048784A1
; GENERAL INFORMATION:
; APPLICANT: Keener, William K.
; APPLICANT: Ward, Thomas E.
; TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: LIT-PI-529
; CURRENT APPLICATION NUMBER: US/10/618,560
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 09/785,921
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Ricinus communis
US-10-618-560-1

Alignment Scores:

Pred. No.:	4.82e-12	Length:	1698
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-10-618-560-1 (1-1698)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db         88 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 147

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        148 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 207

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        208 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 267

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        268 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 327

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        328 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 375

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        376 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 435

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        436 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 495

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147

Db        496 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 552
```

RESULT 57
US-10-394-511-3
; Sequence 3, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cathepsin B linker regions of pAP-214
US-10-394-511-3

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-3 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366
```

```
Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                                :::   |||   |||         ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                  |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                     ||||||   :::|||   |||::::::            |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 58
US-10-394-511-5
; Sequence 5, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-216 insert
US-10-394-511-5

Alignment Scores:
Pred. No.:              5.5e-12         Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-5 (1-1855)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
                 |||      ::::::|||           |||           |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||          :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::          ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||         ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                  |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                     ||||||   :::|||   |||::::::            |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 59
US-10-394-511-7
; Sequence 7, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-218 insert
US-10-394-511-7

Alignment Scores:
Pred. No.:              5.5e-12         Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-7 (1-1855)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
                 |||      ::::::|||           |||           |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||          :::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::          ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||         ::::::
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                  |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474
```

```
Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||::::::::::||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 60
US-10-394-511-9
; Sequence 9, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-220 insert
US-10-394-511-9

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-9 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||::::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||::::::::::||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 61
US-10-394-511-13
; Sequence 13, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-224 insert
US-10-394-511-13

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-13 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::           ::::::||||||:::||||||::::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||::::::::::||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 62
US-10-394-511-15
; Sequence 15, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-226 insert
US-10-394-511-15

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-15 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||        |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 63
US-10-394-511-17
; Sequence 17, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-228 insert
US-10-394-511-17

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-17 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||        |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 64
US-10-394-511-19
; Sequence 19, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
```

```
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-230 insert
US-10-394-511-19

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-19 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||              |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||          ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 65
US-10-394-511-21
; Sequence 21, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-232 insert
US-10-394-511-21

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-21 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||              |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||          ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 66
US-10-394-511-23
; Sequence 23, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
```

```
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-234 insert
US-10-394-511-23
```

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-23 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 67
US-10-394-511-25
; Sequence 25, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-236 insert
US-10-394-511-25
```

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-25 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 68
US-10-394-511-27
; Sequence 27, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: pAP-238 insert
US-10-394-511-27

Alignment Scores:
Pred. No.:              5.5e-12        Length:          1855
Score:                  167.00         Matches:         51
Percent Similarity:     51.6%          Conservative:    31
Best Local Similarity:  32.1%          Mismatches:      61
Query Match:            21.7%          Indels:          16
DB:                     7              Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-27 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 69
US-10-394-511-29
; Sequence 29, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-240 insert
US-10-394-511-29

Alignment Scores:
Pred. No.:              5.5e-12        Length:          1855
Score:                  167.00         Matches:         51
Percent Similarity:     51.6%          Conservative:    31
Best Local Similarity:  32.1%          Mismatches:      61
Query Match:            21.7%          Indels:          16
DB:                     7              Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-29 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 70
US-10-394-511-31
; Sequence 31, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-242 insert
US-10-394-511-31

Alignment Scores:
Pred. No.:              5.5e-12        Length:          1855
Score:                  167.00         Matches:         51
Percent Similarity:     51.6%          Conservative:    31
```

```
Best Local Similarity:  32.1%          Mismatches:     61
Query Match:            21.7%          Indels:         16
DB:                     7              Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-31 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 71
US-10-394-511-33
; Sequence 33, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-244 insert
US-10-394-511-33

Alignment Scores:
Pred. No.:              5.5e-12        Length:         1855
Score:                  167.00         Matches:        51
Percent Similarity:     51.6%          Conservative:   31
Best Local Similarity:  32.1%          Mismatches:     61
Query Match:            21.7%          Indels:         16
DB:                     7              Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-33 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 72
US-10-394-511-35
; Sequence 35, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-246 insert
US-10-394-511-35

Alignment Scores:
Pred. No.:              5.5e-12        Length:         1855
Score:                  167.00         Matches:        51
Percent Similarity:     51.6%          Conservative:   31
Best Local Similarity:  32.1%          Mismatches:     61
Query Match:            21.7%          Indels:         16
DB:                     7              Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-35 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
```

```
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 73
US-10-394-511-37
; Sequence 37, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pPA-248 insert
US-10-394-511-37

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-37 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 74
US-10-394-511-39
; Sequence 39, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-250 insert
US-10-394-511-39

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-39 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::           ::::::||||||:::||||||:::::::::
```

```
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                         :::   |||   |||              ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 75
US-10-394-511-48
; Sequence 48, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-254 insert
US-10-394-511-48

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-48 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                         :::   |||   |||              ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 76
US-10-394-511-50
; Sequence 50, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-258 insert
US-10-394-511-50

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-50 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::          ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                         :::   |||   |||              ::::::
```

```
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 77
US-10-394-511-52
; Sequence 52, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-256 insert
US-10-394-511-52

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-52 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||                  ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 78
US-10-394-511-54
; Sequence 54, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-260 insert
US-10-394-511-54

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-54 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||                  ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
```

```
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                 ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 79
US-10-394-511-74
; Sequence 74, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-262 insert
US-10-394-511-74

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-74 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::           ::::::||||||:::||||||::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||   ||||||   |||      |||:::::::::
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                 ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 80
US-10-394-511-77
; Sequence 77, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-264 insert
US-10-394-511-77

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-77 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::           ::::::||||||:::||||||::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||   ||||||   |||      |||:::::::::
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                 ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 81
US-10-394-511-80

```
; Sequence 80, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-266 insert
US-10-394-511-80

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-80 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 82
US-10-394-511-83
; Sequence 83, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-268 insert
US-10-394-511-83

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-83 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 83
US-10-394-511-86
; Sequence 86, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
```

```
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-270 insert
US-10-394-511-86

Alignment Scores:
Pred. No.:              5.5e-12        Length:          1855
Score:                  167.00         Matches:         51
Percent Similarity:     51.6%          Conservative:    31
Best Local Similarity:  32.1%          Mismatches:      61
Query Match:            21.7%          Indels:          16
DB:                     7              Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-86 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 84
US-10-394-511-89
; Sequence 89, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-272 insert
US-10-394-511-89

Alignment Scores:
Pred. No.:              5.5e-12        Length:          1855
Score:                  167.00         Matches:         51
Percent Similarity:     51.6%          Conservative:    31
Best Local Similarity:  32.1%          Mismatches:      61
Query Match:            21.7%          Indels:          16
DB:                     7              Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-89 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 85
US-10-394-511-92
; Sequence 92, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
```

```
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-274 insert
US-10-394-511-92

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-92 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 86
US-10-394-511-95
; Sequence 95, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-276 insert
US-10-394-511-95

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     7             Gaps:            6

US-10-758-902-9 (1-149) x US-10-394-511-95 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 87
US-10-394-511-98
; Sequence 98, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-278 insert
US-10-394-511-98
```

Alignment Scores:
Pred. No.: 5.5e-12 Length: 1855
Score: 167.00 Matches: 51
Percent Similarity: 51.6% Conservative: 31
Best Local Similarity: 32.1% Mismatches: 61
Query Match: 21.7% Indels: 16
DB: 7 Gaps: 6

US-10-758-902-9 (1-149) x US-10-394-511-98 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                ::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 88
US-10-394-511-101
; Sequence 101, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-280 insert
US-10-394-511-101

Alignment Scores:
Pred. No.: 5.5e-12 Length: 1855
Score: 167.00 Matches: 51
Percent Similarity: 51.6% Conservative: 31
Best Local Similarity: 32.1% Mismatches: 61
Query Match: 21.7% Indels: 16
DB: 7 Gaps: 6

US-10-758-902-9 (1-149) x US-10-394-511-101 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                ::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 89
US-10-394-511-104
; Sequence 104, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-282 insert
US-10-394-511-104

Alignment Scores:
Pred. No.: 5.5e-12 Length: 1855
Score: 167.00 Matches: 51
Percent Similarity: 51.6% Conservative: 31
Best Local Similarity: 32.1% Mismatches: 61
Query Match: 21.7% Indels: 16
DB: 7 Gaps: 6

```
US-10-758-902-9 (1-149) x US-10-394-511-104 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::  :::|||   :::|||:::||||||||:::  |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                     :::  |||  |||              ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||  :::  ||||||     |||  ||||||  |||     |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||  :::|||          |||          |||:::::::|||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||  :::|||  |||::::           |||  ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 90
US-10-394-511-110
; Sequence 110, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-286 insert
US-10-394-511-110

Alignment Scores:
Pred. No.:              5.5e-12         Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-110 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::  :::|||   :::|||:::||||||||:::  |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                     :::  |||  |||              ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||  :::  ||||||     |||  ||||||  |||     |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||  :::|||          |||          |||:::::::|||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||  :::|||  |||::::           |||  ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 91
US-10-394-511-113
; Sequence 113, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-288 insert
US-10-394-511-113

Alignment Scores:
Pred. No.:              5.5e-12         Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-113 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::  :::|||      |||     |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::  :::|||   :::|||:::||||||||:::  |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                     :::  |||  |||              ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||  :::  ||||||     |||  ||||||  |||     |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||  :::|||          |||          |||:::::::|||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||  :::|||  |||::::           |||  ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 91
US-10-394-511-113
; Sequence 113, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-27
;  CURRENT APPLICATION NUMBER: US/10/394,511
;  CURRENT FILING DATE:  2003-03-24
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/063,715
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: US 60/045,148
;  PRIOR FILING DATE: 1997-10-30
;  NUMBER OF SEQ ID NOS: 142
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-288 insert
US-10-394-511-113

Alignment Scores:
Pred. No.:              5.5e-12         Length:         1855
Score:                  167.00          Matches:        51
Percent Similarity:     51.6%           Conservative:   31
Best Local Similarity:  32.1%           Mismatches:     61
Query Match:            21.7%           Indels:         16
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-10-394-511-113 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
```

```
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 92
US-10-394-511-116
; Sequence 116, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-290 insert
US-10-394-511-116

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-116 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 93
US-10-394-511-119
; Sequence 119, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-292 insert
US-10-394-511-119

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-119 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                                                            
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                                                            
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
                                                            
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                                                            
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 94
US-10-394-511-122
; Sequence 122, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-294 insert
US-10-394-511-122

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-122 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
                                                            
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                                                            
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                                                            
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
                                                            
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                                                            
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                                                            
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
                                                            
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                                                            
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 95
US-10-394-511-125
; Sequence 125, Application US/10394511
; Publication No. US20040009551A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-27
; CURRENT APPLICATION NUMBER: US/10/394,511
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/063,715
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 60/045,148
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-296 insert
US-10-394-511-125

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	7	Gaps:	6

US-10-758-902-9 (1-149) x US-10-394-511-125 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
                                                            
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                                                            
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                                                            
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
                                                            
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                                                            
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
```

```
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 96
US-10-893-584-3
; Sequence 3, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Cathepsin B linker regions of pAP-214
US-10-893-584-3

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     10            Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-3 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
```

```
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 97
US-10-893-584-5
; Sequence 5, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-216 insert
US-10-893-584-5

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     10            Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-5 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474
```

```
Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 98
US-10-893-584-7
; Sequence 7, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-218 insert
US-10-893-584-7

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     10            Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-7 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||     |||   ||||||   |||     |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474
```

```
Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 99
US-10-893-584-9
; Sequence 9, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP-220 insert
US-10-893-584-9

Alignment Scores:
Pred. No.:              5.5e-12       Length:          1855
Score:                  167.00        Matches:         51
Percent Similarity:     51.6%         Conservative:    31
Best Local Similarity:  32.1%         Mismatches:      61
Query Match:            21.7%         Indels:          16
DB:                     10            Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-9 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||         :::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||     |||   ||||||   |||     |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
```

```
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 100
US-10-893-584-13
; Sequence 13, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-224 insert
US-10-893-584-13

Alignment Scores:

Pred. No.:	5.5e-12	Length:	1855
Score:	167.00	Matches:	51
Percent Similarity:	51.6%	Conservative:	31
Best Local Similarity:	32.1%	Mismatches:	61
Query Match:	21.7%	Indels:	16
DB:	10	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-13 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGATATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT.474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
```

```
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

Search completed: September 18, 2006, 21:18:18
Job time : 1716.28 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 20:23:47 ; Search time 266.369 Seconds
(without alignments)
1471.519 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2330496 seqs, 876882855 residues

Total number of hits satisfying chosen parameters: 4660992

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/absS/ABSSWEB_spool/US10758902/runat_18092006_162720_11806/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10758902_@CGN_1_1_306_@runat_18092006_162720_11806 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	156.5	20.4	1224	7	US-11-345-661-9	Sequence 9, Appli
2	156.5	20.4	1224	7	US-11-345-661-11	Sequence 11, Appl
3	104.5	13.6	765	7	US-11-361-977A-66	Sequence 66, Appl
4	104.5	13.6	984	7	US-11-361-977A-60	Sequence 60, Appl
5	104.5	13.6	993	7	US-11-361-977A-63	Sequence 63, Appl
6	104.5	13.6	999	7	US-11-361-977A-54	Sequence 54, Appl
7	104.5	13.6	999	7	US-11-361-977A-57	Sequence 57, Appl
8	85.5	11.1	990	6	US-10-953-349-30542	Sequence 30542, A
9	85.5	11.1	990	9	US-11-056-355B-61233	Sequence 61233, A
10	82	10.7	2400	8	US-11-216-545-3907	Sequence 3907, Ap
11	81.5	10.6	2495	9	US-11-218-305-3386	Sequence 3386, Ap
12	81	10.5	6159	9	US-11-013-711-8	Sequence 8, Appli
13	80.5	10.5	1305	9	US-11-316-535A-132	Sequence 132, App
14	80.5	10.5	1443	9	US-11-316-535A-156	Sequence 156, App
15	80	10.4	3111	9	US-11-348-413-4995	Sequence 4995, Ap
c 16	79.5	10.4	1767	9	US-11-174-307B-1881	Sequence 1881, Ap
c 17	79.5	10.4	3426	9	US-11-174-307B-1551	Sequence 1551, Ap
18	77.5	10.1	2928	9	US-11-348-413-270	Sequence 270, App
19	75.5	9.8	1860	8	US-11-266-748A-353475	Sequence 353475,
20	75.5	9.8	1860	8	US-11-266-748A-384474	Sequence 384474,
c 21	75.5	9.8	1860	8	US-11-266-748A-436854	Sequence 436854,
22	75.5	9.8	2598	9	US-11-056-355B-97980	Sequence 97980, A
23	75.5	9.8	2598	9	US-11-056-355B-109219	Sequence 109219,
24	75.5	9.8	2730	6	US-10-449-902-24297	Sequence 24297, A
25	75.5	9.8	5372	8	US-11-266-748A-31618	Sequence 31618, A
26	75	9.8	1095	9	US-11-348-413-13618	Sequence 13618, A
27	75	9.8	1256	9	US-11-218-305-3486	Sequence 3486, Ap
28	75	9.8	3504	9	US-11-348-413-1439	Sequence 1439, Ap
29	74.5	9.7	1283	9	US-11-056-355B-86436	Sequence 86436, A
c 30	74.5	9.7	1487	9	US-11-218-305-13574	Sequence 13574, A
31	74.5	9.7	1823	6	US-10-953-349-5403	Sequence 5403, Ap
32	74.5	9.7	4067	6	US-10-449-902-12843	Sequence 12843, A
33	74	9.6	1437	9	US-11-056-355B-12863	Sequence 12863, A
34	74	9.6	1560	9	US-11-348-413-7411	Sequence 7411, Ap
c 35	73.5	9.6	1998	9	US-11-218-305-9122	Sequence 9122, Ap
36	73.5	9.6	3243	9	US-11-348-413-7015	Sequence 7015, Ap
37	72.5	9.4	1026	9	US-11-348-413-443	Sequence 443, App
38	72.5	9.4	1533	9	US-11-348-413-181	Sequence 181, App
39	72.5	9.4	5479	6	US-10-505-928-472	Sequence 472, App
40	72	9.4	1122	6	US-10-471-571A-705	Sequence 705, App
41	72	9.4	1240	9	US-11-218-305-3485	Sequence 3485, Ap
42	72	9.4	2224	6	US-10-449-902-27052	Sequence 27052, A
43	72	9.4	2832	8	US-11-217-529-77685	Sequence 77685, A
44	71.5	9.3	1374	9	US-11-348-413-13946	Sequence 13946, A
45	71.5	9.3	1788	8	US-11-217-529-77659	Sequence 77659, A
c 46	71.5	9.3	1966	6	US-10-449-902-21229	Sequence 21229, A
c 47	71.5	9.3	2272	6	US-10-449-902-5375	Sequence 5375, Ap
c 48	71.5	9.3	4382	9	US-11-218-305-3302	Sequence 3302, Ap
c 49	71	9.2	1007	9	US-11-218-305-24103	Sequence 24103, A
50	71	9.2	1611	9	US-11-174-307B-3703	Sequence 3703, Ap
51	71	9.2	2055	9	US-11-218-305-12179	Sequence 12179, A
c 52	71	9.2	2704	9	US-11-218-305-24390	Sequence 24390, A
c 53	71	9.2	4066	6	US-10-449-902-19092	Sequence 19092, A
54	71	9.2	4593	9	US-11-333-747A-43	Sequence 43, Appl
55	70.5	9.2	891	9	US-11-348-413-13061	Sequence 13061, A
56	70.5	9.2	1214	6	US-10-953-349-3284	Sequence 3284, Ap
57	70.5	9.2	1461	6	US-10-449-902-9921	Sequence 9921, Ap
58	70.5	9.2	1788	8	US-11-217-529-1712	Sequence 1712, Ap
c 59	70.5	9.2	3960	8	US-11-217-529-79598	Sequence 79598, A
c 60	70.5	9.2	107996	9	US-11-021-837-42	Sequence 42, Appl
c 61	70.5	9.2	165280	9	US-11-021-837-47	Sequence 47, Appl
62	70	9.1	1027	6	US-10-953-349-26017	Sequence 26017, A
63	70	9.1	1347	9	US-11-348-413-332	Sequence 332, App
64	70	9.1	1710	8	US-11-217-529-1986	Sequence 1986, Ap
65	70	9.1	1872	6	US-10-449-902-2365	Sequence 2365, Ap
66	70	9.1	2343	9	US-11-056-355B-86210	Sequence 86210, A
67	70	9.1	2376	9	US-11-056-355B-46134	Sequence 46134, A
68	70	9.1	2520	9	US-11-056-355B-69909	Sequence 69909, A
69	70	9.1	2870	6	US-10-449-902-22262	Sequence 22262, A
70	70	9.1	3828	6	US-10-548-463-73	Sequence 73, Appl
71	70	9.1	3834	9	US-11-348-413-262	Sequence 262, App
c 72	70	9.1	5035	6	US-10-449-902-25475	Sequence 25475, A
73	69.5	9.0	1612	8	US-11-136-524-92	Sequence 92, Appl
c 74	69.5	9.0	4431	8	US-11-266-748A-24600	Sequence 24600, A
c 75	69.5	9.0	4442	8	US-11-266-748A-29633	Sequence 29633, A
c 76	69.5	9.0	4453	8	US-11-266-748A-31417	Sequence 31417, A
77	69.5	9.0	5145	6	US-10-833-833-168	Sequence 168, App
78	69.5	9.0	13938	6	US-10-833-833-167	Sequence 167, App
79	69	9.0	414	8	US-11-217-529-78554	Sequence 78554, A
80	69	9.0	717	6	US-10-526-741-19	Sequence 19, Appl

	81	69	9.0	717	7	US-11-414-676-19 Sequence 19, Appl
	82	69	9.0	1179	6	US-10-471-571A-2101 Sequence 2101, Ap
	83	69	9.0	1217	6	US-10-449-902-28265 Sequence 28265, A
	84	69	9.0	1232	9	US-11-218-305-12178 Sequence 12178, A
	85	69	9.0	4775	8	US-11-266-748A-56767 Sequence 56767, A
	86	69	9.0	4776	9	US-11-300-928-50 Sequence 50, Appl
	87	69	9.0	4874	6	US-10-669-920-834 Sequence 834, App
	88	68.5	8.9	1658	8	US-11-266-748A-183731 Sequence 183731,
	89	68.5	8.9	1658	8	US-11-266-748A-191129 Sequence 191129,
c	90	68.5	8.9	2007	8	US-11-217-529-3048 Sequence 3048, Ap
	91	68.5	8.9	3462	9	US-11-348-413-13606 Sequence 13606, A
	92	68	8.9	434	7	US-11-314-834-2044 Sequence 2044, Ap
c	93	68	8.9	1053	9	US-11-218-305-24102 Sequence 24102, A
	94	68	8.9	1211	9	US-11-056-355B-17912 Sequence 17912, A
	95	68	8.9	1359	9	US-11-218-305-3484 Sequence 3484, Ap
c	96	68	8.9	2285	9	US-11-218-305-21832 Sequence 21832, A
c	97	68	8.9	2358	9	US-11-218-305-21409 Sequence 21409, A
	98	68	8.9	2832	8	US-11-217-529-1740 Sequence 1740, Ap
	99	68	8.9	91278	6	US-10-539-228-341 Sequence 341, App
	100	68	8.9	91278	6	US-10-669-920-858 Sequence 858, App

ALIGNMENTS

RESULT 1
US-11-345-661-9
; Sequence 9, Application US/11345661
; Publication No. US20060171919A1
; GENERAL INFORMATION:
; APPLICANT: Rosenblum, Michael
; APPLICANT: Cheung, Lawrence
; APPLICANT: Lyu, Mi-Ae
; TITLE OF INVENTION: Targeted polypeptides
; FILE REFERENCE: CLFR:059US
; CURRENT APPLICATION NUMBER: US/11/345,661
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: US 60/649,478
; PRIOR FILING DATE: 2005-02-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Polynucleotide encoding the conjugated polypeptide
US-11-345-661-9

Alignment Scores:

Pred. No.:	6.38e-12	Length:	1224
Score:	156.50	Matches:	52
Percent Similarity:	50.0%	Conservative:	23
Best Local Similarity:	34.7%	Mismatches:	54
Query Match:	20.4%	Indels:	21
DB:	7	Gaps:	8

US-10-758-902-9 (1-149) x US-11-345-661-9 (1-1224)

```
Qy          2 AsnThrValSerPheAsnLeu---GlyGluAlaTyr---GluTyrProThrPheIleGln 19
              :::|||||||||||||:::      |||      |||      |||      |||:::
Db        478 GACACCGTGAGCTTTAGCACTAAAGGTGCCACTTATATTACCTACGTGAATTTCTTGAAT 537

Qy         20 AspLeuArgAsnGluLeu--------------AlaLysGlyThrProValCysGlnLeu 34
              :::||||||   :::|||                :::   |||   |||:::
Db        538 GAGCTACGAGTTAAATTGAAACCCGAAGGTAACAGCCATGGAATCCCATTG--------- 588

Qy         35 ProValThrLeuGlnThrIleAlaAspAsp------LysArgPheValLeuValAspIle 52
                 |||:::         ||||||      |||   ||||||||||||   :::
Db        589 ---------CTGCGCAAAAAATGTGATGATCCTGGAAAGTGTTTCGTTTTGGTAGCGCTT 639

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
              :::      :::   :::      ::::::||||||||||||||   ||||||||||||
Db        640 TCAAATGACAATGGACAGTTGGCGGAAATAGCTATAGATGTTACAAGTGTTTATGTGGTG 699

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
              |||||||||                ::::::|||:::   |||              |||
Db        700 GGCTATCAA------------GTAAGAAACAGATCTTACTTCTTTAAAGATGCTCCAGAT 747

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||      ||||||      |||   :::      |||   |||   |||
Db        748 GCTGCTTACGAAGGCCTCTTCAAAAAC---ACAATTAAAACAAGACTTCATTTTGGCGGC 804

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              ||||||      |||      |||      |||:::      :::|||||||:::
Db        805 AGCTATCCCTCGCTG---GAAGGTGAGAAGGCATATAGAGAGACAACAGACTTGGGCATT 861

Qy        133 TyrLysLeuGluPheSerIleGluAlaIle 142
                 |||      |||:::   :::
Db        862 GAACCATTAAGGATTGGCATCAAGAAACTT 891
```

RESULT 2
US-11-345-661-11
; Sequence 11, Application US/11345661
; Publication No. US20060171919A1
; GENERAL INFORMATION:
; APPLICANT: Rosenblum, Michael
; APPLICANT: Cheung, Lawrence
; APPLICANT: Lyu, Mi-Ae
; TITLE OF INVENTION: Targeted polypeptides
; FILE REFERENCE: CLFR:059US
; CURRENT APPLICATION NUMBER: US/11/345,661
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: US 60/649,478
; PRIOR FILING DATE: 2005-02-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Polynucleotide encoding the conjugated polypeptide
US-11-345-661-11

Alignment Scores:

Pred. No.:	6.38e-12	Length:	1224
Score:	156.50	Matches:	52
Percent Similarity:	50.0%	Conservative:	23
Best Local Similarity:	34.7%	Mismatches:	54
Query Match:	20.4%	Indels:	21
DB:	7	Gaps:	8

US-10-758-902-9 (1-149) x US-11-345-661-11 (1-1224)

```
Qy          2 AsnThrValSerPheAsnLeu---GlyGluAlaTyr---GluTyrProThrPheIleGln 19
              :::|||||||||||||:::      |||      |||      |||      |||:::
Db          7 GACACCGTGAGCTTTAGCACTAAAGGTGCCACTTATATTACCTACGTGAATTTCTTGAAT 66

Qy         20 AspLeuArgAsnGluLeu--------------AlaLysGlyThrProValCysGlnLeu 34
              :::||||||   :::|||                :::   |||   |||:::
Db         67 GAGCTACGAGTTAAATTGAAACCCGAAGGTAACAGCCATGGAATCCCATTG--------- 117

Qy         35 ProValThrLeuGlnThrIleAlaAspAsp------LysArgPheValLeuValAspIle 52
                 |||:::         ||||||      |||   ||||||||||||   :::
Db        118 ---------CTGCGCAAAAAATGTGATGATCCTGGAAAGTGTTTCGTTTTGGTAGCGCTT 168

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
              :::      :::   :::      ::::::||||||||||||||   ||||||||||||
Db        169 TCAAATGACAATGGACAGTTGGCGGAAATAGCTATAGATGTTACAAGTGTTTATGTGGTG 228

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
              |||||||||                ::::::|||:::   |||              |||
Db        229 GGCTATCAA------------GTAAGAAACAGATCTTACTTCTTTAAAGATGCTCCAGAT 276

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||      ||||||      |||   :::      |||   |||   |||
```

```
Db        277 GCTGCTTACGAAGGCCTCTTCAAAAAC---ACAATTAAAACAAGACTTCATTTTGGCGGC 333

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              ||||||  |||      |||      |||:::    :::||||||:::
Db        334 AGCTATCCCTCGCTG---GAAGGTGAGAAGGCATATAGAGAGACAACAGACTTGGGCATT 390

Qy        133 TyrLysLeuGluPheSerIleGluAlaIle 142
                  |||      |||:::   :::
Db        391 GAACCATTAAGGATTGGCATCAAGAAACTT 420

RESULT 3
US-11-361-977A-66
; Sequence 66, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 765
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Construct encoding
;   OTHER INFORMATION: Methionine-Saporin fusion protein
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(765)
US-11-361-977A-66

Alignment Scores:
Pred. No.:              7.35e-05      Length:         765
Score:                  104.50        Matches:        35
Percent Similarity:     46.3%         Conservative:   33
Best Local Similarity:  23.8%         Mismatches:     58
Query Match:            13.6%         Indels:         21
DB:                     7             Gaps:           6

US-10-758-902-9 (1-149) x US-11-361-977A-66 (1-765)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
              |||   :::|||   :::|||:::      :::||||||   :::
Db         40 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 99

Qy         28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                       ||||||   :::      :::
Db        100 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG---------------CCGAGCAAA 144

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
              ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
Db        145 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 201

Qy         65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                    ::::::|||||||||  |||      |||      :::
Db        202 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 261

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
                  |||      ::::::   :::      ::::::   |||||||||
Db        262 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 321

Qy        103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              |||      |||:::      |||  :::         ||||||   :::
Db        322 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 381

Qy        121 AlaLysVal--------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
              |||::::::                ||||||:::|||   ||||||:::      |||
Db        382 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 441

Qy        136 GluPheSerIleGluAlaIle 142
                  |||:::||||||:::
Db        442 AGCACGAGCATGGAAGCGGTC 462

RESULT 4
US-11-361-977A-60
; Sequence 60, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
;   LENGTH: 984
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
;   OTHER INFORMATION: toxin fusion protein SDF-1-Beta-AM-SAPORIN
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-11-361-977A-60

Alignment Scores:
Pred. No.:              0.000105      Length:         984
Score:                  104.50        Matches:        35
Percent Similarity:     46.3%         Conservative:   33
Best Local Similarity:  23.8%         Mismatches:     58
Query Match:            13.6%         Indels:         21
DB:                     7             Gaps:           6

US-10-758-902-9 (1-149) x US-11-361-977A-60 (1-984)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
              |||   :::|||   :::|||:::      :::||||||   :::
Db        259 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 318

Qy         28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                       ||||||   :::      :::
Db        319 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG---------------CCGAGCAAA 363

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
              ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
Db        364 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 420

Qy         65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                    ::::::|||||||||  |||      |||      :::
Db        421 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 480

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
                  |||      ::::::   :::      ::::::   |||||||||
Db        481 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 540

Qy        103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              |||      |||:::      |||  :::         ||||||   :::
Db        541 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 600

Qy        121 AlaLysVal--------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
              |||::::::                ||||||:::|||   ||||||:::      |||
Db        601 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 660

Qy        136 GluPheSerIleGluAlaIle 142
                  |||:::||||||:::
Db        661 AGCACGAGCATGGAAGCGGTC 681
```

```
RESULT 5
US-11-361-977A-63
; Sequence 63, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 993
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(993)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
;   OTHER INFORMATION: toxin fusion protein EOTAXIN-AM-SAPORIN
US-11-361-977A-63

Alignment Scores:
Pred. No.:              0.000106        Length:         993
Score:                  104.50          Matches:        35
Percent Similarity:     46.3%           Conservative:   33
Best Local Similarity:  23.8%           Mismatches:     58
Query Match:            13.6%           Indels:         21
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-11-361-977A-63 (1-993)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
              |||   :::|||   :::|||:::      :::||||||   :::
Db        268 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 327

Qy         28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                      ||||||   :::      :::
Db        328 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG--------------CCGAGCAAA 372

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
              ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
Db        373 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 429

Qy         65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                    ::::::|||||||||   |||         |||      :::
Db        430 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 489

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
                  |||      ::::::   :::      ::::::   |||||||||
Db        490 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 549

Qy        103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              |||      |||:::      |||   :::         ||||||   :::
Db        550 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 609

Qy        121 AlaLysVal--------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
              |||::::::                ||||||:::|||   ||||||:::      |||
Db        610 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 669

Qy        136 GluPheSerIleGluAlaIle 142
                 |||:::||||||:::
Db        670 AGCACGAGCATGGAAGCGGTC 690

RESULT 6
US-11-361-977A-54
; Sequence 54, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
;   LENGTH: 999
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(999)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
;   OTHER INFORMATION: toxin fussion protein MCP1-AM-SAPORIN
US-11-361-977A-54

Alignment Scores:
Pred. No.:              0.000107        Length:         999
Score:                  104.50          Matches:        35
Percent Similarity:     46.3%           Conservative:   33
Best Local Similarity:  23.8%           Mismatches:     58
Query Match:            13.6%           Indels:         21
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-11-361-977A-54 (1-999)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
              |||   :::|||   :::|||:::      :::||||||   :::
Db        274 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 333

Qy         28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                      ||||||   :::      :::
Db        334 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG--------------CCGAGCAAA 378

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
              ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
Db        379 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 435

Qy         65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                    ::::::|||||||||   |||         |||      :::
Db        436 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 495

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
                  |||      ::::::   :::      ::::::   |||||||||
Db        496 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 555

Qy        103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              |||      |||:::      |||   :::         ||||||   :::
Db        556 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 615

Qy        121 AlaLysVal--------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
              |||::::::                ||||||:::|||   ||||||:::      |||
Db        616 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 675

Qy        136 GluPheSerIleGluAlaIle 142
                 |||:::||||||:::
Db        676 AGCACGAGCATGGAAGCGGTC 696

RESULT 7
US-11-361-977A-57
; Sequence 57, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
```

```
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
;    LENGTH: 999
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)..(999)
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
;    OTHER INFORMATION: toxin Fusion Protein MCP3-AM-SAPORIN
US-11-361-977A-57

Alignment Scores:
Pred. No.:              0.000107        Length:         999
Score:                  104.50          Matches:        35
Percent Similarity:     46.3%           Conservative:   33
Best Local Similarity:  23.8%           Mismatches:     58
Query Match:            13.6%           Indels:         21
DB:                     7               Gaps:           6

US-10-758-902-9 (1-149) x US-11-361-977A-57 (1-999)

Qy          11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
               |||   :::|||   :::|||:::      :::||||||   :::
Db         274 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 333

Qy          28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                        ||||||   :::      :::
Db         334 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG---------------CCGAGCAAA 378

Qy          45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
               ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
Db         379 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 435

Qy          65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                  ::::::|||||||||   |||       |||      :::
Db         436 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 495

Qy          83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
                  |||      ::::::   :::      ::::::   |||||||||
Db         496 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 555

Qy         103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
               |||      |||:::      |||   :::      ||||||   :::
Db         556 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 615

Qy         121 AlaLysVal--------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
               |||::::::                ||||||:::|||   ||||||:::      |||
Db         616 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 675

Qy         136 GluPheSerIleGluAlaIle 142
                  |||:::||||||:::
Db         676 AGCACGAGCATGGAAGCGGTC 696

RESULT 8
US-10-953-349-30542
; Sequence 30542, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30542
;    LENGTH: 990
;    TYPE: DNA
;    ORGANISM: Triticum aestivum
US-10-953-349-30542

Alignment Scores:
Pred. No.:              0.0511          Length:         990
Score:                  85.50           Matches:        38
Percent Similarity:     41.1%           Conservative:   29
Best Local Similarity:  23.3%           Mismatches:     51
Query Match:            11.1%           Indels:         45
DB:                     6               Gaps:           8

US-10-758-902-9 (1-149) x US-10-953-349-30542 (1-990)

Qy           3 ThrValSerPheAsnLeu---GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
               |||   :::||||||:::         :::  :::|||   |||||||||      :::
Db          95 ACGGCGACGTTCAACGTCCAGGCCAGCTCCACCGACTATGTCACCTTCATCACCGGCATC 154

Qy          22 ArgAsnGluLeu-----------------AlaLysGlyThrProValCysGlnLeuPro 35
               ||||||:::|||                    :::          ||||||      ||||||
Db         155 CGCAACAAGCTCCGCAACCCGGGGCAATCCTCCCACAACCGCCCCGTG------CTACCG 208

Qy          36 ValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::         :::   |||   :::|||      |||:::
Db         209 CCGATCGAGCCCAACGTCCCGCCGAGCAGGTGGTTCCACATCGTGCTCAAGACATCGCCG 268

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               :::         :::   :::|||                ::::::|||      |||::::::
Db         269 GCCAACACCGGGCTCACACTCGCCACCCGCGCCGACAACCTCTATTGGGAGGGCTTCAAG 328

Qy          76 AspLys-----------TrpAspGlyLysAspArgAlaValPheLeuAspLysValPro 91
                           |||:::
Db         329 AGCAGCGACGGCACCTGGTGGGAG---------------------------------- 352

Qy          92 ThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAsp 111
                  |||      |||   ||||||   |||            :::  |||
Db         353 ------CTCACCCCCGGCCTTATCCCCGGTGCCACC---------TATGTCGGGTTTGGC 397

Qy         112 GlySerTyrGln--------------------LysLeuValAsnAlaAlaLysValAsp 124
               |||:::|||:::                  ||||||   |||   |||
Db         398 GGCACCTACCGCGACCTCCTCGGCGACACCGACAAGCTGACCAACGTTGCC--------- 448

Qy         125 ArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGly 144
                              ||||||      ::::::      ::::::   |||:::   |||
Db         449 --------------CTCGGCCGGCAGCAGATGGCCGACGCGGTGACTGCGCTCCACGGG 493

Qy         145 LysThrGln 147
               :::|||:::
Db         494 CGCACCAAG 502

RESULT 9
US-11-056-355B-61233
; Sequence 61233, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61233
;    LENGTH: 990
;    TYPE: DNA
;    ORGANISM: Triticum aestivum
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)..(990)
;    OTHER INFORMATION: Ceres Seq. ID no. 13661987
```

```
US-11-056-355B-61233

Alignment Scores:
Pred. No.:              0.0511          Length:         990
Score:                  85.50           Matches:        38
Percent Similarity:     41.1%           Conservative:   29
Best Local Similarity:  23.3%           Mismatches:     51
Query Match:            11.1%           Indels:         45
DB:                     9               Gaps:           8

US-10-758-902-9 (1-149) x US-11-056-355B-61233 (1-990)

Qy          3 ThrValSerPheAsnLeu---GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||   :::||||||:::         :::   :::|||   |||||||||     :::
Db         95 ACGGCGACGTTCAACGTCCAGGCCAGCTCCACCGACTATGTCACCTTCATCACCGGCATC 154

Qy         22 ArgAsnGluLeu-----------------AlaLysGlyThrProValCysGlnLeuPro 35
              ||||||:::|||                  :::         ||||||      ||||||
Db        155 CGCAACAAGCTCCGCAACCCGGGGCAATCCTCCCACAACCGCCCCGTG------CTACCG 208

Qy         36 ValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::       :::   |||   :::|||     |||:::
Db        209 CCGATCGAGCCCAACGTCCCGCCGAGCAGGTGGTTCCACATCGTGCTCAAGACATCGCCG 268

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              :::         :::   :::|||             ::::::|||      |||::::::
Db        269 GCCAACACCGGGCTCACACTCGCCACCCGCGCCGACAACCTCTATTGGGAGGGCTTCAAG 328

Qy         76 AspLys-----------TrpAspGlyLysAspArgAlaValPheLeuAspLysValPro 91
                           |||:::
Db        329 AGCAGCGACGGCACCTGGTGGGAG---------------------------------- 352

Qy         92 ThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAsp 111
                 |||      |||   ||||||  |||           :::   |||
Db        353 ------CTCACCCCCGGCCTTATCCCCGGTGCCACC---------TATGTCGGGTTTGGC 397

Qy        112 GlySerTyrGln--------------------LysLeuValAsnAlaAlaLysValAsp 124
              |||:::|||:::                  ||||||   |||   |||
Db        398 GGCACCTACCGCGACCTCCTCGGCGACACCGACAAGCTGACCAACGTTGCC--------- 448

Qy        125 ArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGly 144
                        ||||||      ::::::      ::::::   |||:::   |||
Db        449 --------------CTCGGCCGGCAGCAGATGGCCGACGCGGTGACTGCGCTCCACGGG 493

Qy        145 LysThrGln 147
              :::|||:::
Db        494 CGCACCAAG 502

RESULT 10
US-11-216-545-3907
; Sequence 3907, Application US/11216545
; Publication No. US20060135758A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO Technology, LLC
;  APPLICANT:  McLaird, Paul L
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Soybeans.
;  FILE REFERENCE: 38-21 (53659)B
;  CURRENT APPLICATION NUMBER: US/11/216,545
;  CURRENT FILING DATE:  2005-08-31
;  PRIOR APPLICATION NUMBER: US 60/606,062
;  PRIOR FILING DATE: 2004-08-31
;  NUMBER OF SEQ ID NOS: 8783
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3907
;   LENGTH: 2400
;   TYPE: DNA
;   ORGANISM: Glycine max
US-11-216-545-3907

Alignment Scores:
Pred. No.:              0.553           Length:         2400
Score:                  82.00           Matches:        40
Percent Similarity:     33.3%           Conservative:   19
Best Local Similarity:  22.6%           Mismatches:     66
Query Match:            10.7%           Indels:         52
DB:                     8               Gaps:           5

US-10-758-902-9 (1-149) x US-11-216-545-3907 (1-2400)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly---------------- 28
              |||      |||:::   ||||||           :::|||
Db        315 TACCAAGCTTTTGTGCCAGATCTCACTATCTCTGCCTCTAAAACATACTCATCATATCAA 374

Qy         29 --------------ThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAsp 43
                           :::           |||   |||||||||         :::
Db        375 CAAAACCGTGTAGTCTCATCCTACAGTGACCTTGGTGTCACTTTGGACATTCCAAGCTCC 434

Qy         44 AspLysArgPheValLeuValAsp------------IleThrThrThrSerLysLysThr 59
              :::   ||||||   ||||||                ||||||   :::      |||
Db        435 AACCTTAGATTCTTTCTTGTCAGAGGAAGCCCTTATATAACTGCTTCTGTCACAAAGCCA 494

Qy         60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp 79
                    ::::::|||                |||           |||   ::::::
Db        495 ACACCTCTTTCCATCAAAACAGTGCACACCGTAGTTTCCTTGTCTTCAGATGATTACAAC 554

Qy         80 GlyLys-----------------------------------------------AspArgAla 84
                 |||
Db        555 ACCAAACACACCCTTAAGCTTAACAACACTCAGGCATGGATCATATACACCTCCTCTCCA 614

Qy         85 ValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThrAsn 104
              ::::::|||:::   ||||||:::      |||||||||   |||   |||:::
Db        615 ATCTACTTGAACCATGTTCCTTCTGAGGTTACATCCAAGCCATTTTCTGGCATCATTCGT 674

Qy        105 ArgValThrLeu-----------------------------------ThrPheAspGly 112
                    |||                                       |||
Db        675 ATAGCGGCTTTGCCTGATTCTGATTCCAAGTATGTGGAAACTCTTGACAAGTTCAGTTCT 734

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
                 |||            :::||||||
Db        735 TGTTACCCTGTGTCTGGTGATGCAGCA------------------------------- 761

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrpGlyLysThrGlnAsnGly 149
                 |||      ||||||:::|||      |||   |||   ::::::|||
Db        762 CTCAAGAAACCATTCAGTGTTGAGTATAAATGGCAAAAGAAACGTTCTGGG 812

RESULT 11
US-11-218-305-3386
; Sequence 3386, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3386
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-3386

Alignment Scores:
Pred. No.:              0.687           Length:         2495
Score:                  81.50           Matches:        38
Percent Similarity:     44.2%           Conservative:   15
```

```
Best Local Similarity:  31.7%          Mismatches:    38
Query Match:            10.6%          Indels:        29
DB:                     9              Gaps:          8

US-10-758-902-9 (1-149) x US-11-218-305-3386 (1-2495)

Qy         16 ThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuPro 35
Db        680 ACTTTCATCCAGGAGATTCGCCGTGAGCTCGGT---GACACAAGCGTGATGCAGGAGGCG 736

Qy         36 ValThrLeuGlnThrIleAlaAspAspLysArgPheVal---LeuValAspIleThrThr 54
Db        737 TTCCAGCTCCCGCCTCAGACGGACACCCCGAGCTTTCAGGACCTCGTGCTGATCGCCGGC 796

Qy         55 ThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyr 74
Db        797 GAGAGCACCGCCACCCTGCGGCTGCGTACCGAC------AACCTCTACGTCGTCGGCTTC 850

Qy         75 GlnAsp---------LysTrp------------------AspGlyLysAspArgAlaVal 85
Db        851 CGCAACCAAGCCGGCCGGTGGTTCGAGTTCCGGCACGAGGACGGC-------------- 895

Qy         86 PheLeuAspLysValProThrValAlaThrSerLysLeuProGlyValThrAsnArg 105
Db        896 ------GGACTTCCTCCGACCATA------------------CCAGGGGCGACG------ 925

Qy        106 ValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
Db        926 ---ATGCTGCACTTCAGCGGGAGCTACGTGGGCACCAACAGTCTAGCTCCGCTAAATCGT 982

RESULT 12
US-11-013-711-8
; Sequence 8, Application US/11013711
; Publication No. US20060159709A1
; GENERAL INFORMATION:
;  APPLICANT: Loosmore, Sheena M.
;  APPLICANT:  Sasaki, Ken
;  APPLICANT:  Yang, Yan Ping
;  APPLICANT:  Klein, Michel H.
;  TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
;  TITLE OF INVENTION:  PROTEIN OF MORAXELLA
;  FILE REFERENCE: 1038-921MIS:jb
;  CURRENT APPLICATION NUMBER: US/11/013,711
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: US/09/361,619
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 6159
;   TYPE: DNA
;   ORGANISM: Moraxella catarrhalis
US-11-013-711-8

Alignment Scores:
Pred. No.:              2.87           Length:        6159
Score:                  81.00          Matches:       30
Percent Similarity:     42.4%          Conservative:  12
Best Local Similarity:  30.3%          Mismatches:    51
Query Match:            10.5%          Indels:        6
DB:                     9              Gaps:          2

US-10-758-902-9 (1-149) x US-11-013-711-8 (1-6159)

Qy         34 LeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr 53
Db       2413 TTGTCCCCAACACTGCCTAGCATTGCCAGTCCAAGTGGCCGCAACATAGCACTGGGCAAT 2472

Qy         54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73
Db       2473 ACAATCGAAGAAAAAGACAAATCCAACGCTGCCAGCATTGATGATGTGCTAAATGCAGGC 2532

Qy         74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93
Db       2533 TTTAACCTAAAAAATAATGGCAAAGACAAA-----------GACTTTGTCTCCACTTAT 2580

Qy         94 AlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
Db       2581 GACACTGTTGACTTTATCGATGGCAATGCCACCACCGCCACAGTAACTTATGATGAAGCC 2640

Qy        114 TyrGln------LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeu 130
Db       2641 AATCAAACCAGTAAAGTGGCGTATGATGTGAATGTGGATGAGAAAACCATTGAACTG 2697

RESULT 13
US-11-316-535A-132
; Sequence 132, Application US/11316535A
; Publication No. US20060148054A1
; GENERAL INFORMATION:
;  APPLICANT: Fukuyama, Shiro
;  APPLICANT:  Matsui, Tomoko
;  APPLICANT:  Soong, Chee Leong
;  APPLICANT:  Allain, Eric
;  APPLICANT:  Nielsen, Anders Vikso
;  APPLICANT:  Udagawa, Hiroaki
;  APPLICANT:  Liu, Ye
;  APPLICANT:  Duan, Junxin
;  APPLICANT:  Wu, Wenping
;  APPLICANT:  Andersen, Lene Nonboe
;  TITLE OF INVENTION: ENZYMES FOR STARCH PROCESSING
;  FILE REFERENCE: 10729.500-US
;  CURRENT APPLICATION NUMBER: US/11/316,535A
;  CURRENT FILING DATE:  2005-12-22
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 132
;   LENGTH: 1305
;   TYPE: DNA
;   ORGANISM: Absidia crista
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1305)
US-11-316-535A-132

Alignment Scores:
Pred. No.:              0.383          Length:        1305
Score:                  80.50          Matches:       32
Percent Similarity:     40.8%          Conservative:  17
Best Local Similarity:  26.7%          Mismatches:    30
Query Match:            10.5%          Indels:        41
DB:                     9              Gaps:          6

US-10-758-902-9 (1-149) x US-11-316-535A-132 (1-1305)

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
Db        448 GTGGCTGAT-----------GTGTTGCCTGACATCAACACTGAGGATGATAACGTGGTC 495

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyr----------------- 74
Db        496 AAGACGCTCAATGATATTGTCAGCAACTGGGTAACTACATATGGCTTTGATGGTATTCGC 555

Qy         75 ----------------------GlnAspLysTrpAspGlyLysAspArgAla------ 84
Db        556 ATTGACACTGTCAAGCATGTACGTCAAGACTTTTGGGATGGATACAATGAAGCAGCTGGT 615

Qy         85 ValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyValThrAsn 104
Db        616 GTATTT--------------------GCTACAGGAGAAGTCTTTGATGGTGATTCATCC 654

Qy        105 ArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAsp 124
Db        655 TATGTT--------------GGTGGATATCAAAAGCATTTGGACTCG------------ 687

Qy        125 ArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGly 144
```

```
Db        688 ---------------CTTCTCAATTACCCAATGTATTACGCACTCAATGATGTATTTGGT 732

RESULT 14
US-11-316-535A-156
; Sequence 156, Application US/11316535A
; Publication No. US20060148054A1
; GENERAL INFORMATION:
;  APPLICANT: Fukuyama, Shiro
;  APPLICANT:  Matsui, Tomoko
;  APPLICANT:  Soong, Chee Leong
;  APPLICANT:  Allain, Eric
;  APPLICANT:  Nielsen, Anders Vikso
;  APPLICANT:  Udagawa, Hiroaki
;  APPLICANT:  Liu, Ye
;  APPLICANT:  Duan, Junxin
;  APPLICANT:  Wu, Wenping
;  APPLICANT:  Andersen, Lene Nonboe
;  TITLE OF INVENTION: ENZYMES FOR STARCH PROCESSING
;  FILE REFERENCE: 10729.500-US
;  CURRENT APPLICATION NUMBER: US/11/316,535A
;  CURRENT FILING DATE:  2005-12-22
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 156
;   LENGTH: 1443
;   TYPE: DNA
;   ORGANISM: Absidia cristata
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1443)
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: (1)..(120)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (121)..(1443)
;   OTHER INFORMATION: Catalytic domain
US-11-316-535A-156

Alignment Scores:
Pred. No.:              0.441          Length:         1443
Score:                  80.50          Matches:        32
Percent Similarity:     40.8%          Conservative:   17
Best Local Similarity:  26.7%          Mismatches:     30
Query Match:            10.5%          Indels:         41
DB:                     9              Gaps:           6

US-10-758-902-9 (1-149) x US-11-316-535A-156 (1-1443)

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              :::||||||           ||||||  ||||||  |||                  |||
Db        586 GTGGCTGAT-----------GTGTTGCCTGACATCAACACTGAGGATGATAACGTGGTC 633

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyr----------------- 74
              |||         |||:::         :::|||      |||
Db        634 AAGACGCTCAATGATATTGTCAGCAACTGGGTAACTACATATGGCTTTGATGGTATTCGC 693

Qy         75 ------------------------GlnAspLysTrpAspGlyLysAspArgAla------ 84
                                      ||||||  ||||||||   :::   |||
Db        694 ATTGACACTGTCAAGCATGTACGTCAAGACTTTTGGGATGGATACAATGAAGCAGCTGGT 753

Qy         85 ValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThrAsn 104
              ||||||                    ||||||  ::::::|||  |||  ::::::
Db        754 GTATTT--------------------GCTACAGGAGAAGTCTTTGATGGTGATTCATCC 792

Qy        105 ArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAsp 124
                 |||                |||  |||||||||  :::::::::
Db        793 TATGTT--------------GGTGGATATCAAAAGCATTTGGACTCG------------ 825

Qy        125 ArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGly 144
                       |||     |||  :::  :::::::::      ::::::|||
Db        826 ---------------CTTCTCAATTACCCAATGTATTACGCACTCAATGATGTATTTGGT 870
```

```
RESULT 15
US-11-348-413-4995
; Sequence 4995, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  APPLICANT:  Murphy, Ellen
;  APPLICANT:  Olmsted, Stephen
;  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;  FILE REFERENCE: 031896-084100 (AM 101724)
;  CURRENT APPLICATION NUMBER: US/11/348,413
;  CURRENT FILING DATE:  2006-02-07
;  PRIOR APPLICATION NUMBER: PCT/US05/035471
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 11/243,445
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 60/615,573
;  PRIOR FILING DATE: 2004-10-05
;  NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 4995
;   LENGTH: 3111
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(3111)
;   OTHER INFORMATION: WAN01P9X8; ORF; 00000000000000; Singleton contains WAN01P9
;   OTHER INFORMATION: X8::fctX:FctX::AY049087
US-11-348-413-4995

Alignment Scores:
Pred. No.:              1.53           Length:         3111
Score:                  80.00          Matches:        41
Percent Similarity:     36.2%          Conservative:   22
Best Local Similarity:  23.6%          Mismatches:     51
Query Match:            10.4%          Indels:         60
DB:                     9              Gaps:           8

US-10-758-902-9 (1-149) x US-11-348-413-4995 (1-3111)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||         ::::::||||||   :::                  :::|||:::
Db       2029 AACTTGTCAATATATTCATTGGGCGTTTCT--------------------AAAGATATT 2067

Qy         22 ArgAsnGluLeuAlaLysGlyThrProVal------------------------------ 31
              ::::::   |||      :::||||||
Db       2068 AATAGTGATACGGCAAGTTCCAGTCCTGTTGTCCTAAAATACTTGTCAGGTGAGGAGCAT 2127

Qy         32 ---------------------CysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                                   :::|||     ||||||     |||   :::|||
Db       2128 TACTACGGTATTACGGACACAGCAGAATTAGAAAAAACTTTGAATAAAATTGTTGAGGAT 2187

Qy         45 LysArgPheValLeuVal---------------------------------------- 50
              :::         :::
Db       2188 AGTAAGTTATCTCAGCTAGGAATTTCGGATAGTTTAAGTCAGTATGTTGACTACTATGAT 2247

Qy         51 ---------AspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThr 67
                     ||:::      |||  |||      |||             |||   |||
Db       2248 AAACAACCTGATGTACTTGTTACTAGAAAATCGAAGGTTAAT---------GATGAAACA 2298

Qy         68 AspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeu 87
              ::::::           |||  :::      |||||||||              :::
Db       2299 GAGATTTTATACCAAAAAGACCAAGTTCAAGAAGCTGGTAAAGAT---------ATCATT 2349

Qy         88 AspLysValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThr 107
              |||||||||      |||  |||  |||                 :::|||||||
Db       2350 GATAAAGTT------GTATTTACCCCGAAAACTACTAGTCAACCAAAAGGTAAAGTTACT 2403

Qy        108 LeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAsp 127
              |||||||||          |||                 |||||||||
Db       2404 TTAACCTTTAAGTCTGATTAT--------------------AAGGTTGAT--------- 2433
```

```
Qy        128 LeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  :::          |||   |||   |||:::::::::|||
Db       2434 ---GATGAATATACCTATACGCTTTCTTTTAATGTGAAAGCT 2472
```

RESULT 16
US-11-174-307B-1881/c
; Sequence 1881, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 1881
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1767)
; OTHER INFORMATION: Ceres cDNA ID no. 12709994
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1767)
; OTHER INFORMATION: Also known as Ceres CDNA ID no. 23360242
US-11-174-307B-1881

Alignment Scores:

Pred. No.:	0.811	Length:	1767
Score:	79.50	Matches:	26
Percent Similarity:	44.3%	Conservative:	21
Best Local Similarity:	24.5%	Mismatches:	42
Query Match:	10.4%	Indels:	17
DB:	9	Gaps:	3

US-10-758-902-9 (1-149) x US-11-174-307B-1881 (1-1767)

```
Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGln 33
              :::|||:::|||::::::||||||   |||   |||       |||   :::   |||
Db        588 TTCCCTAGCTTCCTTGAAGATCTTCCCAATCCTCTTAGGGTCAACACCACTATAACACAA 529

Qy         34 LeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr 53
                 :::   ||||||      |||           |||:::      |||:::
Db        528 AACATGATGGTTCTCCAGCAAAAAGCC---------TTCTTCATCCAAGAAGACCTTATC 478

Qy         54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73
              |||   ::::::      :::           |||           :::
Db        477 ACAGGGAACCAAATGATTATACTCACTGGGATTCAAACCTGAACTCTC------------ 430

Qy         74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93
                            |||:::|||      |||:::|||:::|||
Db        429 --------------------AAGGAAAGGCTCGAATTCATTGACAGGGTGAAACCGTAG 391

Qy         94 AlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
              :::|||               :::   :::      |||:::   |||
Db        390 ATATCGAGTAATAGATTGGTTGATATCAGAAGCAGTAACACAATCAACTTT--------- 340

Qy        114 TyrGlnLysLeuValAsn 119
                |||||:::::::|||
Db        339 CTTCAAAAGATTATCAAT 322
```

RESULT 17
US-11-174-307B-1551/c
; Sequence 1551, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 1551
; LENGTH: 3426
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3426)
; OTHER INFORMATION: Ceres cDNA ID no. 12653553
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3426)
; OTHER INFORMATION: Also known as Ceres CDNA ID no. 23659454
US-11-174-307B-1551

Alignment Scores:

Pred. No.:	2.06	Length:	3426
Score:	79.50	Matches:	26
Percent Similarity:	44.3%	Conservative:	21
Best Local Similarity:	24.5%	Mismatches:	42
Query Match:	10.4%	Indels:	17
DB:	9	Gaps:	3

US-10-758-902-9 (1-149) x US-11-174-307B-1551 (1-3426)

```
Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGln 33
              :::|||:::|||::::::||||||   |||   |||       |||   :::   |||
Db        588 TTCCCTAGCTTCCTTGAAGATCTTCCCAATCCTCTTAGGGTCAACACCACTATAACACAA 529

Qy         34 LeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr 53
                 :::   ||||||      |||           |||:::      |||:::
Db        528 AACATGATGGTTCTCCAGCAAAAAGCC---------TTCTTCATCCAAGAAGACCTTATC 478

Qy         54 ThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGly 73
              |||   ::::::      :::           |||           :::
Db        477 ACAGGGAACCAAATGATTATACTCACTGGGATTCAAACCTGAACTCTC------------ 430

Qy         74 TyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrVal 93
                            |||:::|||      |||:::|||:::|||
Db        429 --------------------AAGGAAAGGCTCGAATTCATTGACAGGGTGAAACCGTAG 391

Qy         94 AlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySer 113
              :::|||               :::   :::      |||:::   |||
Db        390 ATATCGAGTAATAGATTGGTTGATATCAGAAGCAGTAACACAATCAACTTT--------- 340

Qy        114 TyrGlnLysLeuValAsn 119
                |||||:::::::|||
Db        339 CTTCAAAAGATTATCAAT 322
```

RESULT 18
US-11-348-413-270
; Sequence 270, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen

```
;  APPLICANT:  Olmsted, Stephen
;  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;  FILE REFERENCE: 031896-084100 (AM 101724)
;  CURRENT APPLICATION NUMBER: US/11/348,413
;  CURRENT FILING DATE:  2006-02-07
;  PRIOR APPLICATION NUMBER: PCT/US05/035471
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 11/243,445
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 60/615,573
;  PRIOR FILING DATE: 2004-10-05
;  NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 270
;   LENGTH: 2928
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2928)
;   OTHER INFORMATION: WAN01UJ6O; ORF; 00100000000000; SingletonSubcluster contai
;   OTHER INFORMATION: ns WAN01P47K:spyM18_1880::secreted endoglycosidase:MGAS823
;   OTHER INFORMATION: 2:NC_003485.1
US-11-348-413-270

Alignment Scores:
Pred. No.:              3.16          Length:          2928
Score:                  77.50         Matches:         42
Percent Similarity:     37.2%         Conservative:    16
Best Local Similarity:  26.9%         Mismatches:      63
Query Match:            10.1%         Indels:          35
DB:                     9             Gaps:            7

US-10-758-902-9 (1-149) x US-11-348-413-270 (1-2928)

Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal 31
              |||   |||      |||              |||          |||   |||
Db       2080 TATCATTACAATAACTTTAAAGTTTCTTATGAGAACTATACCGTTAAAGTAACTGATTCC 2139

Qy         32 CysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeu---Val 50
                        |||   :::|||:::|||   ||||||                 |||
Db       2140 ACATTGGGAACCACTACTGACAAAACGCTAGCAACTGATAAAGAAGAGACCTATAAGGTT 2199

Qy         51 AspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyr 70
              |||      :::   :::  ||||||     |||          |||
Db       2200 GACTTCTTTAGCCCAGCAGATAAGACAAAAGCTGTTCAT---------ACTGCTAAAGTG 2250

Qy         71 ValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysVal 90
              :::||||||           |||   |||         |||   |||   :::
Db       2251 ATTGTTGGT--------------GACGAAAAAACCATGATGGTTAATTTGGCAGAAGGC 2295

Qy         91 ProThrValAlaThrSer--------------------LysLeuProGlyVal--- 102
                 ||||||      |||                 |||:::|||   |||:::
Db       2296 GCAACAGTTATTAAGAGTGAAAATGATGAAAATGCCAAAAAAGTTTTTAATGGCATCATG 2355

Qy        103 --------------------ThrAsnArgValThrLeuThrPheAsp------------ 111
                              ||||||   ::::::   |||:::
Db       2356 GAATATAATCCGATATCTACTCAGAATAGAGCTTCGATTATCTTTGAAATTAAAGACCCT 2415

Qy        112 ------GlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
                    |||   :::|||   |||   :::      |||:::||||||
Db       2416 AGTTTAGCAAAATATTGGCGCCTTTTCAATGATAGCAGTAAAGATAAAAAAGAT------ 2469

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGlyLys 145
                 |||      |||      :::|||          |||:::
Db       2470 ---------TATATCAAAGAAGCAAAACTTGAAGTCTTTACAGGCCAG 2508

RESULT 19
US-11-266-748A-353475
; Sequence 353475, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 353475
;   LENGTH: 1860
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (89)..(89)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (169)..(169)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-353475

Alignment Scores:
Pred. No.:              3.2           Length:          1860
Score:                  75.50         Matches:         38
Percent Similarity:     35.4%         Conservative:    24
Best Local Similarity:  21.7%         Mismatches:      66
Query Match:            9.8%          Indels:          47
DB:                     8             Gaps:            8

US-10-758-902-9 (1-149) x US-11-266-748A-353475 (1-1860)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      :::|||:::   :::::::|||   :::   |||  :::|||      |||
Db        923 AGCATGGAAATGGGCCAAGAGCATCAATACCATTCAAAAATAGACGAACTAATTGAAGAA 982

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                 |||         :::      |||                ||||||   :::
Db        983 ACTGTTAAA---GAAATGATAACACTCTTGGTTGCAAAGTTCGTTACTATCTTGGAAGGA 1039

Qy         45 ----------------------------------------LysArgPheValLeuVal 50
                                                      |||:::
Db       1040 GTGCTGGCAAAATTATCCAGATATGACGAAGGGACTTTGTTTTCTTCTTTTCTGTCATTT 1099

Qy         51 AspIleThrThrThrSerLys------LysThrValLysValAlaIleAspValThrAsp 68
                 :::          ||||||                |||      :::||||||   |||
Db       1100 ACCGTGAAGGCAGCTTCCAAATATGTGGATGTACCTAAACCCGGGATGGACGTGGCCGAC 1159

Qy         69 ValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAsp 88
              ||||||          :::          |||                |||      |||
Db       1160 GCCTACGTGACTTTCGTCCGCCATTCTCAGGAT--------------GTCCTGCGTGAT 1204

Qy         89 LysValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeu 108
              ||||||                 :::::::::                      :::
Db       1205 AAGGTC------------AATGAGGAGATGTAC-----------------ATAGAAAGG 1234

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla---------LysValAspArg 125
```

```
Db       1235 TTATTTGATCAATGGTACAACAGCTCCATGAACGTGATCTGCACCTGGTTGACGGACCGG 1294

Qy        126 LysAspLeuGluLeuGlyValTyrLysLeu---------------------------- 135

Db       1295 ATGGACTTACAGCTTCATATTTATCAGTTGAAAACACTAATTAGGATGGTAAAGAAAACC 1354

Qy        136 ------GluPheSerIleGluAlaIleTrpGlyLysThrGlnAsn 148

Db       1355 TACAGAGATTTCCGATTGCAAGGGGTCCTGGACTCCACCTTAAAC 1399

RESULT 20
US-11-266-748A-384474
; Sequence 384474, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 384474
;   LENGTH: 1860
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (89)..(89)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (169)..(169)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-384474

Alignment Scores:
Pred. No.:              3.2          Length:          1860
Score:                  75.50        Matches:         38
Percent Similarity:     35.4%        Conservative:    24
Best Local Similarity:  21.7%        Mismatches:      66
Query Match:            9.8%         Indels:          47
DB:                     8            Gaps:            8

US-10-758-902-9 (1-149) x US-11-266-748A-384474 (1-1860)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24

Db        923 AGCATGGAAATGGGCCAAGAGCATCAATACCATTCAAAAATAGACGAACTAATTGAAGAA 982

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44

Db        983 ACTGTTAAA---GAAATGATAACACTCTTGGTTGCAAAGTTCGTTACTATCTTGGAAGGA 1039

Qy         45 ----------------------------------------LysArgPheValLeuVal 50

Db       1040 GTGCTGGCAAAATTATCCAGATATGACGAAGGGACTTTGTTTTCTTCTTTTCTGTCATTT 1099

Qy         51 AspIleThrThrThrSerLys------LysThrValLysValAlaIleAspValThrAsp 68

Db       1100 ACCGTGAAGGCAGCTTCCAAATATGTGGATGTACCTAAACCCGGGATGGACGTGGCCGAC 1159

Qy         69 ValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAsp 88

Db       1160 GCCTACGTGACTTTCGTCCGCCATTCTCAGGAT--------------GTCCTGCGTGAT 1204

Qy         89 LysValProThrValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeu 108

Db       1205 AAGGTC------------AATGAGGAGATGTAC-----------------ATAGAAAGG 1234

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla---------LysValAspArg 125

Db       1235 TTATTTGATCAATGGTACAACAGCTCCATGAACGTGATCTGCACCTGGTTGACGGACCGG 1294

Qy        126 LysAspLeuGluLeuGlyValTyrLysLeu---------------------------- 135

Db       1295 ATGGACTTACAGCTTCATATTTATCAGTTGAAAACACTAATTAGGATGGTAAAGAAAACC 1354

Qy        136 ------GluPheSerIleGluAlaIleTrpGlyLysThrGlnAsn 148

Db       1355 TACAGAGATTTCCGATTGCAAGGGGTCCTGGACTCCACCTTAAAC 1399

RESULT 21
US-11-266-748A-436854/c
; Sequence 436854, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 436854
;   LENGTH: 1860
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1692)..(1692)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1772)..(1772)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-436854
```

```
Alignment Scores:
Pred. No.:              3.2          Length:        1860
Score:                  75.50        Matches:       38
Percent Similarity:     35.4%        Conservative:  24
Best Local Similarity:  21.7%        Mismatches:    66
Query Match:            9.8%         Indels:        47
DB:                     8            Gaps:          8

US-10-758-902-9 (1-149) x US-11-266-748A-436854 (1-1860)

Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      :::|||:::   :::::::|||   :::   |||   :::|||      |||
Db        938 AGCATGGAAATGGGCCAAGAGCATCAATACCATTCAAAAATAGACGAACTAATTGAAGAA 879

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                 |||         :::      |||                |||||   :::
Db        878 ACTGTTAAA---GAAATGATAACACTCTTGGTTGCAAAGTTCGTTACTATCTTGGAAGGA 822

Qy         45 ----------------------------------------LysArgPheValLeuVal 50
                                                      |||:::
Db        821 GTGCTGGCAAAATTATCCAGATATGACGAAGGGACTTTGTTTTCTTCTTTTCTGTCATTT 762

Qy         51 AspIleThrThrThrSerLys------LysThrValLysValAlaIleAspValThrAsp 68
                 :::        ||||||          |||      :::||||||   |||
Db        761 ACCGTGAAGGCAGCTTCCAAATATGTGGATGTACCTAAACCCGGGATGGACGTGGCCGAC 702

Qy         69 ValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAsp 88
              ||||||        :::         |||              |||       |||
Db        701 GCCTACGTGACTTTCGTCCGCCATTCTCAGGAT--------------GTCCTGCGTGAT 657

Qy         89 LysValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeu 108
              ||||||                 :::::::::                    :::
Db        656 AAGGTC------------AATGAGGAGATGTAC-----------------ATAGAAAGG 627

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla---------LysValAspArg 125
              ||||||    |||          :::|||                  ||||||
Db        626 TTATTTGATCAATGGTACAACAGCTCCATGAACGTGATCTGCACCTGGTTGACGGACCGG 567

Qy        126 LysAspLeuGluLeuGlyValTyrLysLeu---------------------------- 135
              ||||||:::|||   :::|||:::|||
Db        566 ATGGACTTACAGCTTCATATTTATCAGTTGAAAACACTAATTAGGATGGTAAAGAAAACC 507

Qy        136 ------GluPheSerIleGluAlaIleTrpGlyLysThrGlnAsn 148
                    :::|||   ::::::   :::         |||   |||
Db        506 TACAGAGATTTCCGATTGCAAGGGGTCCTGGACTCCACCTTAAAC 462

RESULT 22
US-11-056-355B-97980
; Sequence 97980, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 97980
;   LENGTH: 2598
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2598)
;   OTHER INFORMATION: Ceres Seq. ID no. 13578980
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2598)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13598023
;   OTHER INFORMATION: as cited in SEQ ID NO 66487
US-11-056-355B-97980

Alignment Scores:
Pred. No.:              5.12         Length:        2598
Score:                  75.50        Matches:       34
Percent Similarity:     43.2%        Conservative:  23
Best Local Similarity:  25.8%        Mismatches:    46
Query Match:            9.8%         Indels:        29
DB:                     9            Gaps:          6

US-10-758-902-9 (1-149) x US-11-056-355B-97980 (1-2598)

Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
              |||  |||      |||:::|||:::      |||      ||||||:::   ::::::
Db        939 CAGAGGCCTTTCGTTCTCGAGACTGTGACTGTTGAC---TTGTTTGTGATACGGAATTTA 995

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                        :::|||      :::|||::::::|||               ||||||
Db        996 GGTCTATTTCTGCGGAAGTTCCCTCAGGTGTCAGTAGAT--------------GTTGTT 1040

Qy         73 GlyTyrGlnAspLysTrp----------------------------------AspGly 80
              |||      |||:::|||                                  :::|||
Db       1041 GGACTGGTTGATGAATGGGCTGCTCGCTTTTTTGAGGAGCTGGATTATGTTAACGAGGGA 1100

Qy         81 LysAspArgAlaValPheLeuAsp-----------LysValProThrValAlaThrSer 96
              ::::::          |||   :::          :::|||   |||
Db       1101 GAAAATGGAACATATTTTGCAGAAATGATGAAGAAAGATCTTCCACAAGTTGTTGTACCT 1160

Qy         97 LysLeuPheProGlyValThrAsnArgValThrLeuThr---------PheAspGlySer 113
              |||   :::          |||:::|||      ||||||              ||||||
Db       1161 AAAACCTACCAAAAGTACACGTCAAGGAAGGTTCTTACAACCTCATGGATTGATGGT--- 1217

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAsp--ArgLysAspLeuGluLeuGlyValT 133
                 :::||||||      :::   :::   |||  |||:::      |||         |
Db       1218 ---GAGAAACTGTCACAAAGTATTGAGAGTGATGTCGGCGAACTTGTGAATGTTGGTGTT 1274

Qy        133 yrLysLeuGluPheSerIleGluAlaIleTrp 143
              ||   |||      ::::::        |||
Db       1275 ATTTGTTACCTAAAGCAGTTGCTCGATACTGG 1306

RESULT 23
US-11-056-355B-109219
; Sequence 109219, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 109219
;   LENGTH: 2598
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2598)
;   OTHER INFORMATION: Ceres Seq. ID no. 13578980
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2598)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13598023
;   OTHER INFORMATION: as cited in SEQ ID NO 66487
US-11-056-355B-109219

Alignment Scores:
```

```
Pred. No.:              5.12          Length:        2598
Score:                  75.50         Matches:       34
Percent Similarity:     43.2%         Conservative:  23
Best Local Similarity:  25.8%         Mismatches:    46
Query Match:            9.8%          Indels:        29
DB:                     9             Gaps:          6

US-10-758-902-9 (1-149) x US-11-056-355B-109219 (2598)

Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
              |||   |||       |||:::|||:::      |||      ||||||:::   :::::: 
Db        939 CAGAGGCCTTTCGTTCTCGAGACTGTGACTGTTGAC---TTGTTTGTGATACGGAATTTA 995

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                     :::|||      :::|||::::::|||                 ||||||
Db        996 GGTCTATTTCTGCGGAAGTTCCCTCAGGTGTCAGTAGAT--------------GTTGTT 1040

Qy         73 GlyTyrGlnAspLysTrp-----------------------------------AspGly 80
              |||      |||:::|||                                   :::|||
Db       1041 GGACTGGTTGATGAATGGGCTGCTCGCTTTTTTGAGGAGCTGGATTATGTTAACGAGGGA 1100

Qy         81 LysAspArgAlaValPheLeuAsp-----------LysValProThrValAlaThrSer 96
              ::::::          |||   :::          :::|||   |||
Db       1101 GAAAATGGAACATATTTTGCAGAAATGATGAAGAAAGATCTTCCACAAGTTGTTGTACCT 1160

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThr---------PheAspGlySer 113
              |||   :::          |||:::|||      ||||||             ||||||
Db       1161 AAAACCTACCAAAAGTACACGTCAAGGAAGGTTCTTACAACCTCATGGATTGATGGT--- 1217

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAsp--ArgLysAspLeuGluLeuGlyValT 133
                :::||||||      :::   :::   |||  |||:::      |||          |
Db       1218 ---GAGAAACTGTCACAAAGTATTGAGAGTGATGTCGGCGAACTTGTGAATGTTGGTGTT 1274

Qy        133 yrLysLeuGluPheSerIleGluAlaIleTrp 143
              ||   |||      ::::::         |||
Db       1275 ATTTGTTACCTAAAGCAGTTGCTCGATACTGG 1306

RESULT 24
US-10-449-902-24297
; Sequence 24297, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24297
;   LENGTH: 2730
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK099739
;   DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24297

Alignment Scores:
Pred. No.:              5.49          Length:        2730
Score:                  75.50         Matches:       32
Percent Similarity:     45.8%         Conservative:  17
Best Local Similarity:  29.9%         Mismatches:    31
Query Match:            9.8%          Indels:        27
DB:                     6             Gaps:          8

US-10-758-902-9 (1-149) x US-10-449-902-24297 (1-2730)

Qy         16 ThrPheIleGlnAsp---------LeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              :::|||:::|||||           :::      |||   |||||
Db       2114 TCATTTTTACAGGACAAAGATGAAACGAAACCCAGCCTTCATAAGGGA------------ 2161

Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
              |||||||||         ::::::   |||          |||:::      |||:::
Db       2162 ---TTGCCTGTTGTTTCATTTTCGCTAGGTGACACTGCAGAATTCTTGTATGGTGACGTG 2218

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                        |||   :::   ||||||   ::::::      ||||||   :::
Db       2219 AACGATGTGGATAAAGCTTCA---AAGGTTGATCTGGAATCTGGTGATGTTCTCATATTT 2275

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPhe------LeuAspLysVal 90
              |||                 ||||||   |||  :::|||      :::   ::::::
Db       2276 GGT-----------------GGTAAATCAAGGCTCATATTCCATGGGGTTTCCAGAATC 2317

Qy         91 ---ProThrValAla-----------------ThrSerLysLeuProGlyValThr 103
                 |||       |||                        :::||||||   ||||||
Db       2318 AAACCAAAAACAGCACCAAATTGGCTGACCGATGAAGCAAAACTTCGACCTGGG------ 2371

Qy        104 AsnArgValThrLeuThrPhe 110
                 |||:::   |||||||||
Db       2372 ---CGTCTGAACCTCACATTC 2389

RESULT 25
US-11-266-748A-31618
; Sequence 31618, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31618
;   LENGTH: 5372
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-31618

Alignment Scores:
Pred. No.:              14.2          Length:        5372
Score:                  75.50         Matches:       38
Percent Similarity:     35.4%         Conservative:  24
Best Local Similarity:  21.7%         Mismatches:    66
Query Match:            9.8%          Indels:        47
DB:                     8             Gaps:          8

US-10-758-902-9 (1-149) x US-11-266-748A-31618 (1-5372)
```

```
Qy          5 SerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGlu 24
              |||      :::|||:::   :::::::|||   :::   |||   :::|||      |||
Db       3690 AGCATGGAAATGGGCCAAGAGCATCAATACCATTCAAAAATAGACGAACTAATTGAAGAA 3749

Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                |||          :::      |||                  ||||||   :::
Db       3750 ACTGTTAAA---GAAATGATAACACTCTTGGTTGCAAAGTTCGTTACTATCTTGGAAGGA 3806

Qy         45 -------------------------------------------LysArgPheValLeuVal 50
                                                         |||:::
Db       3807 GTGCTGGCAAAATTATCCAGATATGACGAAGGGACTTTGTTTTCTTCTTTTCTGTCATTT 3866

Qy         51 AspIleThrThrThrSerLys------LysThrValLysValAlaIleAspValThrAsp 68
                :::          ||||||          |||      :::|||||   |||
Db       3867 ACCGTGAAGGCAGCTTCCAAATATGTGGATGTACCTAAACCCGGGATGGACGTGGCCGAC 3926

Qy         69 ValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAsp 88
              ||||||       :::      |||                 |||      |||
Db       3927 GCCTACGTGACTTTCGTCCGCCATTCTCAGGAT--------------GTCCTGCGTGAT 3971

Qy         89 LysValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeu 108
              ||||||              :::::::::                  :::
Db       3972 AAGGTC------------AATGAGGAGATGTAC-----------------ATAGAAAGG 4001

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla---------LysValAspArg 125
                ||||||      |||         :::|||                  ||||||
Db       4002 TTATTTGATCAATGGTACAACAGCTCCATGAACGTGATCTGCACCTGGTTGACGGACCGG 4061

Qy        126 LysAspLeuGluLeuGlyValTyrLysLeu---------------------------- 135
              ||||||:::|||   :::|||:::|||
Db       4062 ATGGACTTACAGCTTCATATTTATCAGTTGAAAACACTAATTAGGATGGTAAAGAAAACC 4121

Qy        136 ------GluPheSerIleGluAlaIleTrpGlyLysThrGlnAsn 148
                   :::|||   ::::::   :::         |||   |||
Db       4122 TACAGAGATTTCCGATTGCAAGGGGTCCTGGACTCCACCTTAAAC 4166

RESULT 26
US-11-348-413-13618
; Sequence 13618, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  APPLICANT:  Murphy, Ellen
;  APPLICANT:  Olmsted, Stephen
;  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;  FILE REFERENCE: 031896-084100 (AM 101724)
;  CURRENT APPLICATION NUMBER: US/11/348,413
;  CURRENT FILING DATE:  2006-02-07
;  PRIOR APPLICATION NUMBER: PCT/US05/035471
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 11/243,445
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 60/615,573
;  PRIOR FILING DATE: 2004-10-05
;  NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 13618
;   LENGTH: 1095
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1095)
;   OTHER INFORMATION: WAN01UPMV; ORF; 00000000011100; Cluster contains WAN01OPY9
;   OTHER INFORMATION: :SE0797:potA:potA protein:ATCC12228:NC_004461.1
US-11-348-413-13618

Alignment Scores:
Pred. No.:              1.79          Length:        1095
Score:                 75.00          Matches:         36
Percent Similarity:    39.4%          Conservative:    18
Best Local Similarity: 26.3%          Mismatches:      61
Query Match:            9.8%          Indels:          22
DB:                        9          Gaps:             6

US-10-758-902-9 (1-149) x US-11-348-413-13618 (1-1095)

Qy         10 GluAlaTyrGluTyrProThr------PheIleGlnAspLeuArgAsnGlu------Leu 25
              :::   |||:::   |||         |||:::   |||          |||      :::
Db       661 GATATATACGATGAACCAGTTAACCGATTTGTTGCTGATTTTATAGGAGAGTCCAACATA 720

Qy         26 AlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
                ||||||   |||         |||   :::          :::
Db       721 GTTCACGGTACAATGGTTGAAGATTTTGTCGTTAATATTTAT-----------GGTCAA 768

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                |||      ||||||:::                |||   |||:::|||   |||
Db       769 AATTTTGATTGTGTAGATATGGGAATAAAAGAAAATAAAAAAGTTGAAGTTGTAATTAGA 828

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
                |||:::   :::|||         |||                        :::
Db       829 CCCGAAGACATTTCACTTGTTTCACAAAATGAT--------------------GGGCTA 867

Qy         86 PheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArg 105
              |||      ||||||            |||   ||||||   ||||||
Db       868 TTTAAAGCCAAAGTT-----------GATTCTATGCTATTTAGAGGTGTACATTATGAA 915

Qy        106 ValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
              :::                  |||:::   ::::::   :::   |||
Db       916 ATTTGTTGTAAAGATAGAAAAGGGTATGAATGGGTAATACAATCAACAAAAAAAGCTAAT 975

Qy        126 LysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
                |||:::|||:::|||         |||      |||||||||
Db       976 GTAGGTAGTGAAGTAGGTCTGTAT---------TTTGAACCAGAAGCAATA 1017

RESULT 27
US-11-218-305-3486
; Sequence 3486, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3486
;   LENGTH: 1256
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-3486

Alignment Scores:
Pred. No.:              2.17          Length:        1256
Score:                 75.00          Matches:         37
Percent Similarity:    41.6%          Conservative:    25
Best Local Similarity: 24.8%          Mismatches:      53
Query Match:            9.8%          Indels:          34
DB:                        9          Gaps:             8

US-10-758-902-9 (1-149) x US-11-218-305-3486 (1-1256)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
              ||||||   |||      ||||||      :::|||   |||:::   |||
Db       200 GCCTACCCTTACAGCGCCTTCATCACCTCCGTCCGGAAAGAAGTGATCAAATACTGCACC 259

Qy         28 ---GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArg 46
                  |||   :::   |||      :::   |||:::            :::
Db       260 AACCATACAGGCATCGTCCAGCCCGTGCTGCCGCTGGAGAAGAATGTCCCCGAGCTCTGG 319
```

```
Qy          47 PheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspVal 66
               |||                 |||       :::::::::   :::||||||   :::
Db         320 TTCTACACCGAG------CTCAAAACGAAGACCAGGTCCATCACGCTCGCCATACGTATG 373

Qy          67 ThrAspValTyrValValGlyTyrGlnAspLys-----------TrpAsp---GlyLys 81
                  ::::::|||:::||||||::::::                  |||:::   ||||||
Db         374 GACAACCTCTACCTGGTCGGCTTCAGGACCCCCGGCGGGGTGTGGTGGGAGTTCGGCAAG 433

Qy          82 AspArgAlaVal---PheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
               |||              ||||||
Db         434 GACGGCGACACCCACCTCCTCGAC---------------------------------- 457

Qy         101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                  |||         |||   |||   |||   ||||||   |||:::   :::
Db         458 ------GACAACGCCAAGTGGCTCGGCTTTGGCGGCCGGTACCAGGACCTCATCGGCAGT 511

Qy         121 AlaLysValAspArgLysAspLeuGlu---------LeuGlyValTyrLysLeuGluPhe 137
                        |||   ||||||         :::|||      ::::::
Db         512 --------------AAGGGCCTGGAGACCGTCACCATGGGCCGTGCCGAAATGACCACG 556

Qy         138 SerIleGluAlaIleTrpGlyLysThr 146
               ::::::      :::      ||||||
Db         557 GCCGTCAACTACCTGGCGAAGAAGACG 583
```

RESULT 28
US-11-348-413-1439
; Sequence 1439, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1439
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3504)
; OTHER INFORMATION: WAN01UKIN; ORF; 11111100000000; Cluster contains WAN01P6WP
; OTHER INFORMATION: :SPy0008:trcF:putative transcription-repair coupling facto
; OTHER INFORMATION: r:SF370:NC_002737.1
US-11-348-413-1439

Alignment Scores:

Pred. No.:	9.17	Length:	3504
Score:	75.00	Matches:	29
Percent Similarity:	40.8%	Conservative:	11
Best Local Similarity:	29.6%	Mismatches:	36
Query Match:	9.8%	Indels:	22
DB:	9	Gaps:	4

US-10-758-902-9 (1-149) x US-11-348-413-1439 (1-3504)

```
Qy          33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
               ||||||      |||||||||      |||   |||:::      |||   |||:::
Db         721 CAATTAGAAAAGGCTCTACAAACAGCACAAGATRATAAAAAATCTTATTTAGAAGATGTA 780

Qy          53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                     ||||||         |||       |||:::               :::
```

```
Db         781 TTAGCTGTTTCAAAAAACGGTTTTAAACATAAG---GATATCCGTAAATTTCAATCATTA 837

Qy          73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
                  |||:::   :::|||                          ||||||   :::|||
Db         838 TTTTAYGAAAAAGAGTGGTCA-----------------TTATTAGATTATATTCCT--- 876

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                                                  :::   |||      |||
Db         877 ----------------------------------AAGGGAACGCCAATCTTTTTTGAT 900

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeu 130
                  :::|||||||||||||:::      |||      |||   |||||||||:::
Db         901 GATTTTCAAAAACTAGTTGAT------AAAAATGCAAGATTTGATTTAGAGATT 948
```

RESULT 29
US-11-056-355B-86436
; Sequence 86436, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86436
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1283)
; OTHER INFORMATION: Ceres Seq. ID no. 12690538
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1283)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 14313471
; OTHER INFORMATION: as cited in SEQ ID NO 64513
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1283)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13591377
; OTHER INFORMATION: as cited in SEQ ID NO 66534
US-11-056-355B-86436

Alignment Scores:

Pred. No.:	2.63	Length:	1283
Score:	74.50	Matches:	28
Percent Similarity:	42.7%	Conservative:	19
Best Local Similarity:	25.5%	Mismatches:	40
Query Match:	9.7%	Indels:	23
DB:	9	Gaps:	4

US-10-758-902-9 (1-149) x US-11-056-355B-86436 (1-1283)

```
Qy          41 IleAlaAspAspLys------ArgPheValLeuValAspIleThrThrThrSerLysLys 58
               ::::::|||   |||      ||||||   |||:::               :::   |||
Db          1 ATGAGTGACACTAAAACGGTGCGTTTTGGTCTTCTTGGATGTATCAGATTCGCATCAAAG 60

Qy          59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
                  |||:::         :::   ::::::      ::::::         |||
Db          61 TTCGTCAGAACAGTAACAGAATCCTCAAACGCCGTCATTATCGCCATCAGCGAT------ 114

Qy          79 AspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeu 98
                                                  |||::::::   |||:::|||
Db         115 ----------------------------------CCATCACTCGAAACCGCAAAAACC 138

Qy          99 PheProGlyValThrAsn------ArgValThrLeuThrPheAspGlySerTyrGlnLys 116
               |||              |||           |||:::|||      |||||||||::::::
```

```
Db        139 TTCGCCACCGGGAACAATTTATCGCCGGAGACCGTCACGATATACGGAAGCTACGAGGAG 198

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              |||:::|||   |||   ||||||         |||   :::   |||   :::
Db        199 CTTTTAAACGATGCAAACGTCGACGCCGTTTACTTGACGATGCCGGTGACGCAA------ 252

Qy        137 PheSerIleGluAlaIleTrpGlyLysThr 146
                          |||   |||       |||
Db        253 ---------CGAGCGAGATGGGCTGTGACG 273

RESULT 30
US-11-218-305-13574/c
; Sequence 13574, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13574
;   LENGTH: 1487
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-13574

Alignment Scores:
Pred. No.:                3.24          Length:          1487
Score:                    74.50         Matches:         28
Percent Similarity:       47.3%         Conservative:    24
Best Local Similarity:    25.5%         Mismatches:      43
Query Match:              9.7%          Indels:          15
DB:                       9             Gaps:            6

US-10-758-902-9 (1-149) x US-11-218-305-13574 (1-1487)

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProVal-----------CysGlnLeuProVal 36
              :::|||                      ||||||:::           |||:::|||
Db       1384 GTTCGGGAACCTGCTTTGAGTGAGACTCCAATCCTTGGGCGCCATTGCCGCCTGTTTTTT 1325

Qy         37 ThrLeu---GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThr 55
                |||   :::   ::::::|||       |||:::|||      ::::::
Db       1324 GTGCTCGGAAAGGCGCTGTCTGATTCCTGTATATTTATTTTGGCAATGCTTTCAGCTGCA 1265

Qy         56 SerLysLysThrValLys---ValAlaIleAspValThrAsp----------------- 68
              :::|||   |||:::         :::   |||:::|||:::
Db       1264 ACAAAACTAACCATGGATGGCACTAGCTTTGACCTGACAGAGCACGAAGGTTCAAATCTG 1205

Qy         69 ---ValTyrValValGlyTyrGlnAspLysTrpAspGly---LysAspArgAlaValPhe 86
                 :::::::::        ::::::||||||      |||   |||   :::|||
Db       1204 TCTCCGTTTCTACTCAAACTTTTTAATGAGTGGGATGATCGCAAGACAAGGGGCTTGTTT 1145

Qy         87 LeuAspLysValProThrValAlaThrSerLysLeuProGlyValThrAsnArgVal 106
                  :::   :::       |||   |||:::   |||||||||   |||   |||
Db       1144 CACCATGACATCAGTTCCTGTGAAACA---AAGGTGCTACCTGGAGTACATAATTTTGTG 1088

Qy        107 ThrLeuThrPheAspGlySerTyrGlnLys 116
                        :::|||      ||||||
Db       1087 GCAACATTAATTGAAGGACGTGACCAAAAG 1058

RESULT 31
US-10-953-349-5403
; Sequence 5403, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5403
;   LENGTH: 1823
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5403

Alignment Scores:
Pred. No.:                4.31          Length:          1823
Score:                    74.50         Matches:         32
Percent Similarity:       40.4%         Conservative:    10
Best Local Similarity:    30.8%         Mismatches:      39
Query Match:              9.7%          Indels:          23
DB:                       6             Gaps:            3

US-10-758-902-9 (1-149) x US-10-953-349-5403 (1-1823)

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              |||   :::   ||||||:::||||||                          |||
Db       1038 ACATTCGAATTGATTGCAGAGGACAAAGAA----------------------ACCCAG 1073

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
                    ||||||:::|||                                    |||
Db       1074 TCGCTCACTGTAGAGGTATTT----------------------------------GAT 1097

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
              |||       |||:::|||       :::   |||   |||:::|||           |||
Db       1098 AAAGACGTAGGTCAAGATGAGCGCCTTGGACTTGTGAAACTTCCC---------TTAAGC 1148

Qy         97 LysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
                 |||       |||||||||       :::   |||           |||
Db       1149 AGTTTGGAAGCCGGAGTTACAAAAGAACTGGAGCTAAATCTGTTGTCTTCACTTGATACT 1208

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              |||           |||   ||||||       :::   |||   |||:::   |||
Db       1209 TTGAAAGTAAAAGATAAGAAAGATAGAGGAAGCATAACTCTTAAGGTACATTATCATGAG 1268

Qy        137 PheSerIleGlu 140
              |||:::   |||
Db       1269 TTCAACAAAGAG 1280

RESULT 32
US-10-449-902-12843
; Sequence 12843, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12843
;   LENGTH: 4067
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK110191
```

```
;  DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-12843

Alignment Scores:
Pred. No.:              13.3          Length:        4067
Score:                  74.50         Matches:       32
Percent Similarity:     37.5%         Conservative:  16
Best Local Similarity:  25.0%         Mismatches:    49
Query Match:            9.7%          Indels:        31
DB:                     6             Gaps:          4

US-10-758-902-9 (1-149) x US-10-449-902-12843 (1-4067)

Qy         26 AlaLysGlyThrProValCysGlnLeuProValThrLeu----------GlnThr 40
              ||||||   |||   :::|||       |||            :::
Db       3608 GCCAAGGATGCACCGGAGCCGCGGCTGCGCGAGGCGCTCAAGGCGGTGTGGCGCCGCGCA 3667

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              :::   |||   |||  |||  :::  |||   |||  :::|||||
Db       3668 GTGGTGCGCGACGACTGGTTCGCGCTGTCCGAGACCACCAATGTTTCGGACCAGACCGTG 3727

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
              :::   |||  :::|||  |||   :::   |||
Db       3728 CTTGCCGACCTGCAAGCTACGGCGTTGTATGCGGTGCTGGGCGAGGTGCTTGCGGACGAT 3787

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
                :::|||:::  :::||||||       |||
Db       3788 GCGAATCGGTCGGCGTATCTGGATGTGCACGAGCTCGTGGGC---------------- 3829

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys---LeuValAsn 119
                                      ||||||   |||  ||||||
Db       3830 ----------------------------GATGGCGAAGATGCAAAGGCGCTCGTGGCG 3859

Qy        120 AlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIle 139
              |||       |||:::  |||:::|||                    :::
Db       3860 GCTAGGATGGCAGATAAGGGCGATGTGGAG-------------------------GTT 3892

Qy        140 GluAlaIleTrpGlyLysThrGln 147
              :::|||:::|||       |||
Db       3893 GACGCTGTCTGGCACGATCGACAG 3916

RESULT 33
US-11-056-355B-12863
; Sequence 12863, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 12863
;   LENGTH: 1437
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1437)
;   OTHER INFORMATION: Ceres Seq. ID no. 12347187
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1437)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13579556
;   OTHER INFORMATION: as cited in SEQ ID NO 53743
US-11-056-355B-12863

Alignment Scores:
Pred. No.:              3.63          Length:        1437
Score:                  74.00         Matches:       31
Percent Similarity:     46.3%         Conservative:  25
Best Local Similarity:  25.6%         Mismatches:    45
Query Match:            9.6%          Indels:        20
DB:                     9             Gaps:          7

US-10-758-902-9 (1-149) x US-11-056-355B-12863 (1-1437)

Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly----------Thr 29
              ||||||   |||   :::       :::       |||            |||
Db         70 CCAACCGAAATCTCAGAGGAAAGTAGGAAACCTCGTTCGGGAACCTGCTTTAGTGAGACT 129

Qy         30 ProVal----------CysGlnLeuProValThrLeu---GlnThrIleAlaAspAsp 44
              |||:::          |||:::|||       |||   :::   ::::::|||
Db        130 CCAATCCTTGGGCGCCATTGCCGCCTGTTTTTTGTGCTAGGAAAGGCGCTGTCTGATTCC 189

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys---ValAla 63
                 |||:::|||      ::::::      :::|||   |||:::         :::
Db        190 TGTATATTTATTTTGGCATTGCTTTCAGCTGCAACAAAACTAACCATGGATGGCACTAGC 249

Qy         64 IleAspValThrAsp--------------------ValTyrValValGlyTyrGlnAsp 76
              |||:::|||:::                     :::::::::      :::
Db        250 TTTGATCTGACAGAGCACGAAGGTTCAAATCTGTCTCCGTTTCTACTCAAACTTTTTAAT 309

Qy         77 LysTrpAspGly---LysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
              :::|||||       |||   |||  :::|||         :::   :::      |||
Db        310 GAGTGGGATGATCGCAAGACAAGGGGCTTGTTTCACCATGACATCAGTTCCTGTGAAACA 369

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
              |||:::   |||||||||   |||   |||            :::|||      |||
Db        370 ---AAGGTGCTACCTGGAGTACATAATTTTGTGGCAACATTAATTGAAGGACGTGACCAA 426

Qy        116 Lys 116
              |||
Db        427 AAG 429

RESULT 34
US-11-348-413-7411
; Sequence 7411, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  APPLICANT:  Murphy, Ellen
;  APPLICANT:  Olmsted, Stephen
;  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;  FILE REFERENCE: 031896-084100 (AM 101724)
;  CURRENT APPLICATION NUMBER: US/11/348,413
;  CURRENT FILING DATE:  2006-02-07
;  PRIOR APPLICATION NUMBER: PCT/US05/035471
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 11/243,445
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 60/615,573
;  PRIOR FILING DATE: 2004-10-05
;  NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 7411
;   LENGTH: 1560
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1560)
;   OTHER INFORMATION: WAN01UM9L; ORF; 00000001000000; Cluster contains WAN01PC4E
;   OTHER INFORMATION: -5::alp2:alpha-like protein 2 Conserved N terminus::AF2081
;   OTHER INFORMATION: 58
US-11-348-413-7411

Alignment Scores:
Pred. No.:              4.08          Length:        1560
Score:                  74.00         Matches:       28
Percent Similarity:     45.6%         Conservative:  13
Best Local Similarity:  31.1%         Mismatches:    47
```

```
Query Match:            9.6%          Indels:        2
DB:                     9             Gaps:          2

US-10-758-902-9 (1-149) x US-11-348-413-7411 (1-1560)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              :::||||||     :::          |||   :::|||   ::::::|||   |||
Db       1294 GTAGGAGAAACACCGAAGGCAGAAGATTCTATTGGTAACTTA---TCAGATCTTCCGAAA 1350

Qy         28 GlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArg 46
              ||||||   |||      :::   ||||||         |||      |||
Db       1351 GGTACAACAGTAGCCTTTGAARCTCCAGTTGATACRGCAACACCGGGAGACAAACCAGCA 1410

Qy         47 PheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspVal 66
                 |||:::|||                 ||||||   ||||||   |||   :::   |||
Db       1411 AAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACGGTTAAGGTT 1470

Qy         67 ThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPhe 86
              |||                 ::::::         |||||||||:::    |||
Db       1471 GTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAGGACCAAACGGTCAAA 1530

Qy         87 LeuAspLysValProThrValAlaThrSer 96
              :::   :::   |||             |||
Db       1531 GTAGGAGAAACACCGAAGGCAGAAGATTCT 1560

RESULT 35
US-11-218-305-9122/c
; Sequence 9122, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9122
;   LENGTH: 1998
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1979)..(1985)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-9122

Alignment Scores:
Pred. No.:              6.79          Length:        1998
Score:                  73.50         Matches:       26
Percent Similarity:     44.2%         Conservative:  12
Best Local Similarity:  30.2%         Mismatches:    33
Query Match:            9.6%          Indels:        15
DB:                     9             Gaps:          5

US-10-758-902-9 (1-149) x US-11-218-305-9122 (1-1998)

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
              |||:::|||      |||:::      |||   |||   |||||||||   ||||||
Db       1437 CTCAAAAACAACAACGCCCAGAGCGACCCATCTTGCAATCTCCCAGTTTTCCTTCAGAAA 1378

Qy         41 IleAlaAspAsp---LysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
              :::      :::   |||                 |||                ||||||:::
Db       1377 GTCATACATAACATCAAAGTTATGTGTTTTGTCCACTGGAATTACCTGCAAAAGAAGTCT 1318

Qy         60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp 79
              :::                 |||   |||         |||      ||||||
```

```
Db       1317 ATT--------------------GATAACTAC------AGCTACTCAAGGAAATGGTAA 1285

Qy         80 GlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr---------Ser 96
              ||||||             :::         ||||||   ::::::|||         :::
Db       1284 GGCAAG------GTACATTATAGTAGTTTAGTTCCTGAGATAAGCACCCAATAGAATACT 1231

Qy         97 LysLeuPheProGlyVal 102
                 :::||||||   :::
Db       1230 CACATCTTTCCAGCCATG 1213

RESULT 36
US-11-348-413-7015
; Sequence 7015, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  APPLICANT:  Murphy, Ellen
;  APPLICANT:  Olmsted, Stephen
;  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;  FILE REFERENCE: 031896-084100 (AM 101724)
;  CURRENT APPLICATION NUMBER: US/11/348,413
;  CURRENT FILING DATE:  2006-02-07
;  PRIOR APPLICATION NUMBER: PCT/US05/035471
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 11/243,445
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 60/615,573
;  PRIOR FILING DATE: 2004-10-05
;  NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 7015
;   LENGTH: 3243
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(3243)
;   OTHER INFORMATION: WAN01ULSG; ORF; 00000000100000; SingletonSubcluster contai
;   OTHER INFORMATION: ns WAN01PIFM:A909_1421_Glim2.02::Glimmer 2.02 orf predicti
;   OTHER INFORMATION: on:A909:WAN01PCPY
US-11-348-413-7015

Alignment Scores:
Pred. No.:              13.4          Length:        3243
Score:                  73.50         Matches:       36
Percent Similarity:     43.3%         Conservative:  22
Best Local Similarity:  26.9%         Mismatches:    53
Query Match:            9.6%          Indels:        23
DB:                     9             Gaps:          6

US-10-758-902-9 (1-149) x US-11-348-413-7015 (1-3243)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              ||||||     |||   ::::::   |||:::|||         ::::::
Db        373 AATCTTTACGGAGCCAAGGATTGGAATACTTATATCGACCAAACTAAATCT------GTA 426

Qy         27 LysGlyThrProValCysGlnLeuProValThrLeuGln---ThrIleAlaAspAspLys 45
                    :::|||:::   |||                |||   :::::::::   ||||||
Db        427 AATAAATCACCTATTATCCAACGTACCGAACAAGGCCAAGTAAGTCTATCCAGCGACAAA 486

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
              |||                                     |||   ||||||   ||||||
Db        487 GGCTTT--------------------AGAGGTGCTGTGACACAAAAAGTGAACATTGAT 525

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||      |||   |||   :::      :::         |||
Db        526 CCCACTAAAAAATATGAGGTCAAGTTTGATATTGAAACAAGTAACAAGGTTGGACAAGCT 585

Qy         86 PheLeu-----------------AspLysValProThrValAlaThrSerLysLeuPhe 99
              ||||||                 ||||||         :::      |||::::::
Db        586 TTCCTTCGTATTATGAAGAAAAAAGACAAGAATACGCGACTTTGGCTTTCTGAGATGACC 645

Qy        100 ProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsn 119
```

```
Db        646 AGCGGTACCACTAACAAACATACCTTAACA-----------------AAGATATATAAC 687

Qy        120 AlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133

Db        688 ---CCAAAGTTAAATGTCTCCGAGGTGACACTTGAACTTTAT 726
```

RESULT 37
US-11-348-413-443
; Sequence 443, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 443
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1026)
; OTHER INFORMATION: WAN01UJCK; ORF; 11111100000000; Cluster contains WAN01P6X1
; OTHER INFORMATION: :SPy2197::conserved hypothetical protein:SF370:NC_002737.1
US-11-348-413-443

Alignment Scores:

Pred. No.:	3.69	Length:	1026
Score:	72.50	Matches:	25
Percent Similarity:	43.7%	Conservative:	20
Best Local Similarity:	24.3%	Mismatches:	35
Query Match:	9.4%	Indels:	23
DB:	9	Gaps:	5

US-10-758-902-9 (1-149) x US-11-348-413-443 (1-1026)

```
Qy         49 LeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAsp 68

Db        739 TTAATAGCGACTGTTACTAAATCTAAAGAGACCGTTGATATCAGTGTGTCTTTAACCGAG 798

Qy         69 ValTyrValValGlyTyrGlnAspLysTrp--------------------------Asp 79

Db        799 GCA--------------CAAAGTAGTTGGATTTCTCTAACAAATTCAGAAATTGGTGAA 843

Qy         80 Gly--------------LysAspArgAlaValPheLeuAspLysValProThrValAla 94

Db        844 GGTGGTATAACATTGACTCAAGACTCGCCAACTTATACAGCGACTTTACCTGCAGAAATA 903

Qy         95 ThrSerLysLeuPhePro---GlyValThrAsnArgValThrLeuThrPheAspGlySer 113

Db        904 ACAGAATCATTGTTGACRCTTGGTGTGACAAAWGGTGTATCTGTAACAATTGATGGA--- 960

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133

Db        961 ------CAACCTGTTGATCTATCACCTTTAACAAGTACTGACTTAAGTTATATCACGTTT 1014

Qy        134 LysLeuGlu 136

Db       1015 AAGATCCAA 1023
```

RESULT 38

US-11-348-413-181
; Sequence 181, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 181
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1533)
; OTHER INFORMATION: WAN01UJ3M; ORF; 01011100000000; Cluster contains WAN01P5OK
; OTHER INFORMATION: :SpyM3_1434::conserved hypothetical protein - phage associ
; OTHER INFORMATION: ated:MGAS315:NC_004070.1
US-11-348-413-181

Alignment Scores:

Pred. No.:	6.48	Length:	1533
Score:	72.50	Matches:	34
Percent Similarity:	42.6%	Conservative:	26
Best Local Similarity:	24.1%	Mismatches:	58
Query Match:	9.4%	Indels:	23
DB:	9	Gaps:	5

US-10-758-902-9 (1-149) x US-11-348-413-181 (1-1533)

```
Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal 31

Db         94 TATGAATCAAAACTTTGGATAGATCAACTTAAGAATTACATTTCAAGGTTTAAA------ 147

Qy         32 CysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAsp 51

Db        148 ---------GCAGAACAATTAGAGCGTTTGAAAGAGTTAAAGCGATACTATCTTGGGGAT 198

Qy         52 ------IleThrThrThrSerLysLysThrValLysValAlaIleAsp------------ 65

Db        199 AATAACATCAAGTATAGACCTGCTAAAACAGATAAATACGCAGCGGATAATCGTATTGCA 258

Qy         66 ---------------ValThrAspValTyrValValGlyTyr------------------ 74

Db        259 AGTGATTTTGCTAAGTATATTACGGTATTTGAGCAAGGTTATATGCTTGGCGTTCCCGTT 318

Qy         75 GlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAla 94

Db        319 GAGTACAAAAATGAAAATAAAGACCTCCAGGCAGCTATTGAC---CTTATGTCGGTCAGA 375

Qy         95 ThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyr 114

Db        376 AACAATGAGGACTACCACAACGTCAAAATAAAAACAGATTTATCAATTTATGGAAGAGCC 435

Qy        115 GlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLys 134

Db        436 TACGAGCTGTTAACTGTTGAGAAAATAGATGACAAAAAAACCGAAGTAAAACTCTACCAG 495

Qy        135 Leu 135

Db        496 CTC 498
```

```
RESULT 39
US-10-505-928-472
; Sequence 472, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 472
;   LENGTH: 5479
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-472

Alignment Scores:
Pred. No.:              38.8          Length:          5479
Score:                  72.50         Matches:         44
Percent Similarity:     34.3%         Conservative:    16
Best Local Similarity:  25.1%         Mismatches:      56
Query Match:            9.4%          Indels:          59
DB:                     6             Gaps:            10

US-10-758-902-9 (1-149) x US-10-505-928-472 (1-5479)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrPro---------- 15
              |||||||||          |||   ||||||      :::   |||
Db       1246 TATAATACC---CGATTAAACCGAGGAGAATATGTAGACGTTCCCTTCCCCAACCAGTAT 1302

Qy         15 ---------------------------------------------------------- 15

Db       1303 CAGTATATTGCTGCAGTGGATTACAATCCAAGAGATAACCAACTTTACGTGTGGAACAAT 1362

Qy         16 ThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrPro---ValCysGlnLeu 34
                ||||||      ||||||      |||      |||   |||         |||:::
Db       1363 AACTTCATT------TTACGATATTCTCTGGAGTTTGGTCCACCTGATCCTGCCCAAGTG 1416

Qy         35 ProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThr 54
              |||   |||      ||||||                              |||:::|||
Db       1417 CCTACCACAGCTGTGACAATAACTTCTTCAGCTGAGCTGTTCAAAACCATAATATCAACC 1476

Qy         55 ThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyr 74
              ||||||      :::   |||      :::      |||         |||   |||
Db       1477 ACAAGCACTACTTCACAGAAAGGCCCCATGAGCACAACT---------GTAGCTGGATCA 1527

Qy         75 GlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAla 94
              |||:::          |||                              |||   |||:::
Db       1528 CAGGAAGGAAGCAAAGGG-----------------ACAAAACCACCTCCAGCAGTTTCT 1569

Qy         95 ThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyr 114
              |||:::|||:::   |||   :::||||||         |||
Db       1570 ACAACCAAAATT---CCACCTATAACAAATATTTTTCCCCTGCCA-------------- 1611

Qy        115 GlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLys 134
              ::::::         |||      :::|||   |||   ::::::
Db       1612 GAGAGATTCTGTGAAGCA------TTAGACTCCAAGGGGATAAAG-------------- 1650

Qy        135 LeuGluPheSerIleGluAlaIleTrpGlyLysThrGlnAsnGly 149
                                  |||   :::||||||   |||
Db       1651 ----------------------TGGCCTCAGACACAAAGGGGA 1671

RESULT 40
US-10-471-571A-705
; Sequence 705, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 705
;   LENGTH: 1122
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-705

Alignment Scores:
Pred. No.:              4.92          Length:          1122
Score:                  72.00         Matches:         36
Percent Similarity:     37.0%         Conservative:    21
Best Local Similarity:  23.4%         Mismatches:      51
Query Match:            9.4%          Indels:          46
DB:                     6             Gaps:            6

US-10-758-902-9 (1-149) x US-10-471-571A-705 (1-1122)

Qy         23 AsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAla 42
              ::::::||||||||||||                  ::::::      |||:::
Db       163 CATGACTTAGCTAAAGGTATTAAAAATGCTGGGCAAATCTTATCTACAATGACAGTGTTA 222

Qy         43 AspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysVal 62
              |||||||||      :::|||      :::         ||      |||:::   |||
Db       223 GATGACAAAGATCGCCTGTTAACTACTGTTAAATTAAAAAGT---AATACATTGAATGTG 279

Qy         63 Ala------------------IleAspValThrAspValTyrValValGlyTyrGlnAsp 76
                                  ||||||:::         ||||||
Db       280 ACGTTACCACGCCAAACATTAATTGACATTATTAAATCTTATGTA-------------- 324

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
                     ||||||   |||:::|||   :::         |||         :::
Db       325 ------------AAAGATGACGCAATATTTACAAATCATGAAGTCACGCATATAGATAAT 372

Qy         97 LysLeuProGlyValThrAsnArgValThrLeuThrPhe------------------ 110
              :::               |||:::::||||||:::   |||
Db       373 GAG--------------ACAGATAAAGTTACCATACATTTCGCGGAACAAGAAAGTGAA 417

Qy        111 ------------------------AspGlySerTyrGlnLysLeuValAsnAlaAlaLys 122
                                     ||||||   :::   |||:::      :::
Db       418 GCATTTGATTTATGTATTGGTGCTGATGGAATTCATTCTAAAGTGAGACAATCTGTAAAT 477

Qy        123 ValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
                 |||   |||   |||      |||                  |||:::   |||
Db       478 GCTGACAGTAAAGTATTATATCAAGGGTATACATGCTTTAGAGGTTTAATTGATGATATT 537

Qy        143 --------------------------------TrpGlyLys 145
                                             |||||||:::
Db       538 GATTTAAAGCATCCGGATTGTGCAAAAGAATACTGGGGAAGA 579

RESULT 41
US-11-218-305-3485
; Sequence 3485, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 3485
;   LENGTH: 1240
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1145)..(1145)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1191)..(1191)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-3485

Alignment Scores:
Pred. No.:              5.66          Length:        1240
Score:                  72.00         Matches:       36
Percent Similarity:     41.6%         Conservative:  26
Best Local Similarity:  24.2%         Mismatches:    53
Query Match:            9.4%          Indels:        34
DB:                     9             Gaps:          8

US-10-758-902-9 (1-149) x US-11-218-305-3485 (1-1240)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
              ||||||   |||     ||||||      :::|||   ::::::   |||
Db        284 GCCTACCCTTACAGCGCCTTCATCACCTCCGTCCGGAAAGACGTGATCAAATACTGCACC 343

Qy         28 ---GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArg 46
                 |||   :::   |||       :::   |||:::             :::
Db        344 AACCATACAGGCATCGTCCAGCCCGTGCTGCCGCTGGAGAAGAATGTCCCCGAGCTCTGG 403

Qy         47 PheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspVal 66
              |||          |||      :::::::::   :::||||||   :::
Db        404 TTCTACACCGAG------CTCAAAACGAAGACCAGGTCCATCACGCTCGCCATACGTATG 457

Qy         67 ThrAspValTyrValValGlyTyrGlnAspLys-----------TrpAsp---GlyLys 81
                 ::::::|||:::||||||::::::                  |||:::   ||||||
Db        458 GACAACCTCTACCTGGTCGGCTTCAGGACCCCCGGCGGGGTGTGGTGGGAGTTCGGCAAG 517

Qy         82 AspArgAlaVal---PheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
              |||           ||||||
Db        518 GACGGCGACACCCACCTCCTCGAC---------------------------------- 541

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                 |||       |||   |||   |||   ||||||   |||:::   :::
Db        542 ------GACAACGCCAAGTGGCTCGGCTTTGGCGGCCGGTACCAGGACCTCATCGGCAGT 595

Qy        121 AlaLysValAspArgLysAspLeuGlu---------LeuGlyValTyrLysLeuGluPhe 137
                       |||   ||||||          :::|||      ::::::
Db        596 --------------AAGGGCCTGGAGACCGTCACCATGGGCCGTGCCGAAATGACCACG 640

Qy        138 SerIleGluAlaIleTrpGlyLysThr 146
              ::::::      :::      ||||||
Db        641 GCCGTCAACTACCTGGCGAAGAAGACG 667

RESULT 42
US-10-449-902-27052
; Sequence 27052, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27052
;   LENGTH: 2224
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK102494
;   DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-27052

Alignment Scores:
Pred. No.:              12.9          Length:        2224
Score:                  72.00         Matches:       28
Percent Similarity:     35.1%         Conservative:  11
Best Local Similarity:  25.2%         Mismatches:    40
Query Match:            9.4%          Indels:        32
DB:                     6             Gaps:          4

US-10-758-902-9 (1-149) x US-10-449-902-27052 (1-2224)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ::::::||||||      |||                  |||   ||||||
Db       1317 GACTTCCCTACTATGCCAATTGAT--------------------GGACCGCCAGTGATG 1355

Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
              :::      |||         |||             |||   |||:::   :::
Db       1356 AAAACTTCTGTCATTAACTCCACATAC---------AAGAATTTCTTGGAAATTGTATTT 1406

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                          |||                 ||||||             :::||||||
Db       1407 CAGAACAATGACACGAAAGTCCAGACCTACCATATCGATGGATATGCATTTTGGGTTGTA 1466

Qy         73 GlyTyrGln-----------------------------------AspLysTrpAspGly 80
              |||                                        :::||||||||||||
Db       1467 GGGATGGACTATGGTGAGTGGACTGAGAATAGCCGTGGGACTTACAACAAGTGGGATGGT 1526

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
                    |||                                  |||:::::::::||||||
Db       1527 GTTTCTCGT-----------------------------TGCACCACACAGGTATTCCCT 1556

Qy        101 GlyValThrAsnArgValThrLeuThrPheAsp 111
              |||          |||   |||:::   |||
Db       1557 GGAGCATGGACTGCTGTGATGCTGTCACTTGAC 1589

RESULT 43
US-11-217-529-77685
; Sequence 77685, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77685
;   LENGTH: 2832
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77685

Alignment Scores:
Pred. No.:              18.1          Length:        2832
Score:                  72.00         Matches:       27
```

```
Percent Similarity:     47.7%          Conservative:  15
Best Local Similarity:  30.7%          Mismatches:    26
Query Match:            9.4%           Indels:        20
DB:                     8              Gaps:          5

US-10-758-902-9 (1-149) x US-11-217-529-77685 (1-2832)

Qy         67 ThrAspValTyrValValGlyTyrGlnAsp-----------LysTrpAspGlyLysAsp 82
              ||||||:::     |||||||||   |||                |||||
Db        271 ACGGATTTATTAGCTGTCGGTTACGCAGATGGTGTCATTAAAGTTTGGGATTTGATGTCT 330

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              :::   |||   |||:::                          |||   |||
Db        331 AAGACTGTGCTTTTGAAT---------------------------TTTAACGGTCAC 360

Qy        103 ThrAsnArgValThr---LeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||   |||   |||||||||:::      :::|||:::::   :::
Db        361 AAAGCAGCTATAACATTATTACAATTTGATGGGACTGGCACAAGATTAATTTCTGGTTCC 420

Qy        122 Lys---------ValAspArgLysAspLeu------GluLeuGlyValTyrLysLeuGlu 136
              |||         :::       ||||||      |||:::|||::::::||||||
Db        421 AAGGACTCCAATATCATTGTATGGGATCTTGTTGGAGAAGTTGGTCTTCATAAACTTAGA 480

Qy        137 PheSerIleGluAlaIleTrpGly 144
                  ::::::|||   |||
Db        481 TCACACAAGGATTCCATTACTGGC 504

RESULT 44
US-11-348-413-13946
; Sequence 13946, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  APPLICANT:  Murphy, Ellen
;  APPLICANT:  Olmsted, Stephen
;  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;  FILE REFERENCE: 031896-084100 (AM 101724)
;  CURRENT APPLICATION NUMBER: US/11/348,413
;  CURRENT FILING DATE:  2006-02-07
;  PRIOR APPLICATION NUMBER: PCT/US05/035471
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 11/243,445
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 60/615,573
;  PRIOR FILING DATE: 2004-10-05
;  NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 13946
;   LENGTH: 1374
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1374)
;   OTHER INFORMATION: WAN01UPWX; ORF; 00000000011111; Cluster contains WAN01OPLO
;   OTHER INFORMATION: :SE0344:vraA:vraA protein:ATCC12228:NC_004461.1
US-11-348-413-13946

Alignment Scores:
Pred. No.:              7.7            Length:        1374
Score:                  71.50          Matches:       31
Percent Similarity:     40.1%          Conservative:  28
Best Local Similarity:  21.1%          Mismatches:    75
Query Match:            9.3%           Indels:        13
DB:                     9              Gaps:          3

US-10-758-902-9 (1-149) x US-11-348-413-13946 (1-1374)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              :::|||:::            |||      :::      |||   |||:::|||   |||
Db        586 ATAGGTCAAAAAAATTTTAATCCACTATCTCTTATGCGTCTTATTAATCARTTGAACAAA 645

Qy         28 GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPhe 47
                  |||   :::      :::|||      :::|||   :::         :::|||
Db        646 RCGACAGCAATATTTGTAGTGCCAACGATGGTACAACAACTTATTTCAACYCAACGACAT 705

Qy         48 ---------ValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
                      :::         :::::::::   :::|||   |||::::::
Db        706 TGTTCATCGATTAAAAGTATTTTGAGTAGTGGTGCTAAACTTACATTGCAACAGTTTCAA 765

Qy         65 AspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAla 84
              :::      :::|||                  ::::::   |||         |||
Db        766 CAAATCAGMAMTTTATATCCACAAGCAAATTTAATAGAATTTTTTGGGACATCTGAAGCA 825

Qy         85 ValPheLeu--------------AspLysValProThrValAlaThrSerLysLeuPhe 99
              |||:::                      |||      :::      |||||||||
Db        826 AGTTTTATAAGCTACAATTTTAACCAATCATCTCCTGCTMATTCTGTWGGTAAACTTTTC 885

Qy        100 ProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsn 119
              |||   |||       |||:::          |||   :::       |||
Db        886 CCTCATGTCGARACRCGATTATTAAATCAAGATGATGATGCAGTAGGATTATTA------ 939

Qy        120 AlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIle 139
                        |||   ::::::          |||      :::   :::
Db        940 ---------GCCGTTAGAAGTGAAATGGTGTTTAGTGGTTATGTKGGACARAGCAATCAA 990

Qy        140 GluAlaIleTrpGlyLysThr 146
              |||       |||   ||||||
Db        991 GAGGGGKCATGGATTAAAACA 1011

RESULT 45
US-11-217-529-77659
; Sequence 77659, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77659
;   LENGTH: 1788
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77659

Alignment Scores:
Pred. No.:              11.1           Length:        1788
Score:                  71.50          Matches:       27
Percent Similarity:     43.9%          Conservative:  27
Best Local Similarity:  22.0%          Mismatches:    52
Query Match:            9.3%           Indels:        17
DB:                     8              Gaps:          4

US-10-758-902-9 (1-149) x US-11-217-529-77659 (1-1788)

Qy         31 ValCysGlnLeuProValThrLeuGlnThr-----------IleAlaAspAspLysArg 46
              ||||||   ||||||      :::   :::           |||:::   :::   |||
Db        655 GTTTGCTCCCTGCCACCATTAATCAATAGTGAACATTCGAAGATCTCTGTGAACACCCGT 714

Qy         47 PheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspVal 66
                 :::|||:::|||||||||   |||   |||          ::::::   :::::::::
Db        715 AACATTTTGATTGATATAACCGCCACCGATAAGACCAAAGCCGAGATCGTTTTGAACATA 774

Qy         67 ThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPhe 86
                                    |||   |||:::
Db        775 TTAACTACAATGTTCTCACGTTATTGTGACGAA-----------------CCATTCACG 816
```

```
Qy          87 LeuAspLysValProThrValAla-----------ThrSerLysLeuPheProGlyVal 102
               ::::::  |||     |||:::           |||:::|||   |||
Db         817 GTTGAGCCTGTAGAAATTGTCTCTGAACACAATGGCCAATCCCGTTTGGCGCCAAACTTC 876

Qy         103 ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLys 122
                 :::|||:::           |||   |||   :::   :::   :::
Db         877 AACGATAGAATT---------ATGGATGTCTCCATTAAGTACATCAACTCCTGTCTTGGC 927

Qy         123 ValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
               :::|||:::         |||:::           :::   |||:::   |||:::
Db         928 CTAGATCAATCCGCTGATGAAATTGCTCATTGTCTAAAGAAGATGTCGTTGCATGCCGTT 987

Qy         143 TrpGlyLys 145
                  |||
Db         988 CAATCAAAG 996
```

RESULT 46
US-10-449-902-21229/c
; Sequence 21229, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21229
; LENGTH: 1966
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK071520
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-21229

Alignment Scores:

Pred. No.:	12.7	Length:	1966
Score:	71.50	Matches:	27
Percent Similarity:	47.8%	Conservative:	16
Best Local Similarity:	30.0%	Mismatches:	34
Query Match:	9.3%	Indels:	13
DB:	6	Gaps:	4

US-10-758-902-9 (1-149) x US-10-449-902-21229 (1-1966)

```
Qy           4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
               ||||||:::   ||||||              ||||||   :::|||   |||
Db        1733 GTTAGTTATCCCCTGGGA---------TCCAATCCCACTGTCCTTCAAGCCCTGGAAGGG 1683

Qy          24 GluLeuAlaLysGlyThrProValCysGlnLeuProValThr---------LeuGlnThr 40
               |||:::   :::   :::      |||::::::   :::            |||
Db        1682 GAAATGGTCAGGTCCTCGAGCCGGTGCAGAGTTGATCTGAACGGTTCCGGTCTCCATCGC 1623

Qy          41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
               |||||||||      |||||||||   :::            ||||||   :::
Db        1622 ATCGCTGATCATGATCGCTTTGTTGATATCTTTAGTGAATACACATCCCTGCAGCCCAAA 1563

Qy          61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp--- 79
                 |||   :::   |||   ::::::           |||:::   |||
Db        1562 ATTGCTGGCATTGCAATGGTGGATGCCTTCCTC-----------GACCGAGTTGATCCT 1515

Qy          80 ------GlyLysAspArgAlaValPheLeu 87
                    :::||||||||||   :::|||
Db        1514 AATCACAGGCAAGACAGGGCCAAATGGCTC 1485
```

RESULT 47
US-10-449-902-5375/c
; Sequence 5375, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5375
; LENGTH: 2272
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK062559
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-5375

Alignment Scores:

Pred. No.:	15.6	Length:	2272
Score:	71.50	Matches:	27
Percent Similarity:	47.8%	Conservative:	16
Best Local Similarity:	30.0%	Mismatches:	34
Query Match:	9.3%	Indels:	13
DB:	6	Gaps:	4

US-10-758-902-9 (1-149) x US-10-449-902-5375 (1-2272)

```
Qy           4 ValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsn 23
               ||||||:::   ||||||              ||||||   :::|||   |||
Db        2039 GTTAGTTATCCCCTGGGA---------TCCAATCCCACTGTCCTTCAAGCCCTGGAAGGG 1989

Qy          24 GluLeuAlaLysGlyThrProValCysGlnLeuProValThr---------LeuGlnThr 40
               |||:::   :::   :::      |||::::::   :::            |||
Db        1988 GAAATGGTCAGGTCCTCGAGCCGGTGCAGAGTTGATCTGAACGGTTCCGGTCTCCATCGC 1929

Qy          41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
               |||||||||      |||||||||   :::            ||||||   :::
Db        1928 ATCGCTGATCATGATCGCTTTGTTGATATCTTTAGTGAATACACATCCCTGCAGCCCAAA 1869

Qy          61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp--- 79
                 |||   :::   |||   ::::::           |||:::   |||
Db        1868 ATTGCTGGCATTGCAATGGTGGATGCCTTCCTC-----------GACCGAGTTGATCCT 1821

Qy          80 ------GlyLysAspArgAlaValPheLeu 87
                    :::||||||||||   :::|||
Db        1820 AATCACAGGCAAGACAGGGCCAAATGGCTC 1791
```

RESULT 48
US-11-218-305-3302/c
; Sequence 3302, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305

```
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3302
;   LENGTH: 4382
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (655)..(655)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-3302

Alignment Scores:
Pred. No.:                39.2          Length:          4382
Score:                    71.50         Matches:         32
Percent Similarity:       40.4%         Conservative:    10
Best Local Similarity:    30.8%         Mismatches:      38
Query Match:              9.3%          Indels:          24
DB:                       9             Gaps:            4

US-10-758-902-9 (1-149) x US-11-218-305-3302 (1-4382)

Qy          69 ValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAsp 88
               |||           |||      |||  |||   |||   ||||||          |||
Db         746 GTACTGGCGACCGGCACGGACGATGCGTGGTTCGGGTCAGATCGGGGTTATTGATTGACT 687

Qy          89 LysValProThrVal-AlaThrSerLysLeuProGlyValThrAsnArg------Va 106
               |||   ||||||||| |||   |||   :::      |||:::   :::|||      ||
Db         686 AAGTAGCCCACGGTGGGCAGTGAGTGCAATGNGTAGTGGGATCTAGTCTAGAACGTATGT 627

Qy         106 lThrLeuThrPheAspGlySerTyr--------------------------------Gl 115
               |            |||||||||                                  ::
Db         626 GAAAAAAGAAGGAGATGGATCACAGAAATGCTCCAGCAGCAGGCATACCCTGAGGACGAA 567

Qy         115 nLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLe 135
               :      :::   |||   |||   ||||||||:::|||          :::||
Db         566 GTCCTGCTGCTCCCAGGCGGCGGTGCAGCGGAAGGACGTGGAGTCGAAGGGCACGAGGCT 507

Qy         135 u--------------------------GluPheSerIleGluAlaIleTrp---GlyLy 145
               |                          |||   :::   ::::::   |||
Db         506 GGCGACCGCGACCTTGGCCCTGGCGCACGAGTCCGCCGCCGACTCCTGGTGGCTCAGCGC 447

Qy         145 sThrGlnAsn 148
               |||||||||
Db         446 GACGCAGAAC 437

RESULT 49
US-11-218-305-24103/c
; Sequence 24103, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT:.MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24103
;   LENGTH: 1007
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-24103

Alignment Scores:
Pred. No.:                5.86          Length:          1007
Score:                    71.00         Matches:         35
Percent Similarity:       34.4%         Conservative:    10
Best Local Similarity:    26.7%         Mismatches:      28
Query Match:              9.2%          Indels:          58
DB:                       9             Gaps:            7

US-10-758-902-9 (1-149) x US-11-218-305-24103 (1-1007)

Qy          35 ProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr--- 53
               |||   ||||||                    ||||||||||||         :::|||
Db         453 CCGTTCACGCTGGACGTGTTCATC---TCCAAGCGCTTCGTCTCGGCGTCCCTCACGCAC 397

Qy          54 ------------------------------ThrThrSerLysLysThrValLysValAla 63
                                             |||:::   |||   :::|||   |||
Db         396 CGGTCGACCTGCAGGCAGGTCGCGGTCGCCGGGACCAACTCCAAGGACATCAAGGCGGCG 337

Qy          64 Ile------------AspVal---------------------------------------- 66
               :::            ||||||
Db         336 CTCAGGTCGAGGTCCGACGTGCCGGCCTGCCTGGCCGTCGGGCGGTTCCTGGCCGAGAGG 277

Qy          67 ---------ThrAspValTyrValValGlyTyr------------GlnAspLysTrpAsp 79
                        |||||||||         |||            :::||||||:::::
Db         276 GCGAAGGAGGCCGACGTGTACACCTGCACGTACACGCCGAGGGAACGGGACAAGTTCGAG 217

Qy          80 GlyLysAspArgAlaVal-----------------------------------------Phe 86
               ||||||   |||||||||                                         :::
Db         216 GGGAAGATCAGGGCGGTTGTTCAGTCGCTGATCGATAACGGGATCAATGTGAAACTTTAC 157

Qy          87 LeuAsp--------------------------LysValProThrValAlaThrSerLys 97
               ||||||                         |||   |||   |||
Db         156 CTTGACTGAGTTTGGTGCTGTATGAGTAGTAGTTCTGTTGGAACTTGCGCGTGGGTTTAT 97

Qy          98 LeuProGlyValThrAsnArgValThrLeu 108
               |||   ||||||:::      |||:::   |||
Db          96 CTGTTGCCAGGGTTGCAGGTTCGAATTATTTTG 64

RESULT 50
US-11-174-307B-3703
; Sequence 3703, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 3703
;   LENGTH: 1611
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1611)
;   OTHER INFORMATION: Ceres cDNA ID no. 21665863
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1611)
;   OTHER INFORMATION: Ceres CLONE  ID no. 779290
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1611)
;   OTHER INFORMATION: Also known as  Ceres CDNA ID no. 25088318
```

US-11-174-307B-3703

Alignment Scores:

Pred. No.:	11.3	Length:	1611
Score:	71.00	Matches:	27
Percent Similarity:	36.3%	Conservative:	14
Best Local Similarity:	23.9%	Mismatches:	36
Query Match:	9.2%	Indels:	36
DB:	9	Gaps:	2

US-10-758-902-9 (1-149) x US-11-174-307B-3703 (1-1611)

```
Qy         55 ThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyr 74
              |||:::   :::      |||   |||:::         ||||||      :::
Db        991 ACGGCGTGCGAGCAGGCCAAGAAGGCGTTGAGCAGCCAAGATGTTGCCGAACTGAGCATC 1050

Qy         75 GlnAspLysTrpAspGlyLysAsp-----------------ArgAlaValPhe------ 86
              :::        ||||||   |||                 ||||||   |||
Db       1051 AAGTCGCTGGTCGATGGTGTCGATTTCTCCGGCTCGCTGACCCGGGCAGAGTTTGAGGAG 1110

Qy         86 ------------------------------------------------------------ 86

Db       1111 CTGAACCATGACTTGTTCCTTAAAGCCATGGCGTTGGTGGAGAGTGCCATGAGACAGGCT 1170

Qy         87 ----------------------LeuAspLysValProThrValAlaThrSerLysLeu 98
                                   ||||||::::::    |||     |||   :::
Db       1171 GGGCTAGACAAGAACAAGGAGCTGCTTGATGAGATTGTGCTGGTTGGTGGAAGCACCATG 1230

Qy         99 PheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuVal 118
              ||||||:::         ||||||      |||||||||          |||   :::
Db       1231 ATCCCTGGGATTCGGAGACTCGTCACCGATTATTTTGATGGGAGGGAGCTGAAAAATATC 1290

Qy        119 AsnAlaAlaLysValAspArgLysAspLeuGluLeuGly 131
              ||||||:::   :::     :::   :::   ||||||
Db       1291 AATGCGTCGGTGATGCCAGATCAAACTGTCACTCTCGGA 1329
```

RESULT 51
US-11-218-305-12179
; Sequence 12179, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12179
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-12179

Alignment Scores:

Pred. No.:	15.9	Length:	2055
Score:	71.00	Matches:	28
Percent Similarity:	43.2%	Conservative:	20
Best Local Similarity:	25.2%	Mismatches:	53
Query Match:	9.2%	Indels:	10
DB:	9	Gaps:	3

US-10-758-902-9 (1-149) x US-11-218-305-12179 (1-2055)

```
Qy         25 LeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
              |||     ||||||||||||   :::|||   :::
Db       1461 CTGCGCGCCGGGACGCCCGTGCTCAGGCTCGGCCTG---------------------- 1496

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
                  ||||||   |||          |||   ::::::                 :::
Db       1497 CACGAGTTCGTGGAGGTGGTGTTCCAGAACACGGAGGAGGAGCTGCAGTCGTGGCACCTC 1556

Qy         65 AspValThrAspValTyrValValGlyTyrGlnAsp---LysTrpAspGlyLysAspArg 83
              |||       |||   :::||||||||||||   |||   :::|||:::          |||
Db       1557 GACGGATACGACTTCTGGGTTGTAGGGTACGGCGATGGCCAGTGGAATGAGACGCAGCGG 1616

Qy         84 AlaValPhe---LeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
                  :::   |||                        |||   :::::::::|||
Db       1617 CAGACGTACAATTTGGTGGACGCGCAGGCAAGACACACCGTTCAGGTGTACCCCAACGGG 1676

Qy        103 ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLys 122
                 :::   :::   ::::::   |||                  :::   :::|||
Db       1677 TGGTCGGCGATCCTGGTGTCGCTGGACAACCAGGGGATGTGGAACCTGCGGTCGGCGATG 1736

Qy        123 ValAspArgLysAspLeuGluLeuGlyValTyr 133
                 ||||||:::   |||          :::|||
Db       1737 TGGGACCGGCAGTACCTCGGGCAGCAGCTCTAC 1769
```

RESULT 52
US-11-218-305-24390/c
; Sequence 24390, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24390
; LENGTH: 2704
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-24390

Alignment Scores:

Pred. No.:	23.4	Length:	2704
Score:	71.00	Matches:	30
Percent Similarity:	41.6%	Conservative:	22
Best Local Similarity:	24.0%	Mismatches:	42
Query Match:	9.2%	Indels:	32
DB:	9	Gaps:	5

US-10-758-902-9 (1-149) x US-11-218-305-24390 (1-2704)

```
Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGly--- 28
              :::::::|||      |||      :::|||   |||      ::::::   ||||||
Db       1803 CAGAGTTATCCCGCTCCCCAATCGCTGCAGCATCTCTG-GGACAGGTTTATAAGGGCCGC 1745

Qy         29 -----------------------ThrProValCysGlnLeuProValThrLeuGlnThr 40
                                                 |||   |||      |||:::|||
Db       1744 TTGAAAGAAACGGGAGAACTAGTAGCTGTCAAAGTTCAGAGGCCATTTGTACTTGAGACT 1685

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
              :::      |||      |||::::::   ::::::          ::::::
Db       1684 GTTACCATCGAT---TTATTCATCATTAGAAACTTGGGTTTGGTACTCAGGAGATTTCCA 1628

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp------ 78
              :::|||:::||||||             |||||||||      |||:::|||
Db       1627 CAGGTGTCCATCGAT--------------GTTGTTGGCCTGGTAGATGAGTGGGCTGCT 1583

Qy         79 -----------------------------AspGlyLysAspArgAlaValPheLeuAsp 88
                                           :::|||::::::         |||   |||
```

```
Db       1582 CGATTTTTTGAAGAACTTGATTATGTAAATGAAGGGGAAAATGGCACTTACTTTGCTGAC 1523

Qy         89 ------------LysValProThrValAlaThrSerLysLeuPheProGlyValThrAsn 104
                          :::|||  |||       |||   :::       |||:::
Db       1522 GTGATGAAAGAAGATCTTCCACAGGTTGTTGTACCAAAGACTTACCATAAATACACGTCT 1463

Qy         105 ArgValThrLeuThr 109
               |||     ||||||
Db       1462 AGAAAAGTTCTTACC 1448

RESULT 53
US-10-449-902-19092/c
; Sequence 19092, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19092
;   LENGTH: 4066
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK069469
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-19092

Alignment Scores:
Pred. No.:              41.5          Length:        4066
Score:                  71.00         Matches:       34
Percent Similarity:     44.8%         Conservative:  18
Best Local Similarity:  29.3%         Mismatches:    42
Query Match:            9.2%          Indels:        22
DB:                     6             Gaps:          6

US-10-758-902-9 (1-149) x US-10-449-902-19092 (1-4066)

Qy          20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGln 39
               ||||||  :::   :::|||       |||     :::|||
Db        2242 GATTTGGCTTCAGCTATAGCATCCCCAGTACCGAACAATAAACTGCTAGCTGGCTTTGCC 2183

Qy          40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
               |||:::               |||||||||   |||:::                   |||
Db        2182 ACTGTA--------------TTTGTACTATCTGATTTAGTTGCTGCC---------ACC 2147

Qy          60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp 79
               ::::::|||               :::|||   :::   |||      |||:::
Db        2146 ATTGAAGTGCTTGAACCAAAATTGAATGTCGGAATTGCAGGGATTGGAGATGAAACAGGT 2087

Qy          80 GlyLysAspArgAlaValPheLeuAsp---------LysValProThrValAlaThrSer 96
               |||           :::   ||||||         |||  ||||||     :::
Db        2086 GGG-----------CTGGTACTGGATGGAGCAAATGTGGTCGATACAGTGGATGGAGCC 2039

Qy          97 LysLeuProGlyValThrAsnArgValThrLeuThrPhe--------------Asp 111
               ||||||      |||::::::      :::   :::||||||              |||
Db        2038 AAGCTAACTTCAGGCTTATCA------ATTGGTGTTACATTTGATAACTTTGATGATGAT 1985

Qy         112 GlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAsp 127
               ||||||  :::  |||:::      |||  ||||||     |||
Db        1984 GGCAGTGAGAAACCATTGCTCAGGCTTGCTGTAGTTGATGCAGCAGAT 1937

RESULT 54
US-11-333-747A-43
; Sequence 43, Application US/11333747A
; Publication No. US20060160159A1
; GENERAL INFORMATION:
;  APPLICANT: Handfield, Martin
;  APPLICANT:  Hillman, Jeffrey
;  APPLICANT:  Progulske-Fox, Ann
;  TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans
;  TITLE OF INVENTION:  Antigens for Use in the Diagnosis, Treatment, and Monitoring
;  TITLE OF INVENTION:  of Periodontal Diseases
;  FILE REFERENCE: MBHB01-662C
;  CURRENT APPLICATION NUMBER: US/11/333,747A
;  CURRENT FILING DATE:  2006-01-17
;  PRIOR APPLICATION NUMBER: US 09/995493
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: PCT/US02/37235
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
;   LENGTH: 4593
;   TYPE: DNA
;   ORGANISM: Actinobacillus actinomycetemcomitans
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(4593)
US-11-333-747A-43

Alignment Scores:
Pred. No.:              49.3          Length:        4593
Score:                  71.00         Matches:       39
Percent Similarity:     40.7%         Conservative:  18
Best Local Similarity:  27.9%         Mismatches:    57
Query Match:            9.2%          Indels:        26
DB:                     9             Gaps:          9

US-10-758-902-9 (1-149) x US-11-333-747A-43 (1-4593)

Qy           4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIle--------- 18
               :::   ||||||:::      |||::::::   :::|||   |||
Db        3436 ATCAAATTTAATATCAAAGGCGGAGACAGCCAAAAATATGTGACGACATCAGGATCCGGC 3495

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeu 38
               |||:::      :::||||||:::   |||                        :::
Db        3496 GATGATGTCACGGTGGATCTTGCCCAAACCACA--------------AAAAATAAGATC 3540

Qy          39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
                  ||||||                |||   :::||||||          ||||||
Db        3541 GACAATGCGGCAGATAAAGAT---------CTCGCCAACATTACCGATAATGGTAAAAAA 3591

Qy          59 ThrValLysVal-----------------AlaIleAspValThrAspValTyrValVal 72
                  :::                     |||  |||  |||   :::  |||
Db        3592 GTTATTACCGCTTTAGGCGCTGTAGTGAAAGCGGCTGATTCTACG---ATTACGGTAACT 3648

Qy          73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
                     |||      |||:::                          :::||||||
Db        3649 GACGAAACCGATAATACGACAGGACAAAAAACCTACAAAATCAAAGCCAATATTCCAACA 3708

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                     :::   :::   ||||||      |||      |||:::      ||||||
Db        3709 CCGGAAAAAAACAGCAATGGCTCCCGGC------AACAATACAACCATTGAAGGTGATGGC 3762

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLys---AspLeuGluLeuGly 131
               |||                |||      ||||||:::   |||   ||||||   ||||||
Db        3763 TCA---------GCCGCCAATCCGTTTAAAGTGAATCTGAAAGATGATTTAGCGCTAGGT 3813

RESULT 55
US-11-348-413-13061
; Sequence 13061, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
```

```
;  APPLICANT:  Murphy, Ellen
;  APPLICANT:  Olmsted, Stephen
;  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;  FILE REFERENCE: 031896-084100 (AM 101724)
;  CURRENT APPLICATION NUMBER: US/11/348,413
;  CURRENT FILING DATE:  2006-02-07
;  PRIOR APPLICATION NUMBER: PCT/US05/035471
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 11/243,445
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 60/615,573
;  PRIOR FILING DATE: 2004-10-05
;  NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 13061
;   LENGTH: 891
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(891)
;   OTHER INFORMATION: WAN01UP50; ORF; 00000000010100; Cluster contains WAN01OQHU
;   OTHER INFORMATION: :SE1502::hypothetical protein:ATCC12228:NC_004461.1
US-11-348-413-13061

Alignment Scores:
Pred. No.:              5.8          Length:          891
Score:                  70.50        Matches:         31
Percent Similarity:     39.5%        Conservative:    18
Best Local Similarity:  25.0%        Mismatches:      30
Query Match:            9.2%         Indels:          45
DB:                     9            Gaps:            6

US-10-758-902-9 (1-149) x US-11-348-413-13061 (1-891)

Qy         40 ThrIleAlaAspAspLysArgPheVal--------------------------LeuVal 50
              ||||||||||||          |||:::                        |||
Db        376 ACTATCGCGGAT---------TTCATAAATTCATTTATTCCATCATTTGAAAAACTTACG 426

Qy         51 AspIleThrThrThrSerLysLysThr--------------------------ValLys 61
              ||||||   |||   |||  |||:::                          :::
Db        427 GATATACTAACCATTTCCTATAAAAGCGCTATAATAGTATTATTAATAATAAATCTTATT 486

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              :::|||:::   |||      :::   ::::::      :::   ||||||
Db        487 ATAGCAGTGCTTGTYATTTTAATWTCAATGTTGAAGTTGAAATTAAAATGG--------- 537

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                                                 ||||||   |||  |||      |||
Db        538 ----------------------------AGAGTTGCAGTTTCAAGTTTATTATATGGA 567

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
              :::   |||                        |||      |||::::::|||:::
Db        568 ATTTTAAAT-------------------------TATTATGTCTTAATTAGTGCATCA 600

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyr------LysLeuGluPheSerIle 139
                 :::|||   ||||||:::         :::         ||||||   |||   |||
Db        601 AGTATAGATAGTAAAGATATTCATTATTCTATTCAAGAACCAAAATTGTCATTTATAATT 660

Qy        140 GluAlaIleTrp 143
                 ::::::
Db        661 TCGTTTTTATAT 672

RESULT 56
US-10-953-349-3284
; Sequence 3284, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3284
;   LENGTH: 1214
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3284

Alignment Scores:
Pred. No.:              8.96         Length:          1214
Score:                  70.50        Matches:         31
Percent Similarity:     37.5%        Conservative:    23
Best Local Similarity:  21.5%        Mismatches:      57
Query Match:            9.2%         Indels:          33
DB:                     6            Gaps:            4

US-10-758-902-9 (1-149) x US-10-953-349-3284 (1-1214)

Qy          5 SerPheAsnLeuGly-----------------------GluAlaTyrGluTyrProThr 16
              ||||||||||||                        |||          :::
Db        524 TCATTCAATTTGGATAATAGTCAGCAAGAGAAGTTGATAAATGCACGCAGCATTGCTTCT 583

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36
                 :::   ::::::      ::::::                          |||
Db        584 GTTTTATATGAAATTCTAAGGAAAATCGAATCAAGTATGGGCCGTGCCTCAACCCCAGAA 643

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56
              ::::::|||          |||::::::          |||:::|||:::   |||:::
Db        644 AGTATACAATTAAACCGGGATGAGGAGATTGGTGAGCTCCTTGATATGGACACCTCAATG 703

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
              ::::::|||   |||:::      |||   |||
Db        704 GAGGAGACCAACAAGATAAATTCGGACGAGACC-------------------------- 736

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96
                                        |||:::|||:::         :::
Db        737 -------------------------TTTGTCGACCAAAAAGCCGAGTTGGTAGTTGAG 769

Qy         97 LysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116
              |||                     |||:::|||      |||   |||   :::|||
Db        770 AAGAGCAAAGTCTTAGAGGACGAGAGACTAACTCAAATGTTTCAAGGAGACCACCAATAT 829

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136
              |||                 |||   ||||||          :::||||||   |||
Db        830 CTCACCCAA-----------GATGAAAAAGAT---------GACATATACAAAGAGGAG 868

Qy        137 PheSerIleGlu 140
                 |||:::
Db        869 GTTCAAATAAAG 880

RESULT 57
US-10-449-902-9921
; Sequence 9921, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9921
;   LENGTH: 1461
;   TYPE: DNA
;   ORGANISM: Oryza sativa
```

```
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK107269
;   DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-9921

Alignment Scores:
Pred. No.:              11.6          Length:         1461
Score:                  70.50         Matches:          31
Percent Similarity:     40.8%         Conservative:     20
Best Local Similarity:  24.8%         Mismatches:       39
Query Match:            9.2%          Indels:           35
DB:                     6             Gaps:              5

US-10-758-902-9 (1-149) x US-10-449-902-9921 (1-1461)

Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGly-----------ThrProValCys 32
              :::|||      |||   ::::::   |||:::|||                ||||||
Db        753 TACATCTACCAGCTCGAGAGCGACGGCGCGCGCGGGGAGCCGAAGCTGGTGCCCGTGGCG 812

Qy         33 GlnLeuProVal--------------ThrLeuGlnThrIleAlaAspAspLysArgPhe 47
                 :::||||||                  |||      :::||||||||||:::|||
Db        813 TACGTGCCCGTGGACGCCCCCTCGTTCCGCCTCACGCTGGTGGCGGACGACGAGAGGGAG 872

Qy         48 ValLeuVal---------------------------------------------------- 50
                 |||:::
Db        873 AGGCTGATGCTGATGAAGGAGGTGTTCTACGTGCACGCGGGCGAGGAGGTGCCACCGGAA 932

Qy         51 ------AspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAsp 68
                   |||:::   |||      :::      |||      |||:::|||:::
Db        933 GGGCCCGACATGCTGACGATGCCCAGGGTGTGCGTCGCGTACGCGGTGGACATGGCGGCG 992

Qy         69 ValTyrVal------------ValGlyTyrGlnAspLysTrpAspGlyLysAspArgAla 84
                 :::            :::|||  :::     ::   |||  |||||||||
Db        993 AGGACGATCGCGCTGTCGAGGCTGGGCGCGCGCGCGCTGTTCATGGGCGACGACCGCGCG 1052

Qy         85 ValPheLeuAspLys---------ValProThrValAlaThrSerLysLeuPheProGly 101
              |||:::                  |||   ||||||         ::::::   |||
Db       1053 GTCTGGGCGTCGCCGGGGGCGTTCTCCCCGGGCGTCGCGGCGGACACCGTCTACGCCGGC 1112

Qy        102 ValThrAsnArgVal 106
                 ||||||:::
Db       1113 CGCCCCAACAGGCTC 1127

RESULT 58
US-11-217-529-1712
; Sequence 1712, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1712
;   LENGTH: 1788
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1712

Alignment Scores:
Pred. No.:              15.4          Length:         1788
Score:                  70.50         Matches:          27
Percent Similarity:     43.1%         Conservative:     26
Best Local Similarity:  22.0%         Mismatches:       53
Query Match:            9.2%          Indels:           17
DB:                     8             Gaps:              4

US-10-758-902-9 (1-149) x US-11-217-529-1712 (1-1788)

Qy         31 ValCysGlnLeuProValThrLeuGlnThr-----------IleAlaAspAspLysArg 46
              :::|||   ||||||      :::   :::           |||:::   |||   |||
Db        655 ATTTGCTCTTTACCACCATTGATCAACAGTGACCACTCCAAGATCTCCGTGGATACACGC 714

Qy         47 PheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspVal 66
                 :::|||:::|||||||||   |||   |||          :::|||   ::::::::
Db        715 AATATCCTAATTGATATTACCGCCACCGATAAGACCAAAGCTGAAGTTGTTTTGAATATA 774

Qy         67 ThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPhe 86
                                     |||   |||:::
Db        775 TTAACCACAATGTTCTCACGTTACTGTGACGAG-----------------CCATTCTCA 816

Qy         87 LeuAspLysValProThrValAla-----------ThrSerLysLeuPheProGlyVal 102
              ::::::   |||      |||:::          |||:::|||   |||
Db        817 GTGGAACCTGTGGAAATTGTTTCTGAGCACAACGGCCAATCTCGTTTGGCACCAAACTTC 876

Qy        103 ThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLys 122
                |||:::          |||   |||   :::   :::   :::
Db        877 AACAAGAGGATC---------ATGGATGTCTCCATCAAATACATCAACTCCTGTCTAGAT 927

Qy        123 ValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              :::::::::        |||:::              :::   |||:::   |||:::
Db        928 CTAAATCAATCTGCCGAGGAAATCGCACACTGTTTGAAGAAAATGTCATTGCACGCCGTT 987

Qy        143 TrpGlyLys 145
                 |||
Db        988 CCATCCAAG 996

RESULT 59
US-11-217-529-79598/c
; Sequence 79598, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79598
;   LENGTH: 3960
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79598

Alignment Scores:
Pred. No.:              47.1          Length:         3960
Score:                  70.50         Matches:          35
Percent Similarity:     37.7%         Conservative:     23
Best Local Similarity:  22.7%         Mismatches:       47
Query Match:            9.2%          Indels:           49
DB:                     8             Gaps:              8

US-10-758-902-9 (1-149) x US-11-217-529-79598 (1-3960)

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeu 38
              |||:::|||         :::   |||         :::|||      |||   |||
Db       2702 CAGAACCTGGCAAAACCGGTGGATAAATATATCAGCCTTTGCAATTTTCCGTCAACT--- 2646

Qy         39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
```

```
                 |||:::|||             |||   |||
Db       2645 ---ACAATGGCAGCTTCCTCGTTATTTGCCTTA-------------------------- 2616

Qy         59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
                                          ::::::    |||         ||||||
Db       2615 --------------------------------TTTATATATGGATGT------AAATGG 2595

Qy         79 AspGlyLysAspArgAlaValPheLeuAspLysValProThr---------ValAlaThr 95
              :::   :::|||                          :::         |||||||||
Db       2594 GAAAGACAGGATGAACATGCTTTAGCTACTCTAGCAGTATCATGACGATGAGTGGCAACA 2535

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPhe-------------- 110
                 ::::::      |||:::   :::   ::::::|||||||||
Db       2534 GACCAGATA---AGAGGCATAGCTTCATCTATCTCTCTTACATTCATCTTTGGTAGCCTA 2478

Qy        111 ---------------AspGlySerTyrGln------------LysLeuValAsnAlaAla 121
                            ||||||:::          ||||||   |||   :::
Db       2477 CTCAAAAGGGTCGTCTCTAAGTCATACAAAAATTTCTGTTTAAAGTTGGCCAATTTTTCA 2418

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
              ||||||      |||      ::::::      :::|||   :::||||||   :::
Db       2417 AAAGTGCATCTAAAGACTTGCAAGATATAATAGTGGAAGTCAGATTTTTCGTCCGATACC 2358

Qy        142 Ile---------------------TrpGlyLysThrGlnAsn 148
              |||                     |||          :::|||
Db       2357 ATATAAGGATACAATGCTGTAATGTGGTCTTTAGTCAAAAAT 2316
```

RESULT 60
US-11-021-837-42/c
; Sequence 42, Application US/11021837
; Publication No. US20060140972A1
; GENERAL INFORMATION:
; APPLICANT: Alm, Richard
; APPLICANT: Manning, Paul
; APPLICANT: Mclaughlin, Robert
; APPLICANT: MacCormack, Kathleen
; TITLE OF INVENTION: Staphlococcus Saprophyticus Nucleic Acids and Polypeptides
; FILE REFERENCE: 101324-US
; CURRENT APPLICATION NUMBER: US/11/021,837
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/533534
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/600680
; PRIOR FILING DATE: 2003-08-31
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 107996
; TYPE: DNA
; ORGANISM: Staphylococcus saprophyticus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)..(65)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34495)..(34495)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (63745)..(63745)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (63826)..(63826)
; OTHER INFORMATION: n is a, c, g, or t
US-11-021-837-42

Alignment Scores:

Pred. No.:	4.88e+03	Length:	107996
Score:	70.50	Matches:	30
Percent Similarity:	38.1%	Conservative:	23
Best Local Similarity:	21.6%	Mismatches:	55
Query Match:	9.2%	Indels:	31
DB:	9	Gaps:	4

US-10-758-902-9 (1-149) x US-11-021-837-42 (1-107996)

```
Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
              :::|||::::::   ::::::      ||||||   |||       |||   |||  |||
Db      23512 TCTATTTCTGAAGGTGAAAAAATAGGACTTGTAGGTATAAACGGTACAGGAAAAAGTACA 23453

Qy         60 ValLysValAlaIleAspValThrAsp-------------------------------- 68
              :::         |||         |||
Db      23452 CTACTCAAAGTGATAGCTGGATTAGATGAAGACTTTAATGCTGAAGTCTCGCATCCTAAC 23393

Qy         69 ValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArg--------------- 83
                 |||   :::   |||       :::             ||||||
Db      23392 GCCTATCGCATTAGATATTCTTCGCAAAAGCAAGAATTTGATCGTAATATGACTGTATTT 23333

Qy         84 ---AlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
                 ||||||         :::      |||:::       :::   :::
Db      23332 GAAGCTGTATTAACTTCAGAAACGAAAACACTACAAGTGATTCGTGCATATGAATCAGCT 23273

Qy        103 ThrAsnArgValThrLeuThr---PheAspGlySerTyrGlnLysLeuValAsnAla--- 120
                 |||:::   |||   |||       |||       ::::::|||::::::||||||
Db      23272 TTAAATCAATATACTGCAACACAAAGCGATGATGATTTCAAAAAAATGATGAATGCACAA 23213

Qy        121 ----------------------------------AlaLysValAspArgLysAspLeu 128
                                                 |||::::::
Db      23212 GAAGAGATGGATAATTATCAGGCGTGGGATTATAGTGCAGAAATTAAAACGATTCTGTCA 23153

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrpGlyLysThrGln 147
              :::||||||:::|||                 :::   |||:::   |||      |||
Db      23152 AAATTAGGTATTTATGACACGACGAAAGAAGTGAGTGCACTTTCTGGTGGTCAACAA 23096
```

RESULT 61
US-11-021-837-47/c
; Sequence 47, Application US/11021837
; Publication No. US20060140972A1
; GENERAL INFORMATION:
; APPLICANT: Alm, Richard
; APPLICANT: Manning, Paul
; APPLICANT: Mclaughlin, Robert
; APPLICANT: MacCormack, Kathleen
; TITLE OF INVENTION: Staphlococcus Saprophyticus Nucleic Acids and Polypeptides
; FILE REFERENCE: 101324-US
; CURRENT APPLICATION NUMBER: US/11/021,837
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/533534
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/600680
; PRIOR FILING DATE: 2003-08-31
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 47
; LENGTH: 165280
; TYPE: DNA
; ORGANISM: Staphylococcus saprophyticus
US-11-021-837-47

Alignment Scores:

Pred. No.:	8.87e+03	Length:	165280
Score:	70.50	Matches:	25
Percent Similarity:	45.8%	Conservative:	24
Best Local Similarity:	23.4%	Mismatches:	37
Query Match:	9.2%	Indels:	21
DB:	9	Gaps:	6

US-10-758-902-9 (1-149) x US-11-021-837-47 (1-165280)

```
Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp------ValThr 67
                 |||   :::         ||||||      :::   |||       |||      :::
Db      25085 GTTTCAATGATTCCATTTTCAAAAGGTGAATTAGCAGTCATAAACGATGCTATAATTGAT 25026

Qy         68 AspValTyrValValGlyTyrGlnAsp-----------------LysTrpAspGlyLys 81
```

```
                ::::::|||          |||::::::                    ||||||:::|||
Db       25025 GAAATTTATTATTGGAAGTATGAAGAAAAGCTACAAGCAGCTAAAAAATGGAATGGACCG 24966

Qy          82 --------------------AspArgAlaValPheLeuAspLysValProThrValAla 94
                                   |||::::::   |||   ::::::      |||
Db       24965 TATATTAATGAACCCAAAATAGATAAATCTACATTTTTTGAGCGA------ACGAAACAA 24912

Qy          95 ThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyr 114
                     ::::::|||   |||   :::   :::   :::      ||||||   :::
Db       24911 GGGCGTTACATTTATCCAAGTGTAGAAAGTACGTTAGCTATTATGGCTGATGGTCAATTT 24852

Qy         115 GlnLysLeuValAsnAlaAlaLysValAspArgLysAsp------LeuGluLeuGly--- 131
               :::      |||   :::      ||||||:::          ||||||:::|||
Db       24851 AAAGGTACAGTTGGATCGTACTGGGTGGATAAAAATACAAATTGGTTAGAAATAGGTATT 24792

Qy         132 ---ValTyrLysLeuGluPhe 137
                  :::|||      :::|||
Db       24791 GTCATCTATGATACAAAGTTT 24771

RESULT 62
US-10-953-349-26017
; Sequence 26017, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26017
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-26017

Alignment Scores:
Pred. No.:              8.33          Length:         1027
Score:                  70.00         Matches:        24
Percent Similarity:     41.1%         Conservative:   15
Best Local Similarity:  25.3%         Mismatches:     40
Query Match:            9.1%          Indels:         16
DB:                     6             Gaps:           2

US-10-758-902-9 (1-149) x US-10-953-349-26017 (1-1027)

Qy          50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
               |||   :::          |||   |||:::|||   :::   |||         ::::::
Db         188 GTCACGCTCAGATGCGGCTCCGGGAAGTCAGTGCTGCTCCGGATACGCGCAGACAACCTC 247

Qy          70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
               |||:::   ||||||:::
Db         248 TACATCTCCGGTTACCGGAGC------------------------------------ 268

Qy          90 ValProThrValAlaThrSerLysLeuProGly------ValThrAsnArgValThr 107
                  |||            |||:::         |||      :::
Db         269 ---CCGGAAGGTCTATGGTCCGAGTTCCTCGGTGGCTCCCTAATCGACGGCGCGGCGCCA 325

Qy         108 LeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAsp 127
               |||:::|||   |||||||||      :::         |||||      :::
Db         326 CTCTCGTTCGCCGGTAGCTACGGCGATATGGCGAGAGTGGCCAAGACGGCACTTGAGGCA 385

Qy         128 LeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
               |||   ||||||      :::||||||   :::   |||   :::
Db         386 CTCACCCTCGGCAAGGAGGAGCTCGAAGCCGCGGCGGAGCGCGTC 430

RESULT 63
US-11-348-413-332
; Sequence 332, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  APPLICANT:  Murphy, Ellen
;  APPLICANT:  Olmsted, Stephen
;  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;  FILE REFERENCE: 031896-084100 (AM 101724)
;  CURRENT APPLICATION NUMBER: US/11/348,413
;  CURRENT FILING DATE:  2006-02-07
;  PRIOR APPLICATION NUMBER: PCT/US05/035471
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 11/243,445
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 60/615,573
;  PRIOR FILING DATE: 2004-10-05
;  NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 332
;   LENGTH: 1347
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1347)
;   OTHER INFORMATION: "WAN01UJ8V; ORF; 11111100000000; Cluster contains WAN01P6S
;   OTHER INFORMATION: R:SPy0242::putative histidine kinase, possibly involved in
;   OTHER INFORMATION: competence:SF370:NC_002737.1"
US-11-348-413-332

Alignment Scores:
Pred. No.:              12.2          Length:         1347
Score:                  70.00         Matches:        33
Percent Similarity:     46.4%         Conservative:   18
Best Local Similarity:  30.0%         Mismatches:     43
Query Match:            9.1%          Indels:         17
DB:                     9             Gaps:           7

US-10-758-902-9 (1-149) x US-11-348-413-332 (1-1347)

Qy          18 IleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr 37
               |||      ||||||      |||               :::|||||||||
Db        1058 ATAACGCCATTGAGGCAGCTCTTGAAGCACARCAACCTCATATGTCAATTGCT-TACTTT 1116

Qy          38 LeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLys 57
               |||      :::   |||   :::   ||||||        :::|||   |||:::|||
Db        1117 TTG------TTAGRTGACTATCAGATGTTTGTT---------GTGACAAATACGACTAAA 1161

Qy          58 LysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLys 77
               |||   |||              |||:::      ::::::      ||||||      |||
Db        1162 AAAAAGGTA------------GACATTAACAAGATCTTTGAAGAAGGCTATTCTTCAAAA 1209

Qy          78 TrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys 97
                  |||   :::|||   :::   |||                 :::         |||
Db        1210 ------GGTTCAGAACGTGGTATCGGCCTTTCTAATGCGCAGCGTATTCTC------AAA 1257

Qy          98 LeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
                  :::|||   ::::::   |||   |||   :::||||||      :::   :::
Db        1258 AAGTATCCTTATTTATCCTTGCGG---ACTAAAAGTTTTGATAAGGAATTTAGCCAAACC 1314

Qy         118 ValAsnAlaAlaLys------ValAspArg 125
               :::          |||      |||||||||
Db        1315 TTGACCATGCCAAAGGAGGAGGTGGATAGA 1344

RESULT 64
US-11-217-529-1986
; Sequence 1986, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
```

```
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1986
;   LENGTH: 1710
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1986

Alignment Scores:
Pred. No.:              17          Length:         1710
Score:                  70.00       Matches:        41
Percent Similarity:     36.8%       Conservative:   23
Best Local Similarity:  23.6%       Mismatches:     46
Query Match:            9.1%        Indels:         64
DB:                     8           Gaps:           9

US-10-758-902-9 (1-149) x US-11-217-529-1986 (1-1710)

Qy          4 ValSerPheAsnLeu---------GlyGluAlaTyrGluTyrProThr---PheIleGln 19
              :::   :::||||||         |||   |||   |||       |||     |||
Db        391 ATCAAGTACAATTTATCCAACGGGGGCCCAGCTCCTGAGTCTGTCACAAATGCTATTTGG 450

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuPro---ValThrLeu 38
              ::::::     :::|||                :::           |||   :::   |||
Db        451 GAAATATCCAAAAAGTTAACTAGCTATAAAACTATCAAAGATTTCCCAGAACTAGACTTG 510

Qy         39 GlnThrIleAlaAspAspLysArgPhe------ValLeuValAspIleThrThrThrSer 56
              |||||||||       |||   ::::::      :::|||:::||||||
Db        511 CAGACGATAGGCAAGGATACGAAATACGGTCCATTATTAATCGATATT------------ 558

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76
                                    ||||||:::|||      ||||||        ::::::
Db        559 --------------------ATCGACATTACAAAAGCCTATGTTGAGTTCTTGAAGGAA 597

Qy         77 LysTrpAsp---------------------------------------------------- 79
              :::|||
Db        598 ATCTTTGACTTCGACCTAATCAAGAAGTTTATCGATAACCAGCGCTCTACTAAGAACTGG 657

Qy         80 ----------------------------------------GlyLysAspArgAlaVal 85
                                                      ||||||     |||:::
Db        658 AAGCTACTGTTCGATAGCATGAATGGTGTCACTGGCCCATACGGAAAG------GCTATT 711

Qy         86 PheLeuAspLysValProThrValAlaThrSerLysLeu--------------------- 98
              |||:::|||:::           |||       |||
Db        712 TTCGTTGACGAATTCGGCTTACCAGCCGATGAAGTCCTACAAAACTGGCATCCTTCTCCG 771

Qy         99 ---PheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
                 |||   |||:::                |||||:::      |||       |||
Db        772 GACTTTGGTGGTATGCATCCAGATCCAAACTTGACTTATGCTAGTTCATTAGTGAAA--- 828

Qy        118 ValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGly 131
                       :::|||||||||:::   :::|||   |||
Db        829 -----------AGGGTTGATCGTGAAAAGATTGAATTTGGT 858

RESULT 65
US-10-449-902-2365
; Sequence 2365, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2365
;   LENGTH: 1872
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK060204
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-2365

Alignment Scores:
Pred. No.:              19.4        Length:         1872
Score:                  70.00       Matches:        28
Percent Similarity:     43.6%       Conservative:   23
Best Local Similarity:  23.9%       Mismatches:     44
Query Match:            9.1%        Indels:         22
DB:                     6           Gaps:           4

US-10-758-902-9 (1-149) x US-10-449-902-2365 (1-1872)

Qy         16 ThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuPro 35
              |||:::|||   |||:::                :::          :::   |||:::
Db        990 ACATATATTTCAGATGTTTCAACAGTTGGTACCCAGGACGCCTGCATTTCACAAGTATCT 1049

Qy         36 ValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThr 55
              |||       |||       |||   :::|||   :::      :::|||       |||
Db       1050 GTGGATCCTCAA------GCTAGAAACAAAGCATATCAAGACATCGATGATTTGACGCTT 1103

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
                 ::::::      :::      :::    :::||||||      :::
Db       1104 TTTCAACAGATAGAGGAAAATTTGATGTCAATAACCGATCGACAGATT------------ 1151

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
                                    |||  |||:::||||||      |||   |||   :::|||
Db       1152 ------------------GATGAGGCCATCTTTCTTAAAGCTGTAAGAACCAGCAGCACA 1193

Qy         96 SerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
                    :::   |||                                  |||:::   |||
Db       1194 GTAGATGTCGTGCCA-------------------------GTCTCTGGTGCAATTCAG 1226

Qy        116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
                  |||       |||   |||   :::   :::::::::|||   :::||||||
Db       1227 AAG---CCTAATGAGGCACCAATACCAAAGGAGGAACTGACCATTGGAGTA 1274

RESULT 66
US-11-056-355B-86210
; Sequence 86210, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86210
;   LENGTH: 2343
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2343)
;   OTHER INFORMATION: Ceres Seq. ID no. 12687655
;   FEATURE:
;   NAME/KEY: misc_feature
```

```
;   LOCATION: (1)..(2343)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12586556
;   OTHER INFORMATION: as cited in SEQ ID NO 64667
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2343)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13656797
;   OTHER INFORMATION: as cited in SEQ ID NO 65756
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2343)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13658498
;   OTHER INFORMATION: as cited in SEQ ID NO 66557
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2343)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 15227053
;   OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-86210

Alignment Scores:
Pred. No.:              26.5          Length:         2343
Score:                  70.00         Matches:        30
Percent Similarity:     42.3%         Conservative:   30
Best Local Similarity:  21.1%         Mismatches:     60
Query Match:            9.1%          Indels:         22
DB:                     9             Gaps:           6

US-10-758-902-9 (1-149) x US-11-056-355B-86210 (1-2343)

Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal 31
              :::   |||      ::::::      ||||||                        ||||||
Db         76 TTCAACTACCAAAACTATGTCAACACTCTGAGA---------ACAACACAGTATCCGGTA 126

Qy         32 CysGlnLeuProValThrLeuGlnThrIleAla------AspAspLysArgPheValLeu 49
                 :::|||          |||   |||   |||      :::::::|||     ::::::
Db        127 GATGAGCTAGAGGCGGCCTTGTATACGGCAGCCGCCGGAAACAACAAGACGGTGATAATA 186

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
                    :::              |||   |||              :::   |||:::
Db        187 ACGATGGTGAACAAAGCGTACGTGAAGGAGGTTGGAAGAGGGAGTACGATGCTTGATCTG 246

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              ::::::      :::         |||:::|||:::                |||||
Db        247 TTTTTGGAGAGTTTT---------TGGGAAGGAGAAGGGACTCTACCACTTTTGGACCAT 297

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              :::      ||||||      :::
Db        298 CTAATGGTGGTGGCAGTGGATCAA----------------------------ACGGCC 327

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAsp---Leu 128
              :::|||           |||   ::::::      |||::::::   :::|||   :::
Db        328 TATGATCGCTGCCGTTTCAAGAGGCTTCACTGCTACAAGATGGAGACTGAAGATGGGGTT 387

Qy        129 GluLeuGlyValTyrLysLeuGluPheSer---------IleGluAlaIleTrpGlyLys 145
              :::|||         |||:::      |||         ||||||   :::|||   :::
Db        388 GACTTAGAGGGAGAGAAAGTATTCATGTCAAAAGATTTCATTGAGATGATGTGGAGAAGG 447

Qy        146 ThrGln 147
              |||:::
Db        448 ACTCGC 453

RESULT 67
US-11-056-355B-46134
; Sequence 46134, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 46134
;   LENGTH: 2376
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2376)
;   OTHER INFORMATION: Ceres Seq. ID no. 12574662
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2376)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12586556
;   OTHER INFORMATION: as cited in SEQ ID NO 64667
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2376)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13656797
;   OTHER INFORMATION: as cited in SEQ ID NO 65756
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2376)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13658498
;   OTHER INFORMATION: as cited in SEQ ID NO 66557
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2376)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13660894
;   OTHER INFORMATION: as cited in SEQ ID NO 67475
US-11-056-355B-46134

Alignment Scores:
Pred. No.:              27.1          Length:         2376
Score:                  70.00         Matches:        30
Percent Similarity:     42.3%         Conservative:   30
Best Local Similarity:  21.1%         Mismatches:     60
Query Match:            9.1%          Indels:         22
DB:                     9             Gaps:           6

US-10-758-902-9 (1-149) x US-11-056-355B-46134 (1-2376)

Qy         12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal 31
              :::   |||      ::::::      ||||||                        ||||||
Db        145 TTCAACTACCAAAACTATGTCAACACTCTGAGA---------ACAACACAGTATCCGGTA 195

Qy         32 CysGlnLeuProValThrLeuGlnThrIleAla------AspAspLysArgPheValLeu 49
                 :::|||          |||   |||   |||      ::::::|||     ::::::
Db        196 GATGAGCTAGAGGCGGCCTTGTATACGGCAGCCGCCGGAAACAACAAGACGGTGATAATA 255

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
                    :::              |||   |||              :::   |||:::
Db        256 ACGATGGTGAACAAAGCGTACGTGAAGGAGGTTGGAAGAGGGAGTACGATGCTTGATCTG 315

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              ::::::      :::         |||:::|||:::                |||||
Db        316 TTTTTGGAGAGTTTT---------TGGGAAGGAGAAGGGACTCTACCACTTTTGGACCAT 366

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              :::      ||||||      :::
Db        367 CTAATGGTGGTGGCAGTGGATCAA----------------------------ACGGCC 396

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAsp---Leu 128
              :::|||           |||   ::::::      |||::::::   :::|||   :::
Db        397 TATGATCGCTGCCGTTTCAAGAGGCTTCACTGCTACAAGATGGAGACTGAAGATGGGGTT 456

Qy        129 GluLeuGlyValTyrLysLeuGluPheSer---------IleGluAlaIleTrpGlyLys 145
              :::|||         |||:::      |||         ||||||   :::|||   :::
Db        457 GACTTAGAGGGAGAGAAAGTATTCATGTCAAAAGATTTCATTGAGATGATGTGGAGAAGG 516

Qy        146 ThrGln 147
```

```
                ||||:::
Db        517 ACTCGC 522

RESULT 68
US-11-056-355B-69909
; Sequence 69909, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 69909
;   LENGTH: 2520
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2520)
;   OTHER INFORMATION: Ceres Seq. ID no. 2041497
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2520)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 12586556
;   OTHER INFORMATION: as cited in SEQ ID NO 64667
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2520)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13656797
;   OTHER INFORMATION: as cited in SEQ ID NO 65756
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2520)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13658498
;   OTHER INFORMATION: as cited in SEQ ID NO 66557
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2520)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13660894
;   OTHER INFORMATION: as cited in SEQ ID NO 67475
US-11-056-355B-69909

Alignment Scores:
Pred. No.:              29.4          Length:         2520
Score:                  70.00         Matches:        30
Percent Similarity:     42.3%         Conservative:   30
Best Local Similarity:  21.1%         Mismatches:     60
Query Match:            9.1%          Indels:         22
DB:                     9             Gaps:           6

US-10-758-902-9 (1-149) x US-11-056-355B-69909 (1-2520)

Qy          12 TyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal 31
               :::   |||     ::::::    ||||||                        ||||||
Db          76 TTCAACTACCAAAACTATGTCAACACTCTGAGA---------ACAACACAGTATCCGGTA 126

Qy          32 CysGlnLeuProValThrLeuGlnThrIleAla------AspAspLysArgPheValLeu 49
                 :::|||         |||   |||   |||      ::::::|||      ::::::
Db         127 GATGAGCTAGAGGCGGCCTTGTATACGGCAGCCGCCGGAAACAACAAGACGGTGATAATA 186

Qy          50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
                  :::             |||   |||             :::   |||:::
Db         187 ACGATGGTGAACAAAGCGTACGTGAAGGAGGTTGGAAGAGGGAGTACGATGCTTGATCTG 246

Qy          70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
               ::::::      :::         |||:::|||:::              ||||||
Db         247 TTTTTGGAGAGTTTT---------TGGGAAGGAGAAGGGACTCTACCACTTTTGGACCAT 297

Qy          90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
               :::      ||||||      :::
Db         298 CTAATGGTGGTGGCAGTGGATCAA----------------------------ACGGCC 327

Qy         110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAsp---Leu 128
               :::|||            |||   ::::::      |||::::::   :::|||   :::
Db         328 TATGATCGCTGCCGTTTCAAGAGGCTTCACTGCTACAAGATGGAGACTGAAGATGGGGTT 387

Qy         129 GluLeuGlyValTyrLysLeuGluPheSer---------IleGluAlaIleTrpGlyLys 145
               :::|||          |||:::      |||         ||||||   :::|||   :::
Db         388 GACTTAGAGGGAGAGAAAGTATTCATGTCAAAAGATTTCATTGAGATGATGTGGAGAAGG 447

Qy         146 ThrGln 147
               |||:::
Db         448 ACTCGC 453

RESULT 69
US-10-449-902-22262
; Sequence 22262, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22262
;   LENGTH: 2870
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK072455
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-22262

Alignment Scores:
Pred. No.:              35.3          Length:         2870
Score:                  70.00         Matches:        25
Percent Similarity:     53.8%         Conservative:   10
Best Local Similarity:  38.5%         Mismatches:     16
Query Match:            9.1%          Indels:         14
DB:                     6             Gaps:           5

US-10-758-902-9 (1-149) x US-10-449-902-22262 (1-2870)

Qy          43 AspAspLysArgPheVal------LeuValAspIleThrThrThrSerLysLysThrVal 60
               |||||||||:::|||         :::||||||         |||:::   |||
Db        1779 GACGACAAGAAGTTTTACAAGGGCATTGTTGACTCATTTGATACAGCTTCAAAAAGGCAC 1838

Qy          61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp---LysTrpAsp 79
               |||:::|||   |||      ||||||   |||:::      :::|||   ||||||:::
Db        1839 AAGATTGCATATGATGATGGAGATGTAGAGGTGCTTCTCCTTAGGGATGAAAAGTGGGAA 1898

Qy          80 GlyLysAspArgAlaValPheLeu-----------AspLysValProThrValAlaThr 95
                                    |||:::            ||||||   |||   ||||||
Db        1899 -----------------TTCGTCAGTGAGGAACAAGACAAAACCCCTGATGTGGCT--- 1937

Qy          96 SerLysLeuPhePro 100
               |||::::::   |||
Db        1938 TCCGAGATTTCCCCG 1952

RESULT 70
US-10-548-463-73
```

```
; Sequence 73, Application US/10548463
; Publication No. US20060194751A1
; GENERAL INFORMATION:
;  APPLICANT: Intercell AG
;  TITLE OF INVENTION: S. pyogenes antigens
;  FILE REFERENCE: R 43092
;  CURRENT APPLICATION NUMBER: US/10/548,463
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: EP03450061.1
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 300
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
;   LENGTH: 3828
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
US-10-548-463-73

Alignment Scores:
Pred. No.:              52.8          Length:         3828
Score:                  70.00         Matches:        30
Percent Similarity:     42.0%         Conservative:   12
Best Local Similarity:  30.0%         Mismatches:     44
Query Match:            9.1%          Indels:         14
DB:                     6             Gaps:           4

US-10-758-902-9 (1-149) x US-10-548-463-73 (1-3828)

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              |||:::|||::::::         :::|||:::||||||      |||
Db        865 GCTGAAGACAGACAATCAACAAAGTTGGATGTCACCACTTTGGAAAAA---------- 912

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
                 ||||||         |||      :::          :::|||         |||
Db        913 ---GCTATCAAAGAAGCGGATGCGATTATTGCTAAAGAAAGCAACAAAGACGCGGTCAAA 969

Qy         82 AspArgAla------------ValPheLeuAspLysValProThrValAlaThrSerLys 97
              |||   |||             |||      |||            :::      ||||||
Db        970 GATCTGGCTGAGAAACTTCAAGTCATCAAGGATTCTTACAAAGAAATCAAAGATAGTAAG 1029

Qy         98 LeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
              |||              |||:::|||:::             |||||||||
Db       1030 CTACTCGCCGAT---ACTCATCGACTGTTAAAAGATACCATCGAGTCTTATCAA------ 1080

Qy        118 ValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPhe 137
                  |||   :::|||         :::|||      |||   |||   |||   |||
Db       1081 ------GCAGGTGAGGTTTCTATTAACAATCTCACAGAAGGAACCTATACGCTAAACTTT 1134

RESULT 71
US-11-348-413-262
; Sequence 262, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  APPLICANT:  Murphy, Ellen
;  APPLICANT:  Olmsted, Stephen
;  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
;  FILE REFERENCE: 031896-084100 (AM 101724)
;  CURRENT APPLICATION NUMBER: US/11/348,413
;  CURRENT FILING DATE:  2006-02-07
;  PRIOR APPLICATION NUMBER: PCT/US05/035471
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 11/243,445
;  PRIOR FILING DATE: 2005-10-05
;  PRIOR APPLICATION NUMBER: US 60/615,573
;  PRIOR FILING DATE: 2004-10-05
;  NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 262
;   LENGTH: 3834
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(3834)
;   OTHER INFORMATION: WAN01UJ6E; ORF; 11111100000000; Cluster contains WAN01P72I
;   OTHER INFORMATION: :SPy1798::hypothetical protein sharing similarity with sev
;   OTHER INFORMATION: eral eukaryotic proteins:SF370:NC_002737.1
US-11-348-413-262

Alignment Scores:
Pred. No.:              53            Length:         3834
Score:                  70.00         Matches:        30
Percent Similarity:     42.0%         Conservative:   12
Best Local Similarity:  30.0%         Mismatches:     44
Query Match:            9.1%          Indels:         14
DB:                     9             Gaps:           4

US-10-758-902-9 (1-149) x US-11-348-413-262 (1-3834)

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              |||:::|||::::::         :::|||:::||||||      |||
Db        871 GCTGAAGACAGACAATCAACAAAGTTGGATGTCACCACTTTGGAAAAA---------- 918

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
                 ||||||         |||      :::          :::|||         |||
Db        919 ---GCTATCAAAGAAGCGGATGCGATTATTGCTAAAGAAAGCAACAAAGACGCGGTCAAA 975

Qy         82 AspArgAla------------ValPheLeuAspLysValProThrValAlaThrSerLys 97
              |||   |||             |||      |||            :::      ||||||
Db        976 GATCTGGCTGAGAAACTTCAAGTCATCAAGGATTCTTAYAAAGAAATCAAAGATAGTAAG 1035

Qy         98 LeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeu 117
              |||              |||:::|||:::             |||||||||
Db       1036 CTACTCGCCGAT---ACTCATCGACTGTTAAAAGATACCATCGAGTCTTATCAA------ 1086

Qy        118 ValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPhe 137
                  |||   :::|||         :::|||      |||   |||   |||   |||
Db       1087 ------GCAGGTGAGGTTTCTATTAACAATCTYACAGAAGGAACCTATACGCTAAACTTT 1140

RESULT 72
US-10-449-902-25475/c
; Sequence 25475, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25475
;   LENGTH: 5035
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK100917
;   DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-25475

Alignment Scores:
Pred. No.:              77.6          Length:         5035
Score:                  70.00         Matches:        28
Percent Similarity:     43.6%         Conservative:   23
Best Local Similarity:  23.9%         Mismatches:     44
Query Match:            9.1%          Indels:         22
DB:                     6             Gaps:           4
```

```
US-10-758-902-9 (1-149) x US-10-449-902-25475 (1-5035)

Qy         16 ThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuPro 35
Db       2353 ACATATATTTCAGATGTTTCAACAGTTGGTACCCAGGACGCCTGCATTTCACAAGTATCT 2294

Qy         36 ValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThr 55
Db       2293 GTGGATCCTCAA------GCTAGAAACAAAGCATATCAAAACATCGATGATTTGACGCTT 2240

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db       2239 TTTCAACAGATAGAGGAAAATTTGATGACAATAACCGATCGACAGATT------------ 2192

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
Db       2191 ------------------GATGAGGCCATCTTTCTTAAAGCTGTAAGAACCAGCAGCACA 2150

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
Db       2149 GTAGATGTCGTGCCA-------------------------GTCTCTGGTGCAATTCAG 2117

Qy        116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db       2116 AAG---CCTAATGAGGCACCAATACCAAAGGAGGAACTGACCATTGGAGTA 2069

RESULT 73
US-11-136-524-92
; Sequence 92, Application US/11136524
; Publication No. US20060094034A1
; GENERAL INFORMATION:
;  APPLICANT: BROUSSEAU, Roland
;  APPLICANT:  HAREL, Josee
;  APPLICANT:  BEKAL, Sadjia
;  TITLE OF INVENTION: ARRAY AND USES THEREOF
;  FILE REFERENCE: 86369-3
;  CURRENT APPLICATION NUMBER: US/11/136,524
;  CURRENT FILING DATE:  2005-05-25
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
;   LENGTH: 1612
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-11-136-524-92

Alignment Scores:
Pred. No.:              18.5          Length:        1612
Score:                  69.50         Matches:       35
Percent Similarity:     41.4%         Conservative:  32
Best Local Similarity:  21.6%         Mismatches:    50
Query Match:            9.0%          Indels:        45
DB:                     8             Gaps:          9

US-10-758-902-9 (1-149) x US-11-136-524-92 (1-1612)

Qy          3 ThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArg 22
Db        275 ACGATAGACTTTTCGACCCAACAAAGT------TATGTCTCTTCGTTAAATAGTATACGG 328

Qy         23 AsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAla 42
Db        329 ACAGAGATATCG------ACCCCT--------------------CTTGAACATATATCT 361

Qy         43 AspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys--- 61
Db        362 CAGGGG-------------------------ACCACATCGGTGTCTGTTATTAACCAC 394

Qy         62 ------------------ValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        395 ACCCCACCGGGCAGTTATTTTGCTGTGGATATACGAGGGCTTGATGTC------TATCAG 448

Qy         76 AspLysTrpAspGly--------------LysAspArgAlaValPheLeuAspLysVal 90
Db        449 GCGCGTTTTGACCATCTTCGTCTGATTATTGAGCAAAATAATTTATATGTGGCCGGGTTC 508

Qy         91 ProThrValAlaThrSerLysLeuPhe----------------------------Pro 100
Db        509 GTTAATACGGCAACAAATACTTTCTACCGTTTTTCAGATTTTACACATATATCAGTGCCC 568

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
Db        569 GGTGTGACAACG---GTTTCCATGACAACGGACAGCAGTTATACCACTCTGCAACGTGTC 625

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
Db        626 GCAGCGCTGGAACGTTCCGGAATGCAAATCAGTCGTCACTCACTGGTTTCATCATATCTG 685

Qy        141 AlaIle 142
Db        686 GCGTTA 691

RESULT 74
US-11-266-748A-24600/c
; Sequence 24600, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24600
;   LENGTH: 4431
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-24600

Alignment Scores:
Pred. No.:              76.4          Length:        4431
Score:                  69.50         Matches:       23
Percent Similarity:     51.5%         Conservative:  11
Best Local Similarity:  34.8%         Mismatches:    11
Query Match:            9.0%          Indels:        21
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-266-748A-24600 (1-4431)

Qy         84 AlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThr 103
Db        714 GCCGTATTTCTAGACAAC------------CCAACTTCAAAGCAATTTCCTGGTCCACTT 667

Qy        104 AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysVal 123
Db        666 GATCAGCTATCTCTAACATATAATCGCTCT--------------------TCACCTGTT 628
```

```
Qy        124 AspArgLysAsp----------------------------LeuGluLeuGlyValTyr 133
              ||||||::::::                            ||||||:::   :::
Db        627 GATAGAAGAAATTCAAAGTTGGCTTATCTTCAGTAAACTGGTTTAGAAATCCTTTTGGCA 568

Qy        134 LysLeuGluPheSerIle 139
                  ||||||||||||
Db        567 AATAACGAATTCTCAATT 550
```

RESULT 75
US-11-266-748A-29633/c
; Sequence 29633, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29633
; LENGTH: 4442
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-29633

Alignment Scores:

Pred. No.:	76.6	Length:	4442
Score:	69.50	Matches:	23
Percent Similarity:	51.5%	Conservative:	11
Best Local Similarity:	34.8%	Mismatches:	11
Query Match:	9.0%	Indels:	21
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-266-748A-29633 (1-4442)

```
Qy         84 AlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThr 103
              ||||||||||||||||                    |||||||||   |||||||||
Db        751 GCCGTATTTCTAGACAAC------------CCAACTTCAAAGCAATTTCCTGGTCCACTT 704

Qy        104 AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysVal 123
              ::::::::::::||||||::::::   |||                      :::   |||
Db        703 GATCAGCTATCTCTAACATATAATCGCTCT--------------------TCACCTGTT 665

Qy        124 AspArgLysAsp----------------------------LeuGluLeuGlyValTyr 133
              ||||||::::::                            ||||||:::   :::
Db        664 GATAGAAGAAATTCAAAGTTGGCTTATCTTCAGTAAACTGGTTTAGAAATCCTTTTGGCA 605

Qy        134 LysLeuGluPheSerIle 139
                  ||||||||||||
Db        604 AATAACGAATTCTCAATT 587
```

RESULT 76

US-11-266-748A-31417/c
; Sequence 31417, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31417
; LENGTH: 4453
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-31417

Alignment Scores:

Pred. No.:	76.9	Length:	4453
Score:	69.50	Matches:	23
Percent Similarity:	51.5%	Conservative:	11
Best Local Similarity:	34.8%	Mismatches:	11
Query Match:	9.0%	Indels:	21
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-266-748A-31417 (1-4453)

```
Qy         84 AlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyValThr 103
              ||||||||||||||||                    |||||||||   |||||||||
Db        762 GCCGTATTTCTAGACAAC------------CCAACTTCAAAGCAATTTCCTGGTCCACTT 715

Qy        104 AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysVal 123
              ::::::::::::||||||::::::   |||                      :::   |||
Db        714 GATCAGCTATCTCTAACATATAATCGCTCT--------------------TCACCTGTT 676

Qy        124 AspArgLysAsp----------------------------LeuGluLeuGlyValTyr 133
              ||||||::::::                            ||||||:::   :::
Db        675 GATAGAAGAAATTCAAAGTTGGCTTATCTTCAGTAAACTGGTTTAGAAATCCTTTTGGCA 616

Qy        134 LysLeuGluPheSerIle 139
                  ||||||||||||
Db        615 AATAACGAATTCTCAATT 598
```

RESULT 77
US-10-833-833-168
; Sequence 168, Application US/10833833
; Publication No. US20060194210A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; APPLICANT: Lai, Albert
; APPLICANT: Tse, Christin
; APPLICANT: Fattaey, Ali
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER

```
;  FILE REFERENCE: 20366-038001
;  CURRENT APPLICATION NUMBER: US/10/833,833
;  CURRENT FILING DATE:  2004-04-27
;  NUMBER OF SEQ ID NOS: 175
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 168
;   LENGTH: 5145
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-833-833-168

Alignment Scores:
Pred. No.:                94.2          Length:        5145
Score:                    69.50         Matches:       28
Percent Similarity:       43.4%         Conservative:  31
Best Local Similarity:    20.6%         Mismatches:    59
Query Match:              9.0%          Indels:        18
DB:                       6             Gaps:          4

US-10-758-902-9 (1-149) x US-10-833-833-168 (1-5145)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::      |||   :::   :::   ::::::||||||                ||||||
Db       1371 TTCAAGCCAGTGGATTATGAAATCACCAAGTCCTATGAGATAGACGTTCAAGCCCAAGAT 1430

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThrLeuGln 39
              |||                          |||       |||::::::   :::   :::
Db       1431 TTGGGT---------CCCAATTCCATTCCTGCTCATTGCAAAATTATAATTAAGGTTGTG 1481

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
                :::   |||:::|||      :::   :::::::::   :::      |||:::
Db       1482 GATGTCAATGACAATAAACCTGAAATTAGCATAAATCTCATGTCCCCTGGAAAAGAAGAA 1541

Qy         60 ValLysValAlaIleAsp-----------ValThrAspValTyrValValGlyTyrGln 75
              |||          :::                |||   |||   :::|||      |||
Db       1542 GTATCTTATGTCTTTGAAGGGGATCCCATTGATACATTCGTTGCTATCGTCAGGGTTCAA 1601

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
              ||||||      |||   :::      :::
Db       1602 GACAAGGATTCTGGGCTGAATGGGGAAATAATC------------------------- 1634

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
                ||||||                 ::::::      |||::::::   :::|||
Db       1635 TGTAAGCTTCATGGGCATGGACATTTTAAACTTCAGAAGACATATGAAAATAACTACTTG 1694

Qy        116 LysLeuValAsnAlaAlaLys-ValAspArgLysAspLeuGluLeu 130
                |||   ||||||       ::::::::::::||||||   :::
Db       1695 ATCTTGACCAATGCCACTCTGGATAGAGAAAAGAGATCTGAGTATA 1740

RESULT 78
US-10-833-833-167
; Sequence 167, Application US/10833833
; Publication No. US20060194210A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  APPLICANT:  Lai, Albert
;  APPLICANT:  Tse, Christin
;  APPLICANT:  Fattaey, Ali
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-038001
;  CURRENT APPLICATION NUMBER: US/10/833,833
;  CURRENT FILING DATE:  2004-04-27
;  NUMBER OF SEQ ID NOS: 175
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167
;   LENGTH: 13938
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-833-833-167

Alignment Scores:
Pred. No.:                382           Length:        13938
Score:                    69.50         Matches:       28
Percent Similarity:       43.4%         Conservative:  31
Best Local Similarity:    20.6%         Mismatches:    59
Query Match:              9.0%          Indels:        18
DB:                       6             Gaps:          4

US-10-758-902-9 (1-149) x US-10-833-833-167 (1-13938)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              :::      |||   :::   :::   ::::::||||||                ||||||
Db       1371 TTCAAGCCAGTGGATTATGAAATCACCAAGTCCTATGAGATAGACGTTCAAGCCCAAGAT 1430

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThrLeuGln 39
              |||                          |||       |||::::::   :::   :::
Db       1431 TTGGGT---------CCCAATTCCATTCCTGCTCATTGCAAAATTATAATTAAGGTTGTG 1481

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
                :::   |||:::|||      :::   :::::::::   :::      |||:::
Db       1482 GATGTCAATGACAATAAACCTGAAATTAGCATAAATCTCATGTCCCCTGGAAAAGAAGAA 1541

Qy         60 ValLysValAlaIleAsp-----------ValThrAspValTyrValValGlyTyrGln 75
              |||          :::                |||   |||   :::|||      |||
Db       1542 GTATCTTATGTCTTTGAAGGGGATCCCATTGATACATTCGTTGCTATCGTCAGGGTTCAA 1601

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThr 95
              ||||||      |||   :::      :::
Db       1602 GACAAGGATTCTGGGCTGAATGGGGAAATAATC------------------------- 1634

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
                ||||||                 ::::::      |||::::::   :::|||
Db       1635 TGTAAGCTTCATGGGCATGGACATTTTAAACTTCAGAAGACATATGAAAATAACTACTTG 1694

Qy        116 LysLeuValAsnAlaAlaLys-ValAspArgLysAspLeuGluLeu 130
                |||   ||||||       ::::::::::::||||||   :::
Db       1695 ATCTTGACCAATGCCACTCTGGATAGAGAAAAGAGATCTGAGTATA 1740

RESULT 79
US-11-217-529-78554
; Sequence 78554, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78554
;   LENGTH: 414
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78554

Alignment Scores:
Pred. No.:                3.22          Length:        414
Score:                    69.00         Matches:       20
Percent Similarity:       42.3%         Conservative:  10
Best Local Similarity:    28.2%         Mismatches:    30
Query Match:              9.0%          Indels:        11
DB:                       8             Gaps:          1

US-10-758-902-9 (1-149) x US-11-217-529-78554 (1-414)

Qy         14 TyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr----------- 29
              |||   |||         ||||||      |||:::|||:::
```

```
Db        193 TACACGACGTGCTACCATGACTTGGATGGTGAAATTGCTGAGGCAAATGATTTCGATGCA 252

Qy         30 ------------------ProValCysGlnLeuProValThrLeuGln-ThrIleAlaAs 43
                                  |||   |||   ||||||   ||||||     |||   :::
Db        253 GTCGCAATATGGAGCCGCCCTGGGTGCCACTTGCCTGCTACACTATCTGACGACGAGTCT 312

Qy         43 pAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAl 63
                  ||||||         |||:::|||             :::   :::   :::
Db        313 TTCAATAAGATTTTTTTTTCACGACTTGACTGTGAGGAAGCACGAAGTCATGCCTCTGGG 372

Qy         63 aIleAspValThrAspValTyrValValGly 73
               :::|||         :::|||   :::|||
Db        373 AATGGACTATTACTACCTTTATGCCATCGGA 403

RESULT 80
US-10-526-741-19
; Sequence 19, Application US/10526741
; Publication No. US20060167232A1
; GENERAL INFORMATION:
;  APPLICANT: ABURATANI, Hiroyuki
;  APPLICANT:  MIDORIKAWA, Yutaka
;  APPLICANT:  NAKANO, Kiyotaka
;  APPLICANT:  OHIZUMI, Iwao
;  APPLICANT:  ITO, Yukio
;  APPLICANT:  TOKITA, Susumu
;  TITLE OF INVENTION: ANTIBODY AGAINST SOLUBLE N-TERMINAL PEPTIDE OR C-TERMINAL PEPTIDE
;  TITLE OF INVENTION:  PRESENT IN BLOOD
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/526,741
;  CURRENT FILING DATE:  2005-03-04
;  PRIOR APPLICATION NUMBER: PCT/JP02/08999
;  PRIOR FILING DATE: 2002-09-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(714)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Mouse-human
;   OTHER INFORMATION: chimeric antibody (M1E07 L chain)
US-10-526-741-19

Alignment Scores:
Pred. No.:              6.97          Length:         717
Score:                  69.00         Matches:        31
Percent Similarity:     39.8%         Conservative:   14
Best Local Similarity:  27.4%         Mismatches:     28
Query Match:            9.0%          Indels:         40
DB:                     6             Gaps:           5

US-10-758-902-9 (1-149) x US-10-526-741-19 (1-717)

Qy         31 ValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuVal 50
              :::|||:::||||||:::      |||   ::::::
Db         86 CTTTGTCGGTTACCATTGGACAACCAGCCTCTATCT----------------------- 121

Qy         51 AspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyr 70
                                          :::|||      |||         |||
Db        122 --------------------------------CTTGCAAGTCAAGTCAGAGCCTCTTAT 148

Qy         71 ValVal--------------------GlyTyrGln-AspLysTrpAspGlyLysAspAr 83
              :::|||                  ||||||    :::   |||   |||
Db        149 ATAGTAATGGAAAGACATATTTGAATTGGTTACAACAGAGGCCTGGCCAGGC-------- 200

Qy         83 gAlaValPheLeuAspLysValProThrValAla-ThrSerLysLeuPheProGlyValT 103
                        |||   |||   |||:::    |||||||||   ||||||:::
Db        201 ------------TCCAAAGCACCTAATGTATCAGGTGTCCAAACTGGACCCTGGCATCC 247

Qy        103 hrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysV 123
                :::|||         |||   ||||||      :::                 |||:
Db        248 CTGACAGG------------TTCAGTGGCAGTGGATCAGAAACAGATTTTACACTTAAAA 295

Qy        123 alAspArgLysAspLeuGlu---LeuGlyValTyr 133
              ::   |||   :::   |||   ||||||||||||
Db        296 TCAGCAGAGTGGAGGCTGAAGATTTGGGAGTTTAT 330

RESULT 81
US-11-414-676-19
; Sequence 19, Application US/11414676
; Publication No. US20060188510A1
; GENERAL INFORMATION:
;  APPLICANT: ABURATANI, Hiroyuki
;  APPLICANT:  MIDORIKAWA, Yutaka
;  APPLICANT:  NAKANO, Kiyotaka
;  APPLICANT:  OHIZUMI, Iwao
;  APPLICANT:  ITO, Yukio
;  APPLICANT:  TOKITA, Susumu
;  TITLE OF INVENTION: ANTIBODY AGAINST SOLUBLE N-TERMINAL PEPTIDE OR C-TERMINAL PEPTIDE
;  TITLE OF INVENTION:  PRESENT IN BLOOD
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/414,676
;  CURRENT FILING DATE:  2006-04-28
;  PRIOR APPLICATION NUMBER: US/10/526,741
;  PRIOR FILING DATE: 2005-11-14
;  PRIOR APPLICATION NUMBER: PCT/JP02/08999
;  PRIOR FILING DATE: 2002-09-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(714)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Mouse-human
;   OTHER INFORMATION: chimeric antibody (M1E07 L chain)
US-11-414-676-19

Alignment Scores:
Pred. No.:              6.97          Length:         717
Score:                  69.00         Matches:        31
Percent Similarity:     39.8%         Conservative:   14
Best Local Similarity:  27.4%         Mismatches:     28
Query Match:            9.0%          Indels:         40
DB:                     7             Gaps:           5

US-10-758-902-9 (1-149) x US-11-414-676-19 (1-717)

Qy         31 ValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuVal 50
              :::|||:::||||||:::      |||   ::::::
Db         86 CTTTGTCGGTTACCATTGGACAACCAGCCTCTATCT----------------------- 121

Qy         51 AspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyr 70
                                          :::|||      |||         |||
Db        122 --------------------------------CTTGCAAGTCAAGTCAGAGCCTCTTAT 148

Qy         71 ValVal--------------------GlyTyrGln-AspLysTrpAspGlyLysAspAr 83
              :::|||                  ||||||    :::   |||   |||
Db        149 ATAGTAATGGAAAGACATATTTGAATTGGTTACAACAGAGGCCTGGCCAGGC-------- 200

Qy         83 gAlaValPheLeuAspLysValProThrValAla-ThrSerLysLeuPheProGlyValT 103
                        |||   |||   |||:::    |||||||||   ||||||:::
Db        201 ------------TCCAAAGCACCTAATGTATCAGGTGTCCAAACTGGACCCTGGCATCC 247

Qy        103 hrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysV 123
                :::|||         |||   ||||||      :::                 |||:
Db        248 CTGACAGG------------TTCAGTGGCAGTGGATCAGAAACAGATTTTACACTTAAAA 295

Qy        123 alAspArgLysAspLeuGlu---LeuGlyValTyr 133
              ::   |||   :::   |||   ||||||||||||
```

```
Db        296 TCAGCAGAGTGGAGGCTGAAGATTTGGGAGTTTAT 330

RESULT 82
US-10-471-571A-2101
; Sequence 2101, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2101
;   LENGTH: 1179
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-2101

Alignment Scores:
Pred. No.:              14          Length:        1179
Score:                  69.00       Matches:       26
Percent Similarity:     37.6%       Conservative:  27
Best Local Similarity:  18.4%       Mismatches:    66
Query Match:            9.0%        Indels:        22
DB:                     6           Gaps:          3

US-10-758-902-9 (1-149) x US-10-471-571A-2101 (1-1179)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPhe----------------------------Ile 18
              ||||||     |||        |||:::
Db        787 TTAGGAAATGACTATCCTGAAGCGACATGGCCAGGTGAAGTCGTAAAAGATGTCGCGTTT 846

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeu 38
                |||   :::::::::        |||           |||:::|||      |||
Db        847 TACGATTACAAATCAAAATATAAAGATGGTAAGGTTCAATTACAAATTCCAGCTGACTTA 906

Qy         39 GlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLys 58
                                                  |||:::      |||   :::
Db        907 GACGAA----------------------------GATGTTCAATTAACGCTTAGAAAT 936

Qy         59 ThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrp 78
                    |||        |||||         :::          |||   :::
Db        937 ATGGCATTAGAGGCATTCAAAGCGACAGATTGTTCTGGTTTAGTCCGTGCTGATTTCTTT 996

Qy         79 AspGlyLysAspArgAlaValPheLeuAspLys---------ValProThrValAlaThr 95
                 :::|||      :::::::::::::::          :::|||
Db        997 GTAACAGAAGACAACCAAATATATATTAATGAAACAAATGCAATGCCTGGATTTACGGCT 1056

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGln 115
                   ::::::|||   :::         :::    |||::::::
Db       1057 TTCAGTATGTATCCAAAGTTATGGGAAAATATGGGCTTATCTTATCCAGAATTGATTACA 1116

Qy        116 LysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
               ||||||:::      ||||||         :::|||   :::         ||||||:::
Db       1117 AAACTTATCGAGCTTGCTAAAGAACGTCACCAGGATAAACAGAAAAATAAATACAAAATT 1176

Qy        136 Glu 136
               :::
Db       1177 GAC 1179

RESULT 83
US-10-449-902-28265
; Sequence 28265, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28265
;   LENGTH: 1217
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK103707
;   DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-28265

Alignment Scores:
Pred. No.:              14.6        Length:        1217
Score:                  69.00       Matches:       39
Percent Similarity:     43.6%       Conservative:  29
Best Local Similarity:  25.0%       Mismatches:    62
Query Match:            9.0%        Indels:        26
DB:                     6           Gaps:          8

US-10-758-902-9 (1-149) x US-10-449-902-28265 (1-1217)

Qy          3 ThrValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||:::||||||:::            :::      |||      ||||||
Db         99 ACCGTGACGTTCAACGTGAGCGGCAGCGGCAGCGACAACTACGGCGACTTCATCGCCGGC 158

Qy         21 LeuArgAsnGluLeuAlaLys-----------------GlyThrProValCysGlnLeu 34
                :::|||      :::|||                                |||||      |||
Db        159 ATCCGCAAGAGGGTGGCCAACCCGAGGCACTTCTCCCACAACCGCCCCGTC------CTC 212

Qy         35 ProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThr 54
              |||                 :::         :::   |||   :::|||      |||
Db        213 CCGCCGGTGGAGCCCGACGTCCCGCCGCGCCGCTGGTTCCACGTCGTGCTCCGGACGCAG 272

Qy         55 ThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyr 74
              ||||||:::   |||:::          |||       ::::::|||:::   |||:::
Db        273 ACCAGCGAGCTCACGCTCGCCACGCGCGCCGAC------AACCTCTACCTGGAGGGCTTC 326

Qy         75 GlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAla 94
              :::         ||||||                                  |||   |||
Db        327 CGCGGCAGC---GACGGC--------------------------------ACCAGCGCG 350

Qy         95 ThrSerLysLeuPheProGlyValThrAsnArgValThr---LeuThrPheAspGlySer 113
                    :::|||      |||:::            |||   |||   |||   ||||||
Db        351 TGGTGGGAGCTCACCCGCGGCCTCATCGCCGGCGCCACCTACCTCGGCTTCGGCGGCTCG 410

Qy        114 TyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyr 133
              |||::::::|||:::            :::       :::   ||||||
Db        411 TACCGCGAGCTCCTCGGGCACACGGAC---AACATGGTCGGTGTCACGCTCGGCCCGCAG 467

Qy        134 LysLeuGluPheSerIleGluAlaIleTrpGlyLysThrGlnAsnGly 149
              ::::::     :::::::::   :::   |||         :::|||
Db        468 CAGATGACGCAGGCCGTGGACACGCTCGCCGGTCTCGCCGCCAGCGGC 515

RESULT 84
US-11-218-305-12178
; Sequence 12178, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
```

```
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12178
;   LENGTH: 1232
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1206)..(1207)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1212)..(1213)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-12178

Alignment Scores:
Pred. No.:              14.9          Length:        1232
Score:                  69.00         Matches:       27
Percent Similarity:     43.5%         Conservative:  20
Best Local Similarity:  25.0%         Mismatches:    51
Query Match:            9.0%          Indels:        10
DB:                     9             Gaps:          3

US-10-758-902-9 (1-149) x US-11-218-305-12178 (1-1232)

Qy         28 GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPhe 47
              ||||||||||||   :::|||   :::                               |||
Db        625 GGGACGCCCGTGCTCAGGCTCGGCCTG----------------------CACGAGTTC 660

Qy         48 ValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThr 67
              |||   |||              |||   ::::::              :::|||
Db        661 GTGGAGGTGGTGTTCCAGAACACGGAGGAGGAGCTGCAGTCGTGGCACCTCGATGGATAC 720

Qy         68 AspValTyrValValGlyTyrGlnAsp---LysTrpAspGlyLysAspArgAlaValPhe 86
              |||   :::|||||||||||||   |||   :::|||:::         |||      :::
Db        721 GACTTCTGGGTTGTAGGGTACGGCGATGGCCAGTGGAATGAGACGCAGCGGCAGACGTAC 780

Qy         87 ---LeuAspLysValProThrValAlaThrSerLysLeuProGlyValThrAsnArg 105
                 |||                        |||   :::::::::|||         :::
Db        781 AACTTGGTGGACGCGCAGGCAAGACACACCGTTCAGGTGTACCCCAACGGGTGGTCGGCG 840

Qy        106 ValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
              :::   ::::::   |||              :::   :::|||     ||||||
Db        841 ATCCTGGTGTCGCTGGACAACCAGGGGATGTGGAACCTGCGGTCGGCGATGTGGGACCGG 900

Qy        126 LysAspLeuGluLeuGlyValTyr 133
              :::   |||         :::|||
Db        901 CAGTACCTCGGGCAGCAGCTCTAC 924

RESULT 85
US-11-266-748A-56767
; Sequence 56767, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56767
;   LENGTH: 4775
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-56767

Alignment Scores:
Pred. No.:              99.8          Length:        4775
Score:                  69.00         Matches:       31
Percent Similarity:     43.7%         Conservative:  24
Best Local Similarity:  24.6%         Mismatches:    43
Query Match:            9.0%          Indels:        28
DB:                     8             Gaps:          6

US-10-758-902-9 (1-149) x US-11-266-748A-56767 (1-4775)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||   ||||||         |||   :::             ::::::|||:::
Db       3733 TCACTCCCAGAGAAATATGAA------ACTAACGTTGGGTCCCAGGGGTCTCAACTCTCT 3786

Qy         27 LysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArg 46
              :::|||            |||                :::   |||      |||   :::
Db       3787 AGAGGGGAGAAA------CAACGCATTGCTATTGCTCGGGCCATTGTACGAGATCCTAAA 3840

Qy         47 PheValLeuValAsp---------------IleThrThrThrSerLysLysThrValLys 61
                 :::|||:::|||               :::   |||   |||:::||||||||:::
Db       3841 ATCTTGCTACTAGATGAAGCCACTTCTGCCTTAGACACAGAAAGTGAAAAGACGGTGCAG 3900

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||                                  :::|||:::
Db       3901 GTTGCTCTAGACAAAGCCAGA----------------------------GAGGGTCGG 3930

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhe------ 99
                 |||          ::::::   |||:::      :::   :::
Db       3931 ACCTGCATTGTCATTGCCCATCGCTTGTCCACCATCCAGAACGCGGATATCATTGCTGTC 3990

Qy        100 ------ProGlyVal--------------ThrAsnArgValThrLeuThrPheAspGly 112
                   ||||||                |||:::         :::          |||
Db       3991 ATGGCACAGGGGGTGGTGATTGAAAAGGGGACCCATGAAGAACTGATGGCCCAAAAAGGA 4050

Qy        113 SerTyrGlnLysLeuVal 118
              :::|||   |||||||||
Db       4051 GCCTACTACAAACTAGTC 4068

RESULT 86
US-11-300-928-50
; Sequence 50, Application US/11300928
; Publication No. US20060166277A1
; GENERAL INFORMATION:
;  APPLICANT: Karumanchi, S. Ananth
;  APPLICANT:  Sukhatme, Vikas P.
;  TITLE OF INVENTION: Nucleic Acids and Polypeptides Useful For Diagnosing and Treating
;  TITLE OF INVENTION:  Complications of Pregnancy
;  FILE REFERENCE: 01948/108002
;  CURRENT APPLICATION NUMBER: US/11/300,928
;  CURRENT FILING DATE:  2005-12-15
;  PRIOR APPLICATION NUMBER: US 60/636,275
;  PRIOR FILING DATE: 2004-12-15
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50
```

```
;   LENGTH: 4776
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4208)..(4208)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4210)..(4212)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4227)..(4229)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4231)..(4231)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4253)..(4253)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4677)..(4677)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4691)..(4691)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4707)..(4707)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4721)..(4721)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4752)..(4752)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4754)..(4754)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4772)..(4773)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-300-928-50

Alignment Scores:
Pred. No.:              99.8          Length:        4776
Score:                  69.00         Matches:       31
Percent Similarity:     43.7%         Conservative:  24
Best Local Similarity:  24.6%         Mismatches:    43
Query Match:            9.0%          Indels:        28
DB:                     9             Gaps:          6

US-10-758-902-9 (1-149) x US-11-300-928-50 (1-4776)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              :::|||   |||  ||||||      |||  :::           ::::::|||:::
Db       3733 TCACTCCCAGAGAAATATGAA------ACTAACGTTGGGTCCCAGGGGTCTCAACTCTCT 3786

Qy         27 LysGlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArg 46
              :::|||          |||          :::  |||      |||   :::
Db       3787 AGAGGGGAGAAA------CAACGCATTGCTATTGCTCGGGCCATTGTACGAGATCCTAAA 3840

Qy         47 PheValLeuValAsp--------------IleThrThrThrSerLysLysThrValLys 61
                :::|||:::|||              :::  |||  |||:::|||||||||:::
```

```
Db       3841 ATCTTGCTACTAGATGAAGCCACTTCTGCCTTAGACACAGAAAGTGAAAAGACGGTGCAG 3900

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||                                    :::|||:::
Db       3901 GTTGCTCTAGACAAAGCCAGA----------------------------GAGGGTCGG 3930

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhe------ 99
                  |||         ::::::   |||:::      :::   :::
Db       3931 ACCTGCATTGTCATTGCCCATCGCTTGTCCACCATCCAGAACGCGGATATCATTGCTGTC 3990

Qy        100 ------ProGlyVal--------------ThrAsnArgValThrLeuThrPheAspGly 112
                   ||||||              |||:::         :::         |||
Db       3991 ATGGCACAGGGGGTGGTGATTGAAAAGGGGACCCATGAAGAACTGATGGCCCAAAAAGGA 4050

Qy        113 SerTyrGlnLysLeuVal 118
              :::|||   |||||||||
Db       4051 GCCTACTACAAACTAGTC 4068

RESULT 87
US-10-669-920-834
; Sequence 834, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-066001
;  CURRENT APPLICATION NUMBER: US/10/669,920
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/004,113
;  PRIOR FILING DATE: 2001-10-23
;  PRIOR APPLICATION NUMBER: US 10/052,482
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 09/997,722
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: US 10/034,650
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: US 10/085,117
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: US 10/087,192
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 10/322,281
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: US 10/322,696
;  PRIOR FILING DATE: 2002-12-17
;  NUMBER OF SEQ ID NOS: 1441
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 834
;   LENGTH: 4874
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-669-920-834

Alignment Scores:
Pred. No.:              103           Length:        4874
Score:                  69.00         Matches:       33
Percent Similarity:     45.5%         Conservative:  12
Best Local Similarity:  33.3%         Mismatches:    42
Query Match:            9.0%          Indels:        12
DB:                     6             Gaps:          6

US-10-758-902-9 (1-149) x US-10-669-920-834 (1-4874)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||          :::      :::|||   ||||||   :::|||   |||:::
Db       1237 GAGTATAAGATCACGGTGGTGCCCATGAGAGGAGAGCTG---GAGGGCAAGCCGATCCTC 1293

Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
                    :::      :::|||     |||              |||:::   |||
Db       1294 ---------CTGAATGGCAGGACAGAAATTGACAGTCCAACCAATGTTGTCACTGATCGA 1344

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAsp-----------ValThrAsp 68
                 |||      :::   |||      |||:::   |||           |||   |||
```

```
Db       1345 GTGACT------GAAGACACAGCAACTGTCTCCTGGGACCCAGTGCAGGCTGTCATAGAC 1398

Qy         69 ValTyrValValGlyTyrGlnAsp---LysTrpAspGlyLysAspArgAlaValPheLeu 87
Db       1399 AAGTATGTAGTGCGCTACACTTCTGCTGATGGGGACACCAAGGAAATGGCAGTGCACAAG 1458

Qy         88 AspLysValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgVal 106
Db       1459 GATGAGAGCAGCACTGTCCTGACGGGC---CTGAAGCCAGGAGAGGCATACAAGGTC 1512

RESULT 88
US-11-266-748A-183731
; Sequence 183731, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 183731
;   LENGTH: 1658
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1431)..(1439)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-183731

Alignment Scores:
Pred. No.:              26.6          Length:          1658
Score:                  68.50         Matches:         27
Percent Similarity:     32.2%         Conservative:    12
Best Local Similarity:  22.3%         Mismatches:      39
Query Match:            8.9%          Indels:          43
DB:                     8             Gaps:            4

US-10-758-902-9 (1-149) x US-11-266-748A-183731 (1-1658)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla--------- 26
Db        690 AAAAGTTACCTTTTCCCC---ATCATCGATGATAGGAATCGGGAGCTTGCCATCCTGTTG 746

Qy         27 ----------------------------LysGlyThrProValCysGln--------- 33
Db        747 GGCATGCTGGATCCAGCAGAGAAGGATGAAAAGGGCATGCCTGTGACAGCTCGTGTGGTG 806

Qy         34 -------------------------------------------LeuProValThrLeuGln 39
Db        807 TTTGTTTTTGGTCCTGATAAGAAGCTGAAGCTGTCTATCCTCTACCCAGCTACCACTGGC 866

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59
Db        867 AGGAACTTTGATGAGATTCTCAGGGTAGTCATCTCTCTCCAGCTGACAGCAGAAAAAGG 926

Qy         60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp 79
Db        927 GTTGCCACCCCAGTTGAT----------------------------------TGGAAG 950

Qy         80 GlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhe 99
Db        951 GATGGGGATAGTGTGATGGTCCTTCCAACCATCCCTGAAGAAGAAGCCAAAAAACTTTTC 1010

Qy        100 Pro 100
Db       1011 CCG 1013

RESULT 89
US-11-266-748A-191129
; Sequence 191129, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191129
;   LENGTH: 1658
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1431)..(1439)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-191129

Alignment Scores:
Pred. No.:              26.6          Length:          1658
Score:                  68.50         Matches:         27
Percent Similarity:     32.2%         Conservative:    12
Best Local Similarity:  22.3%         Mismatches:      39
Query Match:            8.9%          Indels:          43
DB:                     8             Gaps:            4

US-10-758-902-9 (1-149) x US-11-266-748A-191129 (1-1658)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla--------- 26
Db        690 AAAAGTTACCTTTTCCCC---ATCATCGATGATAGGAATCGGGAGCTTGCCATCCTGTTG 746

Qy         27 ----------------------------LysGlyThrProValCysGln--------- 33
```

```
Db        747 GGCATGCTGGATCCAGCAGAGAAGGATGAAAAGGGCATGCCTGTGACAGCTCGTGTGGTG 806

Qy         34 ----------------------------------------LeuProValThrLeuGln 39

Db        807 TTTGTTTTTGGTCCTGATAAGAAGCTGAAGCTGTCTATCCTCTACCCAGCTACCACTGGC 866

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThr 59

Db        867 AGGAACTTTGATGAGATTCTCAGGGTAGTCATCTCTCTCCAGCTGACAGCAGAAAAAAGG 926

Qy         60 ValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAsp 79

Db        927 GTTGCCACCCCAGTTGAT----------------------------------TGGAAG 950

Qy         80 GlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhe 99

Db        951 GATGGGGATAGTGTGATGGTCCTTCCAACCATCCCTGAAGAAGAAGCCAAAAAACTTTTC 1010

Qy        100 Pro 100

Db       1011 CCG 1013
```

RESULT 90
US-11-217-529-3048/c
; Sequence 3048, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3048
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3048

Alignment Scores:

Pred. No.:	34.8	Length:	2007
Score:	68.50	Matches:	39
Percent Similarity:	40.6%	Conservative:	15
Best Local Similarity:	29.3%	Mismatches:	32
Query Match:	8.9%	Indels:	47
DB:	8	Gaps:	8

US-10-758-902-9 (1-149) x US-11-217-529-3048 (1-2007)

```
Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeu------ 25

Db       1697 CTAGGGACTTGCTCGGAAGTATGCACGAGACTA---GATCTTAATGATGATTTGCTTAGG 1641

Qy         26 --------------------------------AlaLysGlyThrProValCysGlnLeu 34

Db       1640 TGCACAGATGACTCATACGGAGCAGAACTGGAAATGAAAGGGCTAGAAGTTTGTGAGTTG 1581

Qy         35 ProValThrLeu------GlnThrIleAlaAspAspLysArgPhe---------ValLeu 49

Db       1580 CTGGCAGAGTTATTAAAGGAATTTATCGCAGATGATGAAAGATTTCTATCGGTGGTCGTA 1521

Qy         50 ValAsp----------------------------------------------------- 51

Db       1520 GTAGACTTTTCAGAGGAAACAGGAGTACCACTAGTGGTTATTGTAGTGTGCCCGGATTTA 1461
```

```
Qy         52 IleThrThrThrSerLysLysThrValLysValAlaIleAsp---ValThrAsp------ 68

Db       1460 GTGCTAACAACCGGGGTATGCGAAGTTTCAAGTTCTGTGGATAAAAAGACTGACGACGTG 1401

Qy         69 ValTyrValValGlyTyrGlnAspLys--------------------TrpAspGlyLys 81

Db       1400 CTATTAATTGTTACAGAAAAAGATGAAGTATAACGCTGTGTGTCAGTTTCCACAGGTTTA 1341

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAla 94

Db       1340 GACCATGCGGTAGTACTAGTTGAAGTTACTACCGTAGCC 1302
```

RESULT 91
US-11-348-413-13606
; Sequence 13606, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 13606
; LENGTH: 3462
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3462)
; OTHER INFORMATION: WAN01UPMI; ORF; 00000000011100; Cluster contains WAN01OPYP
; OTHER INFORMATION: :SE0813:pycA:pyruvate carboxylase:ATCC12228:NC_004461.1
US-11-348-413-13606

Alignment Scores:

Pred. No.:	74.8	Length:	3462
Score:	68.50	Matches:	43
Percent Similarity:	37.3%	Conservative:	26
Best Local Similarity:	23.2%	Mismatches:	67
Query Match:	8.9%	Indels:	49
DB:	9	Gaps:	10

US-10-758-902-9 (1-149) x US-11-348-413-13606 (1-3462)

```
Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21

Db       1213 CATGCCGTTTCATTTAAACAAGCTGAA-----------GAGAAAATGGAACGTTCATTA 1260

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41

Db       1261 CGCGAAATGCGAATTCGTGGCGTAAAGACG---AATATTCCATTTCTCATCAATGTTATG 1317

Qy         42 AlaAspAspLys----------------------ArgPheVal--------------- 48

Db       1318 CGTAATGATAAATTTAGAAGTGGTGATTATACTACTAAATTTATTGAAGAAACACCTGAA 1377

Qy         49 LeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAsp 68

Db       1378 CTTTTCGATATTGCACCGACATTGGACAGAGGTACCAAGACTTTAGAGTATATTGGTAAT 1437

Qy         69 ValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAsp 88

Db       1438 GTGACGATAAACGGATTTCCTAATGTAGAAAAGCGTCCAAAACCAGAATATGAATCTACC 1497
```

```
Qy         89 LysValProThrValAlaThrSerLys---------LeuPhe------------------ 99
              |||:::|||   ::::::      |||        ||||||
Db       1498 AAAATCCCAAAAATTTCTCAAAAGAAAATCAATCAGTTATTTGGAACAAAACAAATTCTT 1557

Qy        100 --------------ProGlyValThrAsnArgVal----------------------- 106
                           ||||||||||||   |||
Db       1558 GAGCAACATGGACCAACAGGTGTTACAAATTGGGTTAGAGAACAAGAAGATGTTTTAATT 1617

Qy        107 ---ThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
                  ||||||      :::::::|||   |||:::   |||   :::|||
Db       1618 ACCGATACTACATTTAGAGATGCACACCAATCTTTACTT---GCAACACGTGTAAGAACA 1674

Qy        126 LysAspLeu-----------------GluLeuGlyValTyrLysLeuGluPheSerIle 139
              ||||||:::                          |||:::|||      ||||||:::
Db       1675 AAAGATATGATGAACATTGCATCTAAAACTGCTGAAGTTTTTAAAGATAGTTTTTCATTA 1734

Qy        140 GluAlaIleTrpGly 144
              |||   :::||||||
Db       1735 GAA---ATGTGGGGT 1746

RESULT 92
US-11-314-834-2044
; Sequence 2044, Application US/11314834
; Publication No. US20060195942A1
; GENERAL INFORMATION:
;  APPLICANT: Fincher, Karen L.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 16517.360 - 38-21(51770)C/US
;  CURRENT APPLICATION NUMBER: US/11/314,834
;  CURRENT FILING DATE:  2005-12-22
;  PRIOR APPLICATION NUMBER: US 09/732,627
;  PRIOR FILING DATE: 2000-12-08
;  NUMBER OF SEQ ID NOS: 4930
; SEQ ID NO 2044
;   LENGTH: 434
;   TYPE: DNA
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3493-030-P1-M1-D11
US-11-314-834-2044

Alignment Scores:
Pred. No.:              4.77          Length:         434
Score:                  68.00         Matches:        31
Percent Similarity:     35.3%         Conservative:   18
Best Local Similarity:  22.3%         Mismatches:     40
Query Match:            8.9%          Indels:         50
DB:                     7             Gaps:           6

US-10-758-902-9 (1-149) x US-11-314-834-2044 (1-434)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              |||:::|||     |||   |||         :::::::::|||
Db         87 TACGATACCGAGAGATTTCAACTTTGAATCATTTCCAATTCCCT-------------- 131

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
                                                      ||||||         :::
Db        132 ---------------------------------------TGGCCTGTAAACCATACATCA 152

Qy         41 IleAlaAspAspLysArgPheValLeuValAsp-----------------------Ile 52
              |||:::   |||:::|||   :::   |||                        :::
Db        153 ATCAGCCCGGATCGGAGACTTATTACTGTAGTTGGAGATCACTTGGATGCGTTGCTTGTG 212

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAsp------------ 68
                 :::   :::   |||   |||       |||:::       |||
Db        213 GATTCACAGAACGGAAAGGCCGTAGCCACAGCAGTAGGTCATCGAGATTACTCCTTTGCA 272

Qy         69 ------------------------ValTyrValValGlyTyrGlnAspLys--------- 77
                                       |||:::      |||   |||||||||
Db        273 TCAGCATGGCACCCAGACGGACGGGTATTTGCCACAGGAAATCAAGACAAGACCTGCCGT 332

Qy         78 ---TrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr---ValAlaThr 95
                |||||                          :::   |||:::   |||   |||||||||
Db        333 GTATGGGAC---------------------ATAAGAAAGCTGGCAACGCCGGTTGCGACT 371

Qy         96 SerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyr 114
              |||          |||              :::      :::   ||||||   :::
Db        372 CTAAAAGGAAACTTGGGTGCTGTAAGATCGATCCGTTTTTCATCCGACGGCCAGTTC 428

RESULT 93
US-11-218-305-24102/c
; Sequence 24102, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24102
;   LENGTH: 1053
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-24102

Alignment Scores:
Pred. No.:              16.5          Length:         1053
Score:                  68.00         Matches:        34
Percent Similarity:     34.1%         Conservative:   10
Best Local Similarity:  26.4%         Mismatches:     27
Query Match:            8.9%          Indels:         58
DB:                     9             Gaps:           7

US-10-758-902-9 (1-149) x US-11-218-305-24102 (1-1053)

Qy         35 ProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThr--- 53
              |||   ||||||                ||||||||||||         :::|||
Db        449 CCGTTCACGCTGGACGTGTTCATC---TCCAAGCGCTTCGTCTCGGCGTCCCTCACGCAC 393

Qy         54 ------------------------------ThrThrSerLysLysThrValLysValAla 63
                                                  |||:::   |||   :::|||   |||
Db        392 CGGTCGACCTGCAGGCAGGTCGCGGTCGCCGGGACCAACTCCAAGGACATCAAGGCGGCG 333

Qy         64 Ile------------AspVal---------------------------------------- 66
              :::             ||||||
Db        332 CTCAGGTCGAGGTCCGACGTGCCGGCCTGCCTGGCCGTCGGGCGGTTCCTGGCCGAGAGG 273

Qy         67 ---------ThrAspValTyrValValGlyTyr------------GlnAspLysTrpAsp 79
                      |||||||||          |||             :::||||||::::::
Db        272 GCGAAGGAGGCCGACGTGTACACCTGCACGTACACGCCGAGGGAACGGGACAAGTTCGAG 213

Qy         80 GlyLysAspArgAlaVal-----------------------------------------Phe 86
              ||||||   |||||||||                                        :::
Db        212 GGGAAGATCAGGGCGGTTGTTCAGTCGCTGATCGATAACGGGATCAATGTGAAACTTTAC 153

Qy         87 LeuAsp--------------------------LysValProThrValAlaThrSerLys 97
              ||||||                          |||   |||   |||
Db        152 CTTGACTGAGTTCGGTGCTGTATGAGTAGTTGTTCTGTTGGAACTTGCGCGTGGGTTTAT 93

Qy         98 LeuPheProGlyValThrAsnArgVal 106
              |||   ||||||:::      |||:::
Db         92 CTGTTGCCAGGGTTGCAGGTTCGAATT 66

RESULT 94
US-11-056-355B-17912
; Sequence 17912, Application US/11056355B
; Publication No. US20060150283A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 17912
;   LENGTH: 1211
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1211)
;   OTHER INFORMATION: Ceres Seq. ID no. 12415232
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1211)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14313167
;   OTHER INFORMATION: as cited in SEQ ID NO 54354
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1211)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 15226238
;   OTHER INFORMATION: as cited in SEQ ID NO 68840
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1211)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14306100
;   OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-17912

Alignment Scores:
Pred. No.:                20.1          Length:         1211
Score:                    68.00         Matches:        30
Percent Similarity:       43.2%         Conservative:   21
Best Local Similarity:    25.4%         Mismatches:     53
Query Match:              8.9%          Indels:         14
DB:                       9             Gaps:           4

US-10-758-902-9 (1-149) x US-11-056-355B-17912 (1-1211)

Qy          28 GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPhe 47
               ||||||||||||   :::|||   :::                             |||
Db         625 GGGACGCCCGTGCTCAGGCTCGGCCTG----------------------CACGAGTTC 660

Qy          48 ValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThr 67
               |||   |||              |||   ::::::                 :::|||
Db         661 GTGGAGGTGGTGTTCCAGAACACGGAGGAGGAGCTGCAGTCGTGGCACCTCGATGGATAC 720

Qy          68 AspValTyrValValGlyTyrGlnAsp---LysTrpAspGlyLysAspArgAlaValPhe 86
               |||   :::||||||||||||   |||   :::|||:::          |||      :::
Db         721 GACTTCTGGGTTGTAGGGTACGGCGATGGCCAGTGGAATGAGACGCAGCGGCAGACGTAC 780

Qy          87 ---LeuAspLysValProThrValAlaThrSerLysLeuProGlyValThrAsnArg 105
                  |||                  |||   :::::::::|||      :::
Db         781 AACTTGGTGGACGCGCAGGCAAGACACACCGTTCAGGTGTACCCCAACGGGTGGTCGGCG 840

Qy         106 ValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
               :::   ::::::   |||                  :::   :::|||      ||||||
Db         841 ATCCTGGTGTCGCTGGACAACCAGGGGATGTGGAACCTGCGGTCGGCGATGTGGGACCGG 900

Qy         126 -----------LysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIle 139
                        :::   |||   |||   |||:::      |||   |||:::
Db         901 CATTACCTCGGGCAGCAGCTCTACCTCAGGGTGTGGACGCCGGAGCAGAGCCTC 954

RESULT 95
US-11-218-305-3484
; Sequence 3484, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3484
;   LENGTH: 1359
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-3484

Alignment Scores:
Pred. No.:                23.7          Length:         1359
Score:                    68.00         Matches:        36
Percent Similarity:       42.3%         Conservative:   27
Best Local Similarity:    24.2%         Mismatches:     52
Query Match:              8.9%          Indels:         34
DB:                       9             Gaps:           9

US-10-758-902-9 (1-149) x US-11-218-305-3484 (1-1359)

Qy          11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
               ||||||   |||      ||||||      :::|||   ::::::   |||
Db         167 GCCTACCCTTACAGCGCCTTCATCACCTCCGTCCGGAAAGACGTGATCAAATACTGCACC 226

Qy          28 ---GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArg 46
                  |||   :::   |||      :::   |||:::                 :::
Db         227 AACCATACAGGCATCGTCCAGCCCGTGCTGCCGCTGGAGAAGAAGGTCCCCGAGCTCTGG 286

Qy          47 PheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspVal 66
               |||                      |||      :::::::::   :::||||||   :::
Db         287 TTCTACACCGAG------CTCAAAACGAAGACCAGGTCCATCACGCTCGCCATACGTATG 340

Qy          67 ThrAspValTyrValValGlyTyrGlnAspLys-----------TrpAsp---GlyLys 81
                  ::::::|||:::||||||::::::                        |||:::   ||||||
Db         341 GACAACCTCTACCTGGTCGGCTTCAGGACCCCCGGCGGGGTGTGGTGGGAGTTCGGCAAG 400

Qy          82 AspArgAlaVal---PheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
               |||            ||||||                        :::|||      |||
Db         401 GACGGCGACACCCACCTCCTCGACGAC--------------AACGCCAAGTGCCGCCCC 445

Qy         101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
               |||                              |||   ||||||   |||:::   :::
Db         446 GGT--------------------------GGCGGCCGGTACCAGGACCTCATCGGCAGT 478

Qy         121 AlaLysValAspArgLysAspLeuGlu---------LeuGlyValTyrLysLeuGluPhe 137
                        |||   ||||||         :::|||      ::::::
Db         479 --------------AAGGGCCTGGAGACCGTCACCATGGGCCGTGCCGAAATGACCACG 523

Qy         138 SerIleGluAlaIleTrpGlyLysThr 146
               ::::::      :::      ||||||
Db         524 GCCGTCAACTACCTGGCGAAGAAGACG 550

RESULT 96
US-11-218-305-21832/c
; Sequence 21832, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
```

```
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21832
;   LENGTH: 2285
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (24)..(25)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(31)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (33)..(34)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (38)..(40)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (58)..(58)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (71)..(71)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (74)..(74)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (83)..(83)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-21832

Alignment Scores:
Pred. No.:              49.1          Length:        2285
Score:                  68.00         Matches:       29
Percent Similarity:     42.2%         Conservative:  14
Best Local Similarity:  28.4%         Mismatches:    37
Query Match:            8.9%          Indels:        22
DB:                     9             Gaps:          4

US-10-758-902-9 (1-149) x US-11-218-305-21832 (1-2285)

Qy         18 IleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThr 37
              |||   |||::::::|||:::   |||:::                  :::|||   |||
Db       1286 ATTGTTGACATTCAGAACAAGGGAGCTGAGAACATT-----------GTTCCTTCCACT 1239

Qy         38 LeuGlnThrIleAlaAspAsp-----------LysArgPheValLeuValAspIleThr 53
                ::::::|||   |||               |||   ||||||      :::
Db       1238 GATTCATCACTTGCTTCAGATGTTGGTGAGAGCTCCCGTTCAGTGCTCTATCCAGTTGAT 1179

Qy         54 ThrThrSerLysLysThrValLysValAlaIleAspVal------ThrAspValTyrVal 71
              ||||||:::    :::|||             |||      |||  |||  :::
Db       1178 ACGACTACTGTGAACTCAGTGTCATCCACGTCTACAGTGGCTGGTACCCCAGTTGAACTT 1119

Qy         72 ValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValPro 91
                |||||||||                                        :::      |||
Db       1118 TCTGGGTATCAG-----------------------------------GAGGGTGCTCCA 1095

Qy         92 ThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAsp 111
              |||   :::|||  |||          |||  |||  ||||||
Db       1094 GTGGTATGTTCTTCATGTTTAACAGCTGATGTTCAGAACAATGTGACATCTGATATGCCA 1035

Qy        112 GlySer 113
              |||:::
Db       1034 GGTGCT 1029

RESULT 97
US-11-218-305-21409/c
; Sequence 21409, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21409
;   LENGTH: 2358
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-21409

Alignment Scores:
Pred. No.:              51.3          Length:        2358
Score:                  68.00         Matches:       28
Percent Similarity:     42.0%         Conservative:  22
Best Local Similarity:  23.5%         Mismatches:    31
Query Match:            8.9%          Indels:        38
DB:                     9             Gaps:          4

US-10-758-902-9 (1-149) x US-11-218-305-21409 (1-2358)

Qy         15 ProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeu 34
              |||       |||   :::||||||   ::::::            ||||||   :::|||
Db       627 CCAGTACTCATATCAAACTTGAGGTTGCAGATA-----------CCGGTTTCAAAACTG 580

Qy         35 ProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThr 54
                :::||||||      :::   |||         ||||||            :::
Db       579 GAGATTACTCTGGGCTACTTGATTGACACAATGTCGTTTGTTGACGCCCTGCCTTCTCTG 520

Qy         55 ThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyr 74
              |||::::::          |||   :::   :::   |||
Db       519 CGATCGAGGCAGTGGCAGGCTGTGGTTCTGGTAATGCTTGAC----------------- 478

Qy         75 GlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAla 94
                                        |||:::   :::   ::::::|||   :::|||
Db       477 -------------------------GCGCTCTCTGTGCACCAGCTTCCCGCCCTTGCT 445

Qy         95 ------------ThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPhe 110
                         |||||||||
Db       444 CCAGTCTTTTCGAATTCGAAGCTT---------------------------------- 421

Qy        111 AspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
                  ||||||::::::||||||||||:::|||   |||:::::::   :::
Db       420 ---------GTGCAAAAGATGTTGAACGCTGCTCAGGTTAGCAGAGAGGAGTATGAC 373

RESULT 98
US-11-217-529-1740
; Sequence 1740, Application US/11217529
; Publication No. US20060099612A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1740
;   LENGTH: 2832
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1740

Alignment Scores:
Pred. No.:              66.4          Length:         2832
Score:                  68.00         Matches:        28
Percent Similarity:     47.7%         Conservative:   14
Best Local Similarity:  31.8%         Mismatches:     26
Query Match:            8.9%          Indels:         20
DB:                     8             Gaps:           5

US-10-758-902-9 (1-149) x US-11-217-529-1740 (1-2832)

Qy         67 ThrAspValTyrValValGlyTyrGlnAsp-----------LysTrpAspGlyLysAsp 82
              |||:::::   ||||||||||||   |||               ||||||
Db        271 ACTAATCTGTTAGTTGTCGGTTATGCAGATGGTGTTATTAAGGTTTGGGATTTGGTATCC 330

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
              :::   |||   |||:::                          |||   |||
Db        331 AAGACAGTGCTCTTAAAC----------------------------TTTAACGGTCAC 360

Qy        103 ThrAsnArgValThr---LeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||   |||   ||||||   :::      :::|||::::::   :::
Db        361 AAGGCGGCTATAACATTATTGCAATTTGATATCACCGGTACAAGGTTGATTTCCGGTTCC 420

Qy        122 Lys---------ValAspArgLysAspLeu------GluLeuGlyValTyrLysLeuGlu 136
              |||         :::       ||||||      |||:::|||:::|||||||||
Db        421 AAGGACTCCAATATCATTGTATGGGACCTTGTTGGTGAAGTTGGTCTTTATAAGCTAAGG 480

Qy        137 PheSerIleGluAlaIleTrpGly 144
                  :::||||||   |||
Db        481 TCACATAAGGATGCCATTACTGGA 504

RESULT 99
US-10-539-228-341
; Sequence 341, Application US/10539228
; Publication No. US20060154250A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc S. Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: CHIR0052-101 (PP023370.0003)
;  CURRENT APPLICATION NUMBER: US/10/539,228
;  CURRENT FILING DATE:  2005-06-17
;  PRIOR APPLICATION NUMBER: US 10/322,281
;  PRIOR FILING DATE: 2002-12-18
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 341
;   LENGTH: 91278
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(91278)
;   OTHER INFORMATION: n = A,T,C or G
US-10-539-228-341

Alignment Scores:
Pred. No.:              8.69e+03      Length:         91278
Score:                  68.00         Matches:        33
Percent Similarity:     41.5%         Conservative:   26
Best Local Similarity:  23.2%         Mismatches:     43
Query Match:            8.9%          Indels:         40
DB:                     6             Gaps:           8

US-10-758-902-9 (1-149) x US-10-539-228-341 (1-91278)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyr------GluTyrProThrPheIleGln 19
              :::::::::      :::||||||      |||            |||:::   :::
Db      59422 GATTCCCTGTGCTTGCATTTGGGTTCTCTGTATCTTCCTGCTCCTCCTTCATTGCTAATC 59481

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGln 39
                 :::||||||||:::::|||   |||       |||
Db      59482 TTCATGAGAAATGAGATTTCAAAGTTTACGAGAAAATGTCAC----------------- 59523

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIle-------------------- 52
                          :::|||||||   |||:::   |||
Db      59524 ------------TAAGAACGATTTCAACTTATTCAAATAATAGATAGAATCATTAATTCA 59571

Qy         53 ------ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyr 70
                    :::   |||       |||   :::|||       :::       |||:::
Db      59572 TTTTTTCTTGTTTCTTGCAAAGTAATTGTCTACTTAGCATTTTTAATCAGAAGTGTTTTT 59631

Qy         71 ValValGlyTyrGlnAspLysTrpAsp---------------GlyLysAspArgAlaVal 85
              :::   ||||||      :::|||                  |||   :::   |||
Db      59632 CCAATTAAATATCAA---GCCTATGATTTTAAATAGCATCTGGCCAAACATAAGGTGGTG 59688

Qy         86 PheLeu-----------------------AspLysValProThrValAlaThrSerLys 97
              ||||||                      |||:::   |||::::::
Db      59689 TTTCTTAGGATGTGGTCCTGAGTCATGTCCAGGAAAATATCCACAATGTCTATTGGAAAT 59748

Qy         98 LeuPhePro---GlyValThrAsnArgVal-----------ThrLeuThrPheAspGly 112
              ::::::|||   |||:::   |||                  :::         ||||||
Db      59749 GTGTATCCTCAGGGCCTAGCAAACACAGAAGTGGATGATCACAGTCAGCTATTGGATGGG 59808

Qy        113 SerTyr 114
              |||:::
Db      59809 TCACAC 59814

RESULT 100
US-10-669-920-858
; Sequence 858, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-066001
;  CURRENT APPLICATION NUMBER: US/10/669,920
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/004,113
;  PRIOR FILING DATE: 2001-10-23
;  PRIOR APPLICATION NUMBER: US 10/052,482
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 09/997,722
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: US 10/034,650
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: US 10/085,117
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: US 10/087,192
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 10/322,281
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: US 10/322,696
;  PRIOR FILING DATE: 2002-12-17
;  NUMBER OF SEQ ID NOS: 1441
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 858
;   LENGTH: 91278
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(91278)
;   OTHER INFORMATION: n = A,T,C or G
US-10-669-920-858

Alignment Scores:
Pred. No.:              8.69e+03        Length:         91278
Score:                  68.00           Matches:        33
Percent Similarity:     41.5%           Conservative:   26
Best Local Similarity:  23.2%           Mismatches:     43
Query Match:            8.9%            Indels:         40
DB:                     6               Gaps:           8

US-10-758-902-9 (1-149) x US-10-669-920-858 (1-91278)

Qy          2 AsnThrValSerPheAsnLeuGlyGluAlaTyr------GluTyrProThrPheIleGln 19
              :::::::::       :::||||||       |||            |||:::   :::
Db      59422 GATTCCCTGTGCTTGCATTTGGGTTCTCTGTATCTTCCTGCTCCTCCTTCATTGCTAATC 59481

Qy         20 AspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGln 39
                :::||||||||:::::::|||   |||       |||
Db      59482 TTCATGAGAAATGAGATTTCAAAGTTTACGAGAAAATGTCAC----------------- 59523

Qy         40 ThrIleAlaAspAspLysArgPheValLeuValAspIle---------------------- 52
                         :::||||||   |||:::   |||
Db      59524 ------------TAAGAACGATTTCAACTTATTCAAATAATAGATAGAATCATTAATTCA 59571

Qy         53 ------ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyr 70
                     :::   |||       |||   :::|||       :::       |||:::
Db      59572 TTTTTTCTTGTTTCTTGCAAAGTAATTGTCTACTTAGCATTTTTAATCAGAAGTGTTTTT 59631

Qy         71 ValValGlyTyrGlnAspLysTrpAsp---------------GlyLysAspArgAlaVal 85
              :::   ||||||      :::|||                  |||   :::   |||
Db      59632 CCAATTAAATATCAA---GCCTATGATTTTAAATAGCATCTGGCCAAACATAAGGTGGTG 59688

Qy         86 PheLeu-----------------------AspLysValProThrValAlaThrSerLys 97
              ||||||                      |||:::   |||::::::
Db      59689 TTTCTTAGGATGTGGTCCTGAGTCATGTCCAGGAAAATATCCACAATGTCTATTGGAAAT 59748

Qy         98 LeuPhePro---GlyValThrAsnArgVal------------ThrLeuThrPheAspGly 112
              :::::::|||   |||:::   |||                :::          ||||||
Db      59749 GTGTATCCTCAGGGCCTAGCAAACACAGAAGTGGATGATCACAGTCAGCTATTGGATGGG 59808

Qy        113 SerTyr 114
              |||:::
Db      59809 TCACAC 59814


Search completed: September 18, 2006, 20:50:09
Job time : 367.369 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 17:40:57 ; Search time 7847.06 Seconds
(without alignments)
1665.017 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 86534536 seqs, 29229259966 residues

Total number of hits satisfying chosen parameters: 173069072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_18092006_162713_11674/app_query.fasta_1
-DB=Pending_Patents_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10758902_@CGN_1_1_10839_@runat_18092006_162713_11674 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pna/PCTUSA_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pna/PCTUSB_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pna/PCTUSC_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pna/US075_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pna/US076_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pna/US077_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pna/US078_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pna/US079_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pna/US080_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pna/US081_COMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pna/US082_COMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pna/US083_COMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pna/US084_COMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pna/US085_COMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pna/US086_COMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pna/US087_COMB.seq:*
17: /EMC_Celerra_SIDS3/ptodata/2/pna/US088_COMB.seq:*
18: /EMC_Celerra_SIDS3/ptodata/2/pna/US089_COMB.seq:*
19: /EMC_Celerra_SIDS3/ptodata/2/pna/US090_COMB.seq:*
20: /EMC_Celerra_SIDS3/ptodata/2/pna/US091_COMB.seq:*
21: /EMC_Celerra_SIDS3/ptodata/2/pna/US092_COMB.seq:*
22: /EMC_Celerra_SIDS3/ptodata/2/pna/US093_COMB.seq:*
23: /EMC_Celerra_SIDS3/ptodata/2/pna/US094_COMB.seq:*
24: /EMC_Celerra_SIDS3/ptodata/2/pna/US095A_COMB.seq:*
25: /EMC_Celerra_SIDS3/ptodata/2/pna/US095B_COMB.seq:*
26: /EMC_Celerra_SIDS3/ptodata/2/pna/US095C_COMB.seq:*
27: /EMC_Celerra_SIDS3/ptodata/2/pna/US096A_COMB.seq:*
28: /EMC_Celerra_SIDS3/ptodata/2/pna/US096B_COMB.seq:*
29: /EMC_Celerra_SIDS3/ptodata/2/pna/US096C_COMB.seq:*
30: /EMC_Celerra_SIDS3/ptodata/2/pna/US097A_COMB.seq:*
31: /EMC_Celerra_SIDS3/ptodata/2/pna/US097B_COMB.seq:*
32: /EMC_Celerra_SIDS3/ptodata/2/pna/US098A_COMB.seq:*
33: /EMC_Celerra_SIDS3/ptodata/2/pna/US098B_COMB.seq:*
34: /EMC_Celerra_SIDS3/ptodata/2/pna/US099A_COMB.seq:*
35: /EMC_Celerra_SIDS3/ptodata/2/pna/US099B_COMB.seq:*
36: /EMC_Celerra_SIDS3/ptodata/2/pna/US099C_COMB.seq:*
37: /EMC_Celerra_SIDS3/ptodata/2/pna/US099D_COMB.seq:*
38: /EMC_Celerra_SIDS3/ptodata/2/pna/US099E_COMB.seq:*
39: /EMC_Celerra_SIDS3/ptodata/2/pna/US100A_COMB.seq:*
40: /EMC_Celerra_SIDS3/ptodata/2/pna/US100B_COMB.seq:*
41: /EMC_Celerra_SIDS3/ptodata/2/pna/US101_COMB.seq:*
42: /EMC_Celerra_SIDS3/ptodata/2/pna/US102A_COMB.seq:*
43: /EMC_Celerra_SIDS3/ptodata/2/pna/US102B_COMB.seq:*
44: /EMC_Celerra_SIDS3/ptodata/2/pna/US103A_COMB.seq:*
45: /EMC_Celerra_SIDS3/ptodata/2/pna/US103B_COMB.seq:*
46: /EMC_Celerra_SIDS3/ptodata/2/pna/US103C_COMB.seq:*
47: /EMC_Celerra_SIDS3/ptodata/2/pna/US103D_COMB.seq:*
48: /EMC_Celerra_SIDS3/ptodata/2/pna/US103E_COMB.seq:*
49: /EMC_Celerra_SIDS3/ptodata/2/pna/US103F_COMB.seq:*
50: /EMC_Celerra_SIDS3/ptodata/2/pna/US104_COMB.seq:*
51: /EMC_Celerra_SIDS3/ptodata/2/pna/US105_COMB.seq:*
52: /EMC_Celerra_SIDS3/ptodata/2/pna/US106A_COMB.seq:*
53: /EMC_Celerra_SIDS3/ptodata/2/pna/US106B_COMB.seq:*
54: /EMC_Celerra_SIDS3/ptodata/2/pna/US107A_COMB.seq:*
55: /EMC_Celerra_SIDS3/ptodata/2/pna/US107B_COMB.seq:*
56: /EMC_Celerra_SIDS3/ptodata/2/pna/US107C_COMB.seq:*
57: /EMC_Celerra_SIDS3/ptodata/2/pna/US107D_COMB.seq:*
58: /EMC_Celerra_SIDS3/ptodata/2/pna/US107E_COMB.seq:*
59: /EMC_Celerra_SIDS3/ptodata/2/pna/US107F_COMB.seq:*
60: /EMC_Celerra_SIDS3/ptodata/2/pna/US107G_COMB.seq:*
61: /EMC_Celerra_SIDS3/ptodata/2/pna/US108_COMB.seq:*
62: /EMC_Celerra_SIDS3/ptodata/2/pna/US109A_COMB.seq:*
63: /EMC_Celerra_SIDS3/ptodata/2/pna/US109B_COMB.seq:*
64: /EMC_Celerra_SIDS3/ptodata/2/pna/US109C_COMB.seq:*
65: /EMC_Celerra_SIDS3/ptodata/2/pna/US110A_COMB.seq:*
66: /EMC_Celerra_SIDS3/ptodata/2/pna/US110B_COMB.seq:*
67: /EMC_Celerra_SIDS3/ptodata/2/pna/US110C_COMB.seq:*
68: /EMC_Celerra_SIDS3/ptodata/2/pna/US110D_COMB.seq:*
69: /EMC_Celerra_SIDS3/ptodata/2/pna/US111A_COMB.seq:*
70: /EMC_Celerra_SIDS3/ptodata/2/pna/US111B_COMB.seq:*
71: /EMC_Celerra_SIDS3/ptodata/2/pna/US112A_COMB.seq:*
72: /EMC_Celerra_SIDS3/ptodata/2/pna/US112B_COMB.seq:*
73: /EMC_Celerra_SIDS3/ptodata/2/pna/US113A_COMB.seq:*
74: /EMC_Celerra_SIDS3/ptodata/2/pna/US113B_COMB.seq:*
75: /EMC_Celerra_SIDS3/ptodata/2/pna/US114_COMB.seq:*
76: /EMC_Celerra_SIDS3/ptodata/2/pna/US117_COMB.seq:*
77: /EMC_Celerra_SIDS3/ptodata/2/pna/US600_COMB.seq:*
78: /EMC_Celerra_SIDS3/ptodata/2/pna/US601_COMB.seq:*
79: /EMC_Celerra_SIDS3/ptodata/2/pna/US602A_COMB.seq:*
80: /EMC_Celerra_SIDS3/ptodata/2/pna/US602B_COMB.seq:*
81: /EMC_Celerra_SIDS3/ptodata/2/pna/US603_COMB.seq:*
82: /EMC_Celerra_SIDS3/ptodata/2/pna/US604A_COMB.seq:*
83: /EMC_Celerra_SIDS3/ptodata/2/pna/US604B_COMB.seq:*
84: /EMC_Celerra_SIDS3/ptodata/2/pna/US605_COMB.seq:*
85: /EMC_Celerra_SIDS3/ptodata/2/pna/US606_COMB.seq:*
86: /EMC_Celerra_SIDS3/ptodata/2/pna/US607_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	726	94.5	2404	66	US-11-084-080-15	Sequence 15, Appl
2	726	94.5	2404	66	US-11-084-080-19	Sequence 19, Appl
3	726	94.5	2404	66	US-11-084-080-21	Sequence 21, Appl
4	726	94.5	2404	66	US-11-084-080-23	Sequence 23, Appl

5	726	94.5	2431	66	US-11-084-080-27	Sequence 27, Appl
6	609	79.3	363	60	US-10-758-902-8	Sequence 8, Appli
7	220.5	28.7	913	6	US-07-787-567A-13	Sequence 13, Appl
8	220.5	28.7	913	41	US-10-127-890-13	Sequence 13, Appl
9	220.5	28.7	913	52	US-10-613-755-13	Sequence 13, Appl
10	220.5	28.7	913	59	US-10-717-243-13	Sequence 13, Appl
11	183.5	23.9	870	34	US-09-905-247-2	Sequence 2, Appli
12	183.5	23.9	870	34	US-09-905-247A-2	Sequence 2, Appli
13	183.5	23.9	886	6	US-07-739-143-3	Sequence 3, Appli
14	183.5	23.9	886	13	US-08-480-432-3	Sequence 3, Appli
15	183.5	23.9	886	42	US-10-280-679B-3	Sequence 3, Appli
16	183.5	23.9	886	42	US-10-280-725B-3	Sequence 3, Appli
17	179.5	23.4	758	28	US-09-663-826-6	Sequence 6, Appli
18	179.5	23.4	762	65	US-11-042-707-16	Sequence 16, Appl
19	179.5	23.4	762	65	US-11-042-707-19	Sequence 19, Appl
20	179.5	23.4	768	65	US-11-042-707-17	Sequence 17, Appl
21	179.5	23.4	768	65	US-11-042-707-20	Sequence 20, Appl
22	179.5	23.4	1499	28	US-09-663-826-14	Sequence 14, Appl
23	176.5	23.0	756	22	US-09-347-064-7	Sequence 7, Appli
24	176.5	23.0	756	22	US-09-347-064-7	Sequence 7, Appli
25	176.5	23.0	756	22	US-09-347-064F-7	Sequence 7, Appli
26	176.5	23.0	756	22	US-09-347-064G-7	Sequence 7, Appli
27	176.5	23.0	756	22	US-09-347-064H-7	Sequence 7, Appli
28	176.5	23.0	756	22	US-09-347-064H-43	Sequence 43, Appl
29	176.5	23.0	762	22	US-09-347-064-1	Sequence 1, Appli
30	176.5	23.0	762	22	US-09-347-064-1	Sequence 1, Appli
31	176.5	23.0	762	22	US-09-347-064F-1	Sequence 1, Appli
32	176.5	23.0	762	22	US-09-347-064G-1	Sequence 1, Appli
33	176.5	23.0	762	22	US-09-347-064H-1	Sequence 1, Appli
34	176.5	23.0	855	50	US-10-499-297-1	Sequence 1, Appli
35	176.5	23.0	1596	65	US-11-042-707-15	Sequence 15, Appl
36	176.5	23.0	1596	65	US-11-042-707-18	Sequence 18, Appl
37	176.5	23.0	1958	50	US-10-499-297-5	Sequence 5, Appli
38	173	22.5	2788	61	US-10-800-052-35	Sequence 35, Appl
39	173	22.5	2803	61	US-10-800-052-2	Sequence 2, Appli
40	173	22.5	2805	61	US-10-800-052-37	Sequence 37, Appl
41	173	22.5	2869	61	US-10-800-052-20	Sequence 20, Appl
42	173	22.5	2878	61	US-10-800-052-26	Sequence 26, Appl
43	169	22.0	807	65	US-11-010-795-23	Sequence 23, Appl
44	169	22.0	1140	13	US-08-406-801-18	Sequence 18, Appl
45	169	22.0	1140	13	US-08-406-801-33	Sequence 33, Appl
46	169	22.0	1623	61	US-10-893-584-273	Sequence 273, App
47	169	22.0	1807	39	US-10-089-058-54	Sequence 54, Appl
48	169	22.0	1807	39	US-10-089-058A-54	Sequence 54, Appl
49	169	22.0	1807	61	US-10-893-584-196	Sequence 196, App
50	169	22.0	1810	39	US-10-089-058-26	Sequence 26, Appl
51	169	22.0	1810	39	US-10-089-058A-26	Sequence 26, Appl
52	169	22.0	1810	61	US-10-893-584-168	Sequence 168, App
53	169	22.0	1813	39	US-10-089-058-103	Sequence 103, App
54	169	22.0	1813	39	US-10-089-058A-103	Sequence 103, App
55	169	22.0	1813	61	US-10-893-584-245	Sequence 245, App
56	169	22.0	1819	39	US-10-089-058-96	Sequence 96, Appl
57	169	22.0	1819	39	US-10-089-058A-96	Sequence 96, Appl
58	169	22.0	1819	61	US-10-893-584-238	Sequence 238, App
59	169	22.0	1822	39	US-10-089-058-33	Sequence 33, Appl
60	169	22.0	1822	39	US-10-089-058-40	Sequence 40, Appl
61	169	22.0	1822	39	US-10-089-058A-33	Sequence 33, Appl
62	169	22.0	1822	39	US-10-089-058A-40	Sequence 40, Appl
63	169	22.0	1822	61	US-10-893-584-175	Sequence 175, App
64	169	22.0	1822	61	US-10-893-584-182	Sequence 182, App
65	169	22.0	1825	39	US-10-089-058-89	Sequence 89, Appl
66	169	22.0	1825	39	US-10-089-058A-89	Sequence 89, Appl
67	169	22.0	1825	61	US-10-893-584-231	Sequence 231, App
68	169	22.0	1828	39	US-10-089-058-68	Sequence 68, Appl
69	169	22.0	1828	39	US-10-089-058A-68	Sequence 68, Appl
70	169	22.0	1828	61	US-10-893-584-210	Sequence 210, App
71	169	22.0	1831	39	US-10-089-058-19	Sequence 19, Appl
72	169	22.0	1831	39	US-10-089-058-61	Sequence 61, Appl
73	169	22.0	1831	39	US-10-089-058A-19	Sequence 19, Appl
74	169	22.0	1831	39	US-10-089-058A-61	Sequence 61, Appl
75	169	22.0	1831	61	US-10-893-584-161	Sequence 161, App
76	169	22.0	1831	61	US-10-893-584-203	Sequence 203, App
77	169	22.0	1834	39	US-10-089-058-12	Sequence 12, Appl
78	169	22.0	1834	39	US-10-089-058A-12	Sequence 12, Appl
79	169	22.0	1834	61	US-10-893-584-154	Sequence 154, App
80	169	22.0	1837	39	US-10-089-058-124	Sequence 124, App
81	169	22.0	1837	39	US-10-089-058A-124	Sequence 124, App
82	169	22.0	1837	61	US-10-893-584-266	Sequence 266, App
83	169	22.0	1843	39	US-10-089-058-117	Sequence 117, App
84	169	22.0	1843	39	US-10-089-058A-117	Sequence 117, App
85	169	22.0	1843	61	US-10-893-584-259	Sequence 259, App
86	169	22.0	1849	39	US-10-089-058-110	Sequence 110, App
87	169	22.0	1849	39	US-10-089-058A-110	Sequence 110, App
88	169	22.0	1849	61	US-10-893-584-252	Sequence 252, App
89	169	22.0	1855	39	US-10-089-058-5	Sequence 5, Appli
90	169	22.0	1855	39	US-10-089-058-47	Sequence 47, Appl
91	169	22.0	1855	39	US-10-089-058-75	Sequence 75, Appl
92	169	22.0	1855	39	US-10-089-058-82	Sequence 82, Appl
93	169	22.0	1855	39	US-10-089-058A-5	Sequence 5; Appli
94	169	22.0	1855	39	US-10-089-058A-47	Sequence 47, Appl
95	169	22.0	1855	39	US-10-089-058A-75	Sequence 75, Appl
96	169	22.0	1855	39	US-10-089-058A-82	Sequence 82, Appl
97	169	22.0	1855	61	US-10-893-584-147	Sequence 147, App
98	169	22.0	1855	61	US-10-893-584-189	Sequence 189, App
99	169	22.0	1855	61	US-10-893-584-217	Sequence 217, App
100	169	22.0	1855	61	US-10-893-584-224	Sequence 224, App

ALIGNMENTS

```
RESULT 1
US-11-084-080-15
; Sequence 15, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-15

Alignment Scores:
Pred. No.:                6.13e-110       Length:          2404
Score:                    726.00          Matches:         144
Percent Similarity:       96.6%           Conservative:    0
Best Local Similarity:    96.6%           Mismatches:      5
Query Match:              94.5%           Indels:          0
DB:                       66              Gaps:            0

US-10-758-902-9 (1-149) x US-11-084-080-15 (1-2404)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 884

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
```

```
Db        885 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 944

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60

Db        945 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1004

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80

Db       1005 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1064

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100

Db       1065 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1124

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120

Db       1125 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1184

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140

Db       1185 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 1244

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149

Db       1245 GCAATCCATGGTAAAACGATAAATGGT 1271
```

RESULT 2
US-11-084-080-19
; Sequence 19, Application US/11084080
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Alignment Scores:

Pred. No.:	6.13e-110	Length:	2404
Score:	726.00	Matches:	144
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	5
Query Match:	94.5%	Indels:	0
DB:	66	Gaps:	0

US-10-758-902-9 (1-149) x US-11-084-080-19 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20

Db       1643 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1702

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40

Db       1703 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 1762

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60

Db       1763 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1822

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80

Db       1823 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1882

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100

Db       1883 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1942

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120

Db       1943 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 2002

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140

Db       2003 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 2062

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149

Db       2063 GCAATCCATGGTAAAACGATAAATGGT 2089
```

RESULT 3
US-11-084-080-21
; Sequence 21, Application US/11084080
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-21

Alignment Scores:

Pred. No.:	6.13e-110	Length:	2404
Score:	726.00	Matches:	144
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	5
Query Match:	94.5%	Indels:	0
DB:	66	Gaps:	0

US-10-758-902-9 (1-149) x US-11-084-080-21 (1-2404)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20

Db        132 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 191

Qy         21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          192 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 251

Qy           41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          252 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 311

Qy           61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          312 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 371

Qy           81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          372 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 431

Qy          101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          432 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 491

Qy          121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                ||||||   |||||||||   |||||||||||||||   |||||||||||||||||||||
Db          492 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 551

Qy          141 AlaIleTrpGlyLysThrGlnAsnGly 149
                ||||||   |||||||||   ||||||
Db          552 GCAATCCATGGTAAAACGATAAATGGT 578
```

```
RESULT 4
US-11-084-080-23
; Sequence 23, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
;   LENGTH: 2404
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Alignment Scores:
Pred. No.:               6.13e-110     Length:        2404
Score:                   726.00        Matches:       144
Percent Similarity:      96.6%         Conservative:  0
Best Local Similarity:   96.6%         Mismatches:    5
Query Match:             94.5%         Indels:        0
DB:                      66            Gaps:          0

US-10-758-902-9 (1-149) x US-11-084-080-23 (1-2404)

Qy            1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          950 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 1009

Qy           21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1010 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 1069

Qy           41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1070 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1129

Qy           61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1130 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1189

Qy           81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1190 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1249

Qy          101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1250 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1309

Qy          121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
                ||||||   |||||||||   |||||||||||||||   |||||||||||||||||||||
Db         1310 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 1369

Qy          141 AlaIleTrpGlyLysThrGlnAsnGly 149
                ||||||   |||||||||   ||||||
Db         1370 GCAATCCATGGTAAAACGATAAATGGT 1396
```

```
RESULT 5
US-11-084-080-27
; Sequence 27, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 2431
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-011
US-11-084-080-27

Alignment Scores:
Pred. No.:               6.25e-110     Length:        2431
Score:                   726.00        Matches:       144
Percent Similarity:      96.6%         Conservative:  0
Best Local Similarity:   96.6%         Mismatches:    5
Query Match:             94.5%         Indels:        0
DB:                      66            Gaps:          0

US-10-758-902-9 (1-149) x US-11-084-080-27 (1-2431)

Qy            1 TyrAsnThrValSerPheAsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAsp 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          852 TACAACACCGTGTCATTTAACCTTGGAGAAGCTTATGAGTACCCCACTTTTATACAAGAT 911

Qy           21 LeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThr 40
```

```
Db        912 TTGCGCAATGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTGACACTACAAACC 971

Qy         41 IleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrVal 60

Db        972 ATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCGAAGAAAACAGTT 1031

Qy         61 LysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGly 80

Db       1032 AAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGACAAATGGGATGGC 1091

Qy         81 LysAspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPhePro 100

Db       1092 AAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGTAAACTTTTCCCA 1151

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120

Db       1152 GGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAACTTGTGAATGCT 1211

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140

Db       1212 GCCAAAGCTGATAGAAAGGCTCTCGAACTGGGGGTTAACAAATTGGAATTTTCCATTGAA 1271

Qy        141 AlaIleTrpGlyLysThrGlnAsnGly 149

Db       1272 GCAATCCATGGTAAAACGATAAATGGT 1298
```

RESULT 6
US-10-758-902-8
; Sequence 8, Application US/10758902
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenzo
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
; FILE REFERENCE: PNJ-005CN
; CURRENT APPLICATION NUMBER: US/10/758,902
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 09/445160
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: PCT/NL98/0336
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Bougainvillaea Spectabilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(361)
US-10-758-902-8

Alignment Scores:

Pred. No.:	1.66e-91	Length:	363
Score:	609.00	Matches:	120
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	79.3%	Indels:	0
DB:	60	Gaps:	0

US-10-758-902-9 (1-149) x US-10-758-902-8 (1-363)

```
Qy         17 PheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProVal 36

Db          2 TTTATACAAGATTTGCGCAACGAATTGGCTAAGGGCACACCAGTATGTCAACTTCCAGTG 61

Qy         37 ThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIleThrThrThrSer 56

Db         62 ACACTACAAACCATAGCCGATGACAAGCGATTTGTTCTAGTTGATATCACTACGACCTCG 121

Qy         57 LysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGlnAsp 76

Db        122 AAGAAAACAGTTAAGGTTGCTATAGATGTGACAGATGTGTATGTTGTGGGTTATCAAGAC 181

Qy         77 LysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThrValAlaThrSer 96

Db        182 AAATGGGATGGCAAAGATCGAGCTGTTTTCCTTGACAAGGTTCCTACTGTTGCAACTAGT 241

Qy         97 LysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLys 116

Db        242 AAACTTTTCCCAGGGGTGACTAATCGTGTAACGTTAACATTTGATGGCAGCTATCAGAAA 301

Qy        117 LeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGlu 136

Db        302 CTTGTGAATGCTGCCAAAGTGGATAGAAAGGATCTCGAACTGGGCGTCTACAAACTCGAG 361
```

RESULT 7
US-07-787-567A-13
; Sequence 13, Application US/07787567A
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/787,567A
; FILING DATE: 19911104
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Gruber, Lewis S.
; REGISTRATION NUMBER: 30,060
; REFERENCE/DOCKET NUMBER: 27129/30545
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-787-567A-13

Alignment Scores:

Pred. No.:	7.73e-25	Length:	913
Score:	220.50	Matches:	52
Percent Similarity:	59.9%	Conservative:	33
Best Local Similarity:	36.6%	Mismatches:	50
Query Match:	28.7%	Indels:	7
DB:	6	Gaps:	3

US-10-758-902-9 (1-149) x US-07-787-567A-13 (1-913)

```
Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21

Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141
```

```
Qy          22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
               |||       |||                 |||       :::|||:::          ||||||
Db         142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy          42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
               :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db         202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy          62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
               ||||||||||||||||||:::||||||||||||   |||:::                :::
Db         262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy          82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
               |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db         310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy         102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
               |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db         370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::::||||||:::       |||       :::|||
Db         427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy         142 IleTrp 143
               ::::::
Db         487 TTGTTT 492

RESULT 8
US-10-127-890-13
; Sequence 13, Application US/10127890
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 913 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-127-890-13

Alignment Scores:
Pred. No.:                7.73e-25        Length:          913
Score:                    220.50          Matches:         52
Percent Similarity:       59.9%           Conservative:    33
Best Local Similarity:    36.6%           Mismatches:      50
Query Match:              28.7%           Indels:          7
DB:                       41              Gaps:            3

US-10-758-902-9 (1-149) x US-10-127-890-13 (1-913)

Qy           4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
               |||:::|||:::|||           |||       |||       ||||||:::|||
Db          82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy          22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
               |||       |||                 |||       :::|||:::          ||||||
Db         142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy          42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
               :::|||   :::||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db         202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy          62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
               ||||||||||||||||||:::||||||||||||   |||:::                :::
Db         262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy          82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
               |||   :::   |||       :::   |||       |||   :::   ||||||   |||
Db         310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy         102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
               |||   ::::::||||||   :::   |||:::|||:::   |||       ||||||
Db         370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy         122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::::||||||:::       |||       :::|||
Db         427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy         142 IleTrp 143
               ::::::
Db         487 TTGTTT 492

RESULT 9
US-10-613-755-13
; Sequence 13, Application US/10613755
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
```

```
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/613,755
;           FILING DATE: 02-Jul-2003
;           CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/08/646,360
;           FILING DATE: 13-MAY-1996
;           APPLICATION NUMBER: PCT/US94/05348
;           FILING DATE: 12-MAY-1994
;           APPLICATION NUMBER: US 08/064,691
;           FILING DATE: 12-MAY-1993
;           APPLICATION NUMBER: US 07/988,430
;           FILING DATE: 09-DEC-1992
;           APPLICATION NUMBER: US 07/901,707
;           FILING DATE: 19-JUN-1992
;           APPLICATION NUMBER: US 07/787,567
;           FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;           NAME: McNicholas, Janet M.
;           REGISTRATION NUMBER: 32,918
;           REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 312/707-8889
;           TELEFAX: 312/707-9155
;           TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 913 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-613-755-13

Alignment Scores:
Pred. No.:              7.73e-25        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     52              Gaps:           3

US-10-758-902-9 (1-149) x US-10-613-755-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||          |||     |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              |||      :::|||:::         ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::              :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC-----------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                      |||::::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 10
US-10-717-243-13
; Sequence 13, Application US/10717243
;   GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 169
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;           STREET: 500 West Madison Street, 34th floor
;           CITY: Chicago
;           STATE: Illinois
;           COUNTRY: USA
;           ZIP: 60661
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/717,243
;           FILING DATE: 18-Nov-2003
;           CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/08/839,765
;           FILING DATE: 15-APR-1997
;           APPLICATION NUMBER: US 08/425,336
;           FILING DATE: 18-APR-1995
;           APPLICATION NUMBER: US 08/064,691
;           FILING DATE: 12-MAY-1993
;           APPLICATION NUMBER: US 07/988,430
;           FILING DATE: 09-DEC-1992
;           APPLICATION NUMBER: US 07/901,707
;           FILING DATE: 19-JUN-1992
;           APPLICATION NUMBER: US 07/787,567
;           FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;           NAME: McNicholas, Janet M.
;           REGISTRATION NUMBER: 32,918
;           REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 312/707-8889
;           TELEFAX: 312/707-9155
;           TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 913 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-717-243-13

Alignment Scores:
Pred. No.:              7.73e-25        Length:         913
Score:                  220.50          Matches:        52
Percent Similarity:     59.9%           Conservative:   33
Best Local Similarity:  36.6%           Mismatches:     50
Query Match:            28.7%           Indels:         7
DB:                     59              Gaps:           3
```

```
US-10-758-902-9 (1-149) x US-10-717-243-13 (1-913)

Qy          4 ValSerPheAsnLeu------GlyGluAlaTyrGluTyrProThrPheIleGlnAspLeu 21
              |||:::|||:::|||              |||      |||      ||||||:::|||
Db         82 GTTAACTTCGATTTGTCGACTGCCACTGCAAAAACCTACACAAAATTTATCGAAGATTTC 141

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                 |||      :::|||:::          ||||||
Db        142 AGGGCGACTCTTCCATTTAGCCATAAAGTGTATGATATACCTCTACTGTATTCCACTATT 201

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||   :::|||||||:::|||:::|||:::|||:::   :::   :::|||:::
Db        202 TCCGACTCCAGACGTTTCATACTCCTCGATCTTACAAGTTATGCATATGAAACCATCTCG 261

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||||||||   |||:::              :::
Db        262 GTGGCCATAGATGTGACGAACGTTTATGTTGTGGCGTATCGCACC------------CGC 309

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
              |||   :::   |||      :::   |||      |||   :::   ||||||   |||
Db        310 GATGTATCCTACTTTTTTAAAGAATCTCCTCCTGAAGCTTATAACATCCTATTCAAAGGT 369

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 |||   ::::::||||||   :::   |||:::|||:::   |||      ||||||
Db        370 ---ACGCGGAAAATTACACTGCCATATACCGGTAATTATGAAAATCTTCAAACTGCTGCA 426

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::::::||||||:::      |||      :::|||
Db        427 CACAAAATAAGAGAGAATATTGATCTTGGACTCCCTGCCTTGAGTAGTGCCATTACCACA 486

Qy        142 IleTrp 143
              ::::::
Db        487 TTGTTT 492

RESULT 11
US-09-905-247-2
; Sequence 2, Application US/09905247
; GENERAL INFORMATION:
;  APPLICANT: KE, YI-BAO
;  APPLICANT:  NIE, HUI-LING
;  TITLE OF INVENTION: Mutant Trichosanthin
;  FILE REFERENCE: 04399/000J615-US0
;  CURRENT APPLICATION NUMBER: US/09/905,247
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: CN 00119553.0
;  PRIOR FILING DATE: 2000-08-02
;  PRIOR APPLICATION NUMBER: CN 01103102.6
;  PRIOR FILING DATE: 2001-01-18
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 870
;   TYPE: DNA
;   ORGANISM: Trichosanthes Kirilowii M.
US-09-905-247-2

Alignment Scores:
Pred. No.:              1.36e-18      Length:          870
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     34            Gaps:            2

US-10-758-902-9 (1-149) x US-09-905-247-2 (1-870)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||            |||      ||||||   :::|||
Db         73 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 132

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                 :::      :::|||:::          ::::::
Db        133 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCAGTCTT 192

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        193 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 252

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||::::::||||||:::              |||
Db        253 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 303

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::          |||   |||          :::|||
Db        304 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 363

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::||||||||||   :::   |||:::|||::::::|||      ||||||
Db        364 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCA 423

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||::::::::::   ||||||:::      |||:::   :::|||
Db        424 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCTGCTTTGGACAGTGCCATTACCACT 483

Qy        142 IleTrp 143
              ::::::
Db        484 TTGTTT 489

RESULT 12
US-09-905-247A-2
; Sequence 2, Application US/09905247A
; GENERAL INFORMATION:
;  APPLICANT: Ke, Yi-Bao
;  APPLICANT:  Nie, Hui-Ling
;  TITLE OF INVENTION: MUTANT TRICHOSANTHIN
;  FILE REFERENCE: 04399/000J615-US0
;  CURRENT APPLICATION NUMBER: US/09/905,247A
;  CURRENT FILING DATE:  2001-07-13
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 870
;   TYPE: DNA
;   ORGANISM: Trichosanthes Kirilowii M.
US-09-905-247A-2

Alignment Scores:
Pred. No.:              1.36e-18      Length:          870
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     34            Gaps:            2

US-10-758-902-9 (1-149) x US-09-905-247A-2 (1-870)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||            |||      ||||||   :::|||
Db         73 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 132

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                 :::      :::|||:::          ::::::
Db        133 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCAGTCTT 192

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        193 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 252

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||::::::||||||:::              |||
Db        253 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 303

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::          |||   |||          :::|||
Db        304 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 363
```

```
Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||:::::::|||      ||||||
Db        364 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCA 423

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::      |||:::   :::|||
Db        424 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCTGCTTTGGACAGTGCCATTACCACT 483

Qy        142 IleTrp 143
                :::::
Db        484 TTGTTT 489

RESULT 13
US-07-739-143-3
; Sequence 3, Application US/07739143
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Venable, Baetjer, Howard & Civiletti
;      STREET:  1201 New York Avenue N.W., Suite 1000
;      CITY:  Washington
;      STATE:  DC
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/739,143
;      FILING DATE:  19910801
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ihnen, Jeffrey L.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  18604-090574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-962-4810
;      TELEFAX:  202-962-8300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  886 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chinese cucumber
;    IMMEDIATE SOURCE:
;      CLONE:  alpha-trichosanthin
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  8..877
US-07-739-143-3

Alignment Scores:
Pred. No.:              1.41e-18      Length:          886
Score:                  183.50        Matches:         44
Percent Similarity:     53.5%         Conservative:    32
Best Local Similarity:  31.0%         Mismatches:      61
Query Match:            23.9%         Indels:          5
DB:                     6             Gaps:            2

US-10-758-902-9 (1-149) x US-07-739-143-3 (1-886)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||           |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||           :::     :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::::||||||:::          |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::          |||   |||          :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::|||||||||   :::   |||:::|||:::::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                  |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                :::::
Db        491 TTGTTT 496

RESULT 14
US-08-480-432-3
; Sequence 3, Application US/08480432
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William 0.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
```

```
;       STREET:  1155 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  Patent in Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/480,432
;       FILING DATE:  07-JUNE-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 184,237
;       FILING DATE:  19-JAN-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 600,244
;       FILING DATE:  22-OCT-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 641,617
;       FILING DATE:  16-JAN-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 310,881
;       FILING DATE:  17-FEB-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 160,766
;       FILING DATE:  26-FEB-1988
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 160,771
;       FILING DATE:  26-FEB-1988
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 347,637
;       FILING DATE:  05-MAY-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 363,138
;       FILING DATE:  08-JUN-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 219,279
;       FILING DATE:  15-JUL-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Halluin, Albert P.
;       REGISTRATION NUMBER:  28,957
;       REFERENCE/DOCKET NUMBER:  8129-111
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-854-3660
;       TELEFAX:  415-854-3694
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  886 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Chinese cucumber
;     IMMEDIATE SOURCE:
;       CLONE:  alpha-trichosanthin
;     FEATURE:
;       NAME/KEY:  CDS (B) LOCATION: 8. .877
;       LOCATION:  8. .877
US-08-480-432-3

Alignment Scores:
Pred. No.:              1.41e-18        Length:         886
Score:                  183.50          Matches:        44
Percent Similarity:     53.5%           Conservative:   32
Best Local Similarity:  31.0%           Mismatches:     61
Query Match:            23.9%           Indels:         5
DB:                     13              Gaps:           2

US-10-758-902-9 (1-149) x US-08-480-432-3 (1-886)
```

```
Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||             |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||             :::      :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                    :::|||:::   |||:::   :::|||      :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::             |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                       |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                    :::||||||||||   :::   |||:::|||::::::|||      ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::   ||||||:::      |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
                 ::::::
Db        491 TTGTTT 496

RESULT 15
US-10-280-679B-3
; Sequence 3, Application US/10280679B
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
;  FILE REFERENCE: LSBC-0109-US03
;  CURRENT APPLICATION NUMBER: US/10/280,679B
;  CURRENT FILING DATE:  2000-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 886
;   TYPE: DNA
;   ORGANISM: Chinese Cucumber
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (8)..(877)
;   OTHER INFORMATION:
```

US-10-280-679B-3

Alignment Scores:

Pred. No.:	1.41e-18	Length:	886
Score:	183.50	Matches:	44
Percent Similarity:	53.5%	Conservative:	32
Best Local Similarity:	31.0%	Mismatches:	61
Query Match:	23.9%	Indels:	5
DB:	42	Gaps:	2

US-10-758-902-9 (1-149) x US-10-280-679B-3 (1-886)

```
Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||     |||         |||     ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||     |||              :::     :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::  :::|||     :::  :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::|||||:::           |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 :::|||||||||   :::  |||:::|||::::::|||     ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                |||:::::::::   ||||||:::     |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496
```

RESULT 16
US-10-280-725B-3
; Sequence 3, Application US/10280725B
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Recombinant Viral Nucleic Acids
; FILE REFERENCE: LSBC-0109-US02
; CURRENT APPLICATION NUMBER: US/10/280,725B
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/557,941
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 08/484,341
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600,244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641,617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737,899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739,143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310,881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160,766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160,771
; PRIOR FILING DATE: 1988-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 886
; TYPE: DNA
; ORGANISM: Chinese Cucumber
; FEATURE:
; NAME/KEY: exon
; LOCATION: (8)..(877)
; OTHER INFORMATION:
US-10-280-725B-3

Alignment Scores:

Pred. No.:	1.41e-18	Length:	886
Score:	183.50	Matches:	44
Percent Similarity:	53.5%	Conservative:	32
Best Local Similarity:	31.0%	Mismatches:	61
Query Match:	23.9%	Indels:	5
DB:	42	Gaps:	2

US-10-758-902-9 (1-149) x US-10-280-725B-3 (1-886)

```
Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||     |||         |||     ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||     |||              :::     :::|||:::         ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                 :::|||:::   |||:::  :::|||     :::  :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::|||||:::           |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                    |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                 :::|||||||||   :::  |||:::|||::::::|||     ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                |||:::::::::   ||||||:::     |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496
```

RESULT 17
US-09-663-826-6
; Sequence 6, Application US/09663826
; GENERAL INFORMATION:
; APPLICANT: Russel, David R.
; Fuller, James T.
; TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
; PROTEIN TOXINS IN PLANT CELLS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,826
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/902,486
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Seay, Nicholas J.
;             REGISTRATION NUMBER: 27386
;             REFERENCE/DOCKET NUMBER: 670513.90261
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 608-251-5000
;             TELEFAX: 608-251-9166
;    INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 758 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  3..748
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-663-826-6

Alignment Scores:
Pred. No.:              5.11e-18        Length:         758
Score:                  179.50          Matches:        44
Percent Similarity:     54.5%           Conservative:   34
Best Local Similarity:  30.8%           Mismatches:     58
Query Match:            23.4%           Indels:         7
DB:                     28              Gaps:           3

US-10-758-902-9 (1-149) x US-09-663-826-6 (1-758)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||  |||     |||           |||      ||||||:::|||
Db          9 GTGAGCTTTCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 68

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||       |||                 |||       :::|||:::          :::|||
Db         69 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 128

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::          |||:::   |||:::   :::|||      :::   :::|||:::
Db        129 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 188

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||:::::||||||
Db        189 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT-----------GCCGGT 236

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||   :::   |||   ::::::                    :::|||   :::|||
Db        237 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 296

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                     :::|||||||||   :::   |||:::|||:::::|||      |||
Db        297 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 356

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||          |||:::::::::   ||||||:::      |||:::   :::|||
Db        357 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 416

Qy        141 AlaIleTrp 143
                 ::::::
Db        417 ACTTTGTAT 425

RESULT 18
US-11-042-707-16
; Sequence 16, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 16
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1
US-11-042-707-16

Alignment Scores:
Pred. No.:              5.16e-18        Length:         762
Score:                  179.50          Matches:        50
Percent Similarity:     57.1%           Conservative:   26
Best Local Similarity:  37.6%           Mismatches:     48
Query Match:            23.4%           Indels:         9
DB:                     65              Gaps:           4

US-10-758-902-9 (1-149) x US-11-042-707-16 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   :::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::|||   :::||||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   :::|||      ||||||||||||||:::
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGGTTACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||  ||||||                |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||       |||   :::   ||||||  |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||           |||           |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 19
US-11-042-707-19
; Sequence 19, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
```

```
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 19
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1
US-11-042-707-19

Alignment Scores:
Pred. No.:              5.16e-18      Length:         762
Score:                  179.50        Matches:        50
Percent Similarity:     57.1%         Conservative:   26
Best Local Similarity:  37.6%         Mismatches:     48
Query Match:            23.4%         Indels:         9
DB:                     65            Gaps:           4

US-10-758-902-9 (1-149) x US-11-042-707-19 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   :::|||      |||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTGTTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 20
US-11-042-707-17
; Sequence 17, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 17
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-11-042-707-17

Alignment Scores:
Pred. No.:              5.23e-18      Length:         768
Score:                  179.50        Matches:        49
Percent Similarity:     56.7%         Conservative:   27
Best Local Similarity:  36.6%         Mismatches:     49
Query Match:            23.4%         Indels:         9
DB:                     65            Gaps:           4

US-10-758-902-9 (1-149) x US-11-042-707-17 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   :::|||      |||||||||||||||:::
Db        166 GTGGAGCTCACCAACCAGGGGCAGGACTCGATCACGGCCGCCATCGACGTTACCAATGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThr---AsnArgValThrLeu 108
              |||      |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGCACCACCCGAGATAGATCCTCTCTC 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||      |||         |||         |||      :::
Db        334 CCATTCACTGGAAGCTACACCGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATC 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        391 CCTCTCGGTATAGAGCAACTCATTCAATCCGTCTCTGCGCTT 432

RESULT 21
US-11-042-707-20
; Sequence 20, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 20
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-11-042-707-20

Alignment Scores:
Pred. No.:              5.23e-18      Length:         768
Score:                  179.50        Matches:        49
Percent Similarity:     56.7%         Conservative:   27
Best Local Similarity:  36.6%         Mismatches:     49
Query Match:            23.4%         Indels:         9
```

```
DB:                    65            Gaps:          4

US-10-758-902-9 (1-149) x US-11-042-707-20 (1-768)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::        ::::::|||   :::||||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||         :::   ::::::      ||||||||||||||:::
Db        166 GTTGAATTGACTAACCAAGGACAGGATAGTATTACTGCTGCTATTGATGTGACTAACGCT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                ||:::::::   ||||||
Db        226 TATGTTGTTGCATATCAG------------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuProProGlyValThr---AsnArgValThrLeu 108
              |||       |||   :::   ||||||   |||   |||   :::|||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGTACAACACGGGATAGAAGTTCTTTG 333

Qy        109 ThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeu 128
              |||   |||||||||       |||           |||           |||      :::
Db        334 CCTTTTACTGGTTCTTATACAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATT 390

Qy        129 GluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||       |||:::   |||:::
Db        391 CCATTGGGAATTGAGCAGTTGATCCAGAGTGTTTCTGCTTTG 432

RESULT 22
US-09-663-826-14
; Sequence 14, Application US/09663826
;   GENERAL INFORMATION:
;        APPLICANT: Russel, David R.
;                   Fuller, James T.
;        TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
;                            PROTEIN TOXINS IN PLANT CELLS
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Quarles & Brady
;             STREET: 1 South Pinckney Street
;             CITY: Madison
;             STATE: WI
;             COUNTRY: US
;             ZIP: 53701-2113
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,826
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/902,486
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Seay, Nicholas J.
;             REGISTRATION NUMBER: 27386
;             REFERENCE/DOCKET NUMBER: 670513.90261
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 608-251-5000
;             TELEFAX: 608-251-9166
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1499 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  3..1493
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-663-826-14

Alignment Scores:
Pred. No.:                1.68e-17        Length:          1499
Score:                    179.50          Matches:         44
Percent Similarity:       54.5%           Conservative:    34
Best Local Similarity:    30.8%           Mismatches:      58
Query Match:              23.4%           Indels:          7
DB:                       28              Gaps:            3

US-10-758-902-9 (1-149) x US-09-663-826-14 (1-1499)

Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||      |||          |||       ||||||::::::|||
Db          9 GTGAGCTTTCGTTTATCAGGTGCTACAACCACATCCTATGGAGTTTTCATTAAAAATCTG 68

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||                |||      :::|||:::         :::|||
Db         69 AGAGAAGCTCTTCCATACGAAAGGAAAGTGTACAATATACCGCTATTACGTTCAAGTATT 128

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
              :::        |||:::   |||:::   :::|||      :::   :::|||:::
Db        129 TCAGGTTCAGGACGCTACACATTACTCCATCTCACAAATTACGCGGATGAAACCATCTCA 188

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||:::|||||||||:::||||||::::::||||||
Db        189 GTGGCAGTAGACGTAACAAACGTCTATATTATGGGGTATCTT------------GCCGGT 236

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLys---LeuPhePro 100
              |||   :::   |||   ::::::                   :::|||   :::|||
Db        237 GATGTGTCCTATTTTTTCAACGAGGCTTCAGCAACAGAAGCTGCAAAATTCGTATTCAAA 296

Qy        101 GlyValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                      :::|||||||||   :::   |||:::|||::::::|||      |||
Db        297 GATGCTAAGAAAAAAGTGACGCTTCCATATTCAGGCAATTACGAAAGGCTTCAAACTGCT 356

Qy        121 AlaLysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGlu 140
              |||         |||:::::::::   ||||||:::      |||:::   :::|||
Db        357 GCAGGAAAAATAAGAGAAAATATTCCACTTGGACTCCCAGCTTTGGACAGTGCCATTACC 416

Qy        141 AlaIleTrp 143
                 ::::::
Db        417 ACTTTGTAT 425

RESULT 23
US-09-347-064-7
; Sequence 7, Application US/09347064
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064-7
```

```
Alignment Scores:
Pred. No.:              1.64e-17        Length:         756
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     22              Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064-7 (1-756)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::      ||||||||||||||::::::
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||  ||||||                    |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||  |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||         |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 24
US-09-347-064-7
; Sequence 7, Application US/09347064A
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064-7

Alignment Scores:
Pred. No.:              1.64e-17        Length:         756
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     22              Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064-7 (1-756)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::      ||||||||||||||::::::
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||  ||||||                    |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||  |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||         |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 25
US-09-347-064F-7
; Sequence 7, Application US/09347064F
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION:  Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION:  album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064F
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064F-7

Alignment Scores:
Pred. No.:              1.64e-17        Length:         756
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     22              Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064F-7 (1-756)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
```

```
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
Db        274 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 26
US-09-347-064G-7
; Sequence 7, Application US/09347064G
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION:  Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION:  album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064G
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064G-7

Alignment Scores:
Pred. No.:                1.64e-17      Length:          756
Score:                    176.50        Matches:         49
Percent Similarity:       57.1%         Conservative:    27
Best Local Similarity:    36.8%         Mismatches:      48
Query Match:              23.0%         Indels:          9
DB:                       22            Gaps:            4

US-10-758-902-9 (1-149) x US-09-347-064G-7 (1-756)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
Db        274 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 27
US-09-347-064H-7
; Sequence 7, Application US/09347064H
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on Ribosome-
;  TITLE OF INVENTION:  Inactivating Proteins of
;  TITLE OF INVENTION:  the Mistletoe Viscum album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064H
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064H-7

Alignment Scores:
Pred. No.:                1.64e-17      Length:          756
Score:                    176.50        Matches:         49
Percent Similarity:       57.1%         Conservative:    27
Best Local Similarity:    36.8%         Mismatches:      48
Query Match:              23.0%         Indels:          9
DB:                       22            Gaps:            4

US-10-758-902-9 (1-149) x US-09-347-064H-7 (1-756)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
Db        274 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 28
```

```
US-09-347-064H-43
; Sequence 43, Application US/09347064H
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on Ribosome-
;  TITLE OF INVENTION:  Inactivating Proteins of
;  TITLE OF INVENTION:  the Mistletoe Viscum album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064H
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064H-43

Alignment Scores:
Pred. No.:              1.64e-17        Length:         756
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     22              Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064H-43 (1-756)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||           ::::::      |||||||||||||||::::::
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                        |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 29
US-09-347-064-1
; Sequence 1, Application US/09347064
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064-1

Alignment Scores:
Pred. No.:              1.67e-17        Length:         762
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     22              Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064-1 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||           ::::::      |||||||||||||||::::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                        |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 30
US-09-347-064-1
; Sequence 1, Application US/09347064A
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 762
```

```
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064-1

Alignment Scores:
Pred. No.:              1.67e-17        Length:         762
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     22              Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064-1 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||               ::::::      ||||||||||||||||::::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 31
US-09-347-064F-1
; Sequence 1, Application US/09347064F
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION:  Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION:  album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064F
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064F-1

Alignment Scores:
Pred. No.:              1.67e-17        Length:         762
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     22              Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064F-1 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||               ::::::      ||||||||||||||||::::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||                  |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||         |||         |||      :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 32
US-09-347-064G-1
; Sequence 1, Application US/09347064G
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION:  Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION:  album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064G
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064G-1

Alignment Scores:
Pred. No.:              1.67e-17        Length:         762
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     22              Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064G-1 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::||||||||||||
```

```
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||:::::::|||                :::::      |||||||||||||||:::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||  ||||||                    |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 33
US-09-347-064H-1
; Sequence 1, Application US/09347064H
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on Ribosome-
;  TITLE OF INVENTION:  Inactivating Proteins of
;  TITLE OF INVENTION:  the Mistletoe Viscum album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064H
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Viscum album
US-09-347-064H-1

Alignment Scores:
Pred. No.:              1.67e-17        Length:         762
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     22              Gaps:           4

US-10-758-902-9 (1-149) x US-09-347-064H-1 (1-762)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         52 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 111

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        112 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 171

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                :::::      |||||||||||||||:::::
Db        172 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 231

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||  ||||||                    |||::::::   ||||||
Db        232 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 279

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        280 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 336

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        337 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 393

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        394 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 432

RESULT 34
US-10-499-297-1
; Sequence 1, Application US/10499297
; GENERAL INFORMATION:
;  APPLICANT: Muthing, Johannes
;  APPLICANT:  Peter-Katalinic, Jasna
;  APPLICANT:  Langer, Martin
;  APPLICANT:  Mockel, Babette
;  APPLICANT:  Eck, Jurgen
;  TITLE OF INVENTION: METHOD FOR DETERMINATION OF THE
;  TITLE OF INVENTION:  RESPONSIVENESS OF AN INDIVIDUAL TO MISTLETOE LECTIN
;  FILE REFERENCE: VOSS-P01-010
;  CURRENT APPLICATION NUMBER: US/10/499,297
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: EP 01130745.1
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 855
;   TYPE: DNA
;   ORGANISM: Viscum album
US-10-499-297-1

Alignment Scores:
Pred. No.:              2.04e-17        Length:         855
Score:                  176.50          Matches:        49
Percent Similarity:     57.1%           Conservative:   27
Best Local Similarity:  36.8%           Mismatches:     48
Query Match:            23.0%           Indels:         9
DB:                     50              Gaps:           4

US-10-758-902-9 (1-149) x US-10-499-297-1 (1-855)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db        145 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 204

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         :::::::|||   :::|||||||||||
Db        205 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 264

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                :::::      |||||||||||||||:::::
Db        265 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 324

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||  ||||||                    |||::::::   ||||||
Db        325 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 372

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
                 |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        373 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 429

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        430 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 486

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::   :::|||      |||:::   |||:::
Db        487 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 525
```

```
RESULT 35
US-11-042-707-15
; Sequence 15, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 15
;   LENGTH: 1596
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: MLA-I
US-11-042-707-15

Alignment Scores:
Pred. No.:              6.06e-17      Length:          1596
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     65            Gaps:            4

US-10-758-902-9 (1-149) x US-11-042-707-15 (1-1596)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAATACTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::      |||||||||||||||::::::
Db        166 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||           |||::::::   ||||||
Db        226 TACGTCGTGGCTTACCAA-----------GCAGGCGACCAATCCTACTTTTTGCGCGAC 273

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCACCACGCGGCGCGGAAACGCACCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        331 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::  :::|||      |||:::   |||:::
Db        388 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 426

RESULT 36
US-11-042-707-18
; Sequence 18, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 18
;   LENGTH: 1596
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: MLI (matched)
US-11-042-707-18

Alignment Scores:
Pred. No.:              6.06e-17      Length:          1596
Score:                  176.50        Matches:         49
Percent Similarity:     57.1%         Conservative:    27
Best Local Similarity:  36.8%         Mismatches:      48
Query Match:            23.0%         Indels:          9
DB:                     65            Gaps:            4

US-10-758-902-9 (1-149) x US-11-042-707-18 (1-1596)

Qy         13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
              ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         46 GAGTATTTTAGATTTATTACTTTGTTGAGGGATTACGTTAGTTCTGGTTCTTTCAGTAAC 105

Qy         33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
              ::::::|||:::      |||:::         ::::::|||   :::|||||||||||
Db        106 GAAATTCCTTTGCTTAGACAATCTACTATTCCAGTTTCTGATGCTCAGCGTTTCGTTCTT 165

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
              |||::::::|||                ::::::      |||||||||||||||::::::
Db        166 GTTGAATTGACTAACCAAGGAGGTGATAGTATTACTGCTGCTATTGATGTGACTAACCTT 225

Qy         70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
              |||||||||   ||||||           |||::::::   ||||||
Db        226 TATGTTGTTGCATATCAG-----------GCTGGTGATCAGTCTTATTTCCTTAGGGAT 273

Qy         90 ValProThrValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThr 109
              |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db        274 GCTCCTAGAGGAGCTGAGACTCATTTGTTTACTGGT---ACAACACGGAGTTCTTTGCCT 330

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              |||:::|||||||||      |||          |||          |||      :::
Db        331 TTTAACGGTTCTTATCCAGACTTGGAAAGATATGCTGGT---CACAGAGATCAAATTCCA 387

Qy        130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
              ||||||:::  :::|||      |||:::   |||:::
Db        388 TTGGGAATTGATCAGTTGATCCAGAGTGTTACTGCTTTG 426

RESULT 37
US-10-499-297-5
; Sequence 5, Application US/10499297
; GENERAL INFORMATION:
;  APPLICANT: Muthing, Johannes
;  APPLICANT:  Peter-Katalinic, Jasna
;  APPLICANT:  Langer, Martin
;  APPLICANT:  Mockel, Babette
;  APPLICANT:  Eck, Jurgen
;  TITLE OF INVENTION: METHOD FOR DETERMINATION OF THE
;  TITLE OF INVENTION:  RESPONSIVENESS OF AN INDIVIDUAL TO MISTLETOE LECTIN
;  FILE REFERENCE: VOSS-P01-010
;  CURRENT APPLICATION NUMBER: US/10/499,297
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: EP 01130745.1
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
```

```
;   LENGTH: 1958
;   TYPE: DNA
;   ORGANISM: Viscum album
US-10-499-297-5

Alignment Scores:
Pred. No.:                8.66e-17        Length:         1958
Score:                    176.50          Matches:        49
Percent Similarity:       57.1%           Conservative:   27
Best Local Similarity:    36.8%           Mismatches:     48
Query Match:              23.0%           Indels:         9
DB:                       50              Gaps:           4

US-10-758-902-9 (1-149) x US-10-499-297-5 (1-1958)

Qy          13 GluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCys 32
               ||||||      ||||||      ||||||:::   ::::::   |||:::
Db         199 GAATATTTCCGGTTCATCACGCTTCTCCGAGATTATGTCTCAAGCGGAAGCTTTTCCAAT 258

Qy          33 GlnLeuProValThrLeuGlnThr---------IleAlaAspAspLysArgPheValLeu 49
               ::::::|||:::      |||:::         :::::::|||   :::||||||||||||
Db         259 GAGATACCACTCTTGCGTCAGTCTACGATCCCCGTCTCCGATGCGCAAAGATTTGTCTTG 318

Qy          50 ValAspIleThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspVal 69
               |||::::::|||               ::::::      |||||||||||||||::::::
Db         319 GTGGAGCTCACCAACCAGGGGGGAGACTCGATCACGGCCGCCATCGACGTTACCAATCTG 378

Qy          70 TyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLys 89
               |||||||||  ||||||                  |||::::::   ||||||
Db         379 TACGTCGTGGCTTACCAA------------GCAGGCGACCAATCCTACTTTTTGCGCGAC 426

Qy          90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
               |||      |||   :::   ||||||   |||   |||   |||   :::|||
Db         427 GCACCACGCGGCGCGGAAACGCATCTCTTCACCGGC---ACCACCCGATCCTCTCTCCCA 483

Qy         110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
               |||:::||||||||||      |||         |||         |||       :::
Db         484 TTCAACGGAAGCTACCCTGATCTGGAGCGATACGCCGGA---CATAGGGACCAGATCCCT 540

Qy         130 LeuGlyValTyrLysLeuGluPheSerIleGluAlaIle 142
               ||||||:::   :::|||      |||:::   |||:::
Db         541 CTCGGTATAGACCAACTCATTCAATCCGTCACGGCGCTT 579

RESULT 38
US-10-800-052-35
; Sequence 35, Application US/10800052
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 2788
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: pWKK-21
US-10-800-052-35

Alignment Scores:
Pred. No.:                6.31e-16        Length:         2788
Score:                    173.00          Matches:        52
Percent Similarity:       52.2%           Conservative:   31
Best Local Similarity:    32.7%           Mismatches:     60
Query Match:              22.5%           Indels:         16
DB:                       61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-35 (1-2788)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||             |||             |||      ||||||
Db        1288 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1347

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db        1348 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1407

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::|||||||||:::::::
Db        1408 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1467

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        1468 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1527

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                              :::   |||   |||              ::::::
Db        1528 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1575

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        1576 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1635

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||           |||          |||:::::::::|||||||||
Db        1636 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1695

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::              |||   ||||||
Db        1696 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1752

RESULT 39
US-10-800-052-2
; Sequence 2, Application US/10800052
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 2803
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Plasmid pWKK-500.
US-10-800-052-2

Alignment Scores:
Pred. No.:                6.37e-16        Length:         2803
Score:                    173.00          Matches:        52
Percent Similarity:       52.2%           Conservative:   31
Best Local Similarity:    32.7%           Mismatches:     60
Query Match:              22.5%           Indels:         16
DB:                       61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-2 (1-2803)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||             |||             |||      ||||||
Db        1402 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1461

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db        1462 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1521

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::|||||||||:::::::
Db        1522 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1581

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
```

```
Db       1582 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1641

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db       1642 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1689

Qy         93 ValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db       1690 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1749

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db       1750 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1809

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147

Db       1810 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1866
```

RESULT 40
US-10-800-052-37
; Sequence 37, Application US/10800052
; GENERAL INFORMATION:
; APPLICANT: Keener, William K
; TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
; FILE REFERENCE: B-221
; CURRENT APPLICATION NUMBER: US/10/800,052
; CURRENT FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pWKK-15
US-10-800-052-37

Alignment Scores:

Pred. No.:	6.38e-16	Length:	2805
Score:	173.00	Matches:	52
Percent Similarity:	52.2%	Conservative:	31
Best Local Similarity:	32.7%	Mismatches:	60
Query Match:	22.5%	Indels:	16
DB:	61	Gaps:	6

US-10-758-902-9 (1-149) x US-10-800-052-37 (1-2805)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db       1405 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1464

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db       1465 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1524

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db       1525 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1584

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db       1585 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1644

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db       1645 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1692

Qy         93 ValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db       1693 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1752

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db       1753 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1812

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147

Db       1813 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1869
```

RESULT 41
US-10-800-052-20
; Sequence 20, Application US/10800052
; GENERAL INFORMATION:
; APPLICANT: Keener, William K
; TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
; FILE REFERENCE: B-221
; CURRENT APPLICATION NUMBER: US/10/800,052
; CURRENT FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 2869
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Coding region of pWKK-700.
US-10-800-052-20

Alignment Scores:

Pred. No.:	6.63e-16	Length:	2869
Score:	173.00	Matches:	52
Percent Similarity:	52.2%	Conservative:	31
Best Local Similarity:	32.7%	Mismatches:	60
Query Match:	22.5%	Indels:	16
DB:	61	Gaps:	6

US-10-758-902-9 (1-149) x US-10-800-052-20 (1-2869)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db       1486 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1545

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db       1546 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1605

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db       1606 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1665

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db       1666 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1725

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db       1726 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1773

Qy         93 ValAlaThrSerLysLeuProProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db       1774 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1833

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db       1834 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1893

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147

Db       1894 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1950
```

RESULT 42
US-10-800-052-26
; Sequence 26, Application US/10800052
; GENERAL INFORMATION:
; APPLICANT: Keener, William K

```
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 2878
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: pWKK-800
US-10-800-052-26

Alignment Scores:
Pred. No.:              6.67e-16        Length:         2878
Score:                  173.00          Matches:        52
Percent Similarity:     52.2%           Conservative:   31
Best Local Similarity:  32.7%           Mismatches:     60
Query Match:            22.5%           Indels:         16
DB:                     61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-800-052-26 (1-2878)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||              |||      ||||||
Db       1495 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 1554

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                :::   :::|||      |||      |||      |||      ::::::||||||
Db       1555 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 1614

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::|||||:::|||||||::::::
Db       1615 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGACCTCTCAAATCAT 1674

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db       1675 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 1734

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||            ::::::
Db       1735 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 1782

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db       1783 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 1842

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db       1843 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 1902

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                ||||||   :::|||   |||::::::            |||   ||||||
Db       1903 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 1959

RESULT 43
US-11-010-795-23
; Sequence 23, Application US/11010795
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  DI, RONG
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
;  TITLE OF INVENTION:  RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
;  FILE REFERENCE: OCIRS 3.0-085
;  CURRENT APPLICATION NUMBER: US/11/010,795
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: 60/529,348
;  PRIOR FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
;   LENGTH: 807
;   TYPE: DNA
;   ORGANISM: Ricinus communis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(804)
US-11-010-795-23

Alignment Scores:
Pred. No.:              3.46e-16        Length:         807
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     65              Gaps:           6

US-10-758-902-9 (1-149) x US-11-010-795-23 (1-807)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||              |||      ||||||
Db         19 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 78

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                :::   :::|||      |||      |||      |||      ::::::||||||
Db         79 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 138

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::|||||:::|||||||::::::
Db        139 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 198

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        199 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTAGGCTACCGT 258

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||            ::::::
Db        259 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 306

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        307 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 366

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        367 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 426

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                ||||||   :::|||   |||::::::            |||   ||||||
Db        427 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 483

RESULT 44
US-08-406-801-18
; Sequence 18, Application US/08406801
;  GENERAL INFORMATION:
;    APPLICANT:  Wright, Andrew F.
;    APPLICANT:  Blakey, David C.
;    APPLICANT:  Fitton, John E.
;    APPLICANT:  Lindholm, Leif
;    APPLICANT:  Lind, Peter
;    APPLICANT:  Holmgren, Jan
;    TITLE OF INVENTION:  Conjugates
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/406,801
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/908,269
;      FILING DATE:  02-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  PNK/3893/96491/MJW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1140 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-406-801-18

Alignment Scores:
Pred. No.:              6.33e-16        Length:         1140
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     13              Gaps:           6

US-10-758-902-9 (1-149) x US-08-406-801-18 (1-1140)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        158 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 217

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                :::   :::|||      |||      |||      |||      ::::::||||||
Db        218 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 277

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::|||||:::|||||:::::::::
Db        278 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 337

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        338 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 397

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||            ::::::
Db        398 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 445

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        446 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 505

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        506 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 565

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        566 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 622

RESULT 45
US-08-406-801-33
; Sequence 33, Application US/08406801
;  GENERAL INFORMATION:
;    APPLICANT:  Wright, Andrew F.
;    APPLICANT:  Blakey, David C.
;    APPLICANT:  Fitton, John E.
;    APPLICANT:  Lindholm, Leif
;    APPLICANT:  Lind, Peter
;    APPLICANT:  Holmgren, Jan
;    TITLE OF INVENTION:  Conjugates
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/406,801
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/908,269
;      FILING DATE:  02-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  PNK/3893/96491/MJW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1140 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  143..943
US-08-406-801-33

Alignment Scores:
Pred. No.:              6.33e-16        Length:         1140
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     13              Gaps:           6

US-10-758-902-9 (1-149) x US-08-406-801-33 (1-1140)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        158 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 217

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                :::   :::|||      |||      |||      |||      ::::::||||||
Db        218 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 277

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::|||||:::|||||:::::::::
Db        278 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 337

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   ||||||||||||||:::
Db        338 GCAGAGCTTTCTGTTACATTAGCCCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 397

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                           :::   |||   |||            ::::::
Db        398 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 445
```

```
Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        446 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 505

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        506 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 565

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        566 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 622
```

RESULT 46
US-10-893-584-273
; Sequence 273, Application US/10893584
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 273
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ricin-like toxin (TST10054)
US-10-893-584-273

Alignment Scores:

Pred. No.:	1.17e-15	Length:	1623
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	61	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-273 (1-1623)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db         16 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 75

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db         76 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 135

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        136 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 195

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        196 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 255

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        256 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 303

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        304 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 363

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        364 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 423

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        424 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 480
```

RESULT 47
US-10-089-058-54
; Sequence 54, Application US/10089058
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP 313
US-10-089-058-54

Alignment Scores:

Pred. No.:	1.41e-15	Length:	1807
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058-54 (1-1807)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534
```

```
Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 48
US-10-089-058A-54
; Sequence 54, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 1807
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-54

Alignment Scores:
Pred. No.:              1.41e-15      Length:          1807
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     39            Gaps:            6

US-10-758-902-9 (1-149) x US-10-089-058A-54 (1-1807)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      :::::::|||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 49
US-10-893-584-196
; Sequence 196, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
;   LENGTH: 1807
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-196

Alignment Scores:
Pred. No.:              1.41e-15      Length:          1807
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     61            Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-196 (1-1807)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      :::::::|||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 50
US-10-089-058-26
; Sequence 26, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
```

```
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 1810
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP304
US-10-089-058-26

Alignment Scores:
Pred. No.:              1.42e-15        Length:         1810
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058-26 (1-1810)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::|||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                      :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 51
US-10-089-058A-26
; Sequence 26, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 1810
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-26

Alignment Scores:
Pred. No.:              1.42e-15        Length:         1810
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058A-26 (1-1810)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::|||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                      :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 52
US-10-893-584-168
; Sequence 168, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 168
;   LENGTH: 1810
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-168

Alignment Scores:
Pred. No.:              1.42e-15        Length:         1810
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-168 (1-1810)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||              ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::              |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 53
US-10-089-058-103
; Sequence 103, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 1813
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP322
US-10-089-058-103

Alignment Scores:
Pred. No.:              1.42e-15        Length:         1813
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058-103 (1-1813)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||              ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::              |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 54
US-10-089-058A-103
; Sequence 103, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 1813
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-103

Alignment Scores:
Pred. No.:              1.42e-15        Length:         1813
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     39              Gaps:           6
```

```
US-10-758-902-9 (1-149) x US-10-089-058A-103 (1-1813)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 55
US-10-893-584-245
; Sequence 245, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
;   LENGTH: 1813
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-245

Alignment Scores:
Pred. No.:              1.42e-15      Length:          1813
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     61            Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-245 (1-1813)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 56
US-10-089-058-96
; Sequence 96, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
;   LENGTH: 1819
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP321
US-10-089-058-96

Alignment Scores:
Pred. No.:              1.43e-15      Length:          1819
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     39            Gaps:            6

US-10-758-902-9 (1-149) x US-10-089-058-96 (1-1819)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246
```

```
Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 57
US-10-089-058A-96
; Sequence 96, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
;   LENGTH: 1819
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-96

Alignment Scores:
Pred. No.:              1.43e-15      Length:          1819
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     39            Gaps:            6

US-10-758-902-9 (1-149) x US-10-089-058A-96 (1-1819)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 58
US-10-893-584-238
; Sequence 238, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
;   LENGTH: 1819
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-238

Alignment Scores:
Pred. No.:              1.43e-15      Length:          1819
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     61            Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-238 (1-1819)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414
```

```
Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 59
US-10-089-058-33
; Sequence 33, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP305
US-10-089-058-33

Alignment Scores:
Pred. No.:              1.43e-15      Length:          1822
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     39            Gaps:            6

US-10-758-902-9 (1-149) x US-10-089-058-33 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 60
US-10-089-058-40
; Sequence 40, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP308
US-10-089-058-40

Alignment Scores:
Pred. No.:              1.43e-15      Length:          1822
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     39            Gaps:            6

US-10-758-902-9 (1-149) x US-10-089-058-40 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                 :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||         |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
              ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 61
US-10-089-058A-33
; Sequence 33, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-33

Alignment Scores:
Pred. No.:              1.43e-15      Length:          1822
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     39            Gaps:            6

US-10-758-902-9 (1-149) x US-10-089-058A-33 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||       |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||  |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 62
US-10-089-058A-40
; Sequence 40, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-40

Alignment Scores:
Pred. No.:              1.43e-15      Length:          1822
Score:                  169.00        Matches:         51
Percent Similarity:     52.2%         Conservative:    32
Best Local Similarity:  32.1%         Mismatches:      60
Query Match:            22.0%         Indels:          16
DB:                     39            Gaps:            6

US-10-758-902-9 (1-149) x US-10-089-058A-40 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||       |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||  |||           ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 63
US-10-893-584-175
; Sequence 175, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
```

```
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-175

Alignment Scores:
Pred. No.:              1.43e-15        Length:         1822
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-175 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||       ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                 :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 64
US-10-893-584-182
; Sequence 182, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-182

Alignment Scores:
Pred. No.:              1.43e-15        Length:         1822
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-182 (1-1822)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||       ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                 :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 65
US-10-089-058-89
; Sequence 89, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
;   LENGTH: 1825
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP320
US-10-089-058-89
```

```
Alignment Scores:
Pred. No.:                1.44e-15        Length:         1825
Score:                    169.00          Matches:        51
Percent Similarity:       52.2%           Conservative:   32
Best Local Similarity:    32.1%           Mismatches:     60
Query Match:              22.0%           Indels:         16
DB:                       39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058-89 (1-1825)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   ::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 66
US-10-089-058A-89
; Sequence 89, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
;   LENGTH: 1825
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-89

Alignment Scores:
Pred. No.:                1.44e-15        Length:         1825
Score:                    169.00          Matches:        51
Percent Similarity:       52.2%           Conservative:   32
Best Local Similarity:    32.1%           Mismatches:     60
Query Match:              22.0%           Indels:         16
DB:                       39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058A-89 (1-1825)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   ::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::          |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 67
US-10-893-584-231
; Sequence 231, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 231
;   LENGTH: 1825
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-231

Alignment Scores:
Pred. No.:                1.44e-15        Length:         1825
Score:                    169.00          Matches:        51
Percent Similarity:       52.2%           Conservative:   32
Best Local Similarity:    32.1%           Mismatches:     60
Query Match:              22.0%           Indels:         16
DB:                       61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-231 (1-1825)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
```

```
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 68
US-10-089-058-68
; Sequence 68, Application US/10089058
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1828
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP315
US-10-089-058-68

Alignment Scores:

Pred. No.:	1.44e-15	Length:	1828
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058-68 (1-1828)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 69
US-10-089-058A-68
; Sequence 68, Application US/10089058A
; GENERAL INFORMATION:
; APPLICANT: Braun, Curtis
; APPLICANT: Borgford, Thor
; APPLICANT: Purac, Admir
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1828
; TYPE: DNA
; ORGANISM: E. coli
US-10-089-058A-68

Alignment Scores:

Pred. No.:	1.44e-15	Length:	1828
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058A-68 (1-1828)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366
```

```
Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db         367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 70
US-10-893-584-210
; Sequence 210, Application US/10893584
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; LENGTH: 1828
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-210

Alignment Scores:

Pred. No.:	1.44e-15	Length:	1828
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	61	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-210 (1-1828)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db         367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 71
US-10-089-058-19
; Sequence 19, Application US/10089058
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP303
US-10-089-058-19

Alignment Scores:

Pred. No.:	1.45e-15	Length:	1831
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058-19 (1-1831)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db         367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
```

```
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 72
US-10-089-058-61
; Sequence 61, Application US/10089058
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP314
US-10-089-058-61

Alignment Scores:

Pred. No.:	1.45e-15	Length:	1831
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058-61 (1-1831)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 73
US-10-089-058A-19
; Sequence 19, Application US/10089058A
; GENERAL INFORMATION:
; APPLICANT: Braun, Curtis
; APPLICANT: Borgford, Thor
; APPLICANT: Purac, Admir
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: E. coli
US-10-089-058A-19

Alignment Scores:

Pred. No.:	1.45e-15	Length:	1831
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058A-19 (1-1831)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 74
US-10-089-058A-61
; Sequence 61, Application US/10089058A
; GENERAL INFORMATION:
; APPLICANT: Braun, Curtis
; APPLICANT: Borgford, Thor
; APPLICANT: Purac, Admir

```
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1831
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-61

Alignment Scores:
Pred. No.:              1.45e-15        Length:         1831
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058A-61 (1-1831)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 75
US-10-893-584-161
; Sequence 161, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 161
;   LENGTH: 1831
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-161

Alignment Scores:
Pred. No.:              1.45e-15        Length:         1831
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-161 (1-1831)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 76
US-10-893-584-203
; Sequence 203, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
```

```
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
;   LENGTH: 1831
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-203
```

Alignment Scores:

Pred. No.:	1.45e-15	Length:	1831
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	61	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-203 (1-1831)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                ::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 77
US-10-089-058-12
; Sequence 12, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 1834
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP302
US-10-089-058-12
```

Alignment Scores:

Pred. No.:	1.45e-15	Length:	1834
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058-12 (1-1834)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
                ::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::          ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 78
US-10-089-058A-12
; Sequence 12, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 1834
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-12
```

Alignment Scores:

Pred. No.:	1.45e-15	Length:	1834
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16

```
DB:                    39            Gaps:          6

US-10-758-902-9 (1-149) x US-10-089-058A-12 (1-1834)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 79
US-10-893-584-154
; Sequence 154, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
;   LENGTH: 1834
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-154

Alignment Scores:
Pred. No.:              1.45e-15      Length:          1834
Score:                  169.00        Matches:           51
Percent Similarity:     52.2%         Conservative:      32
Best Local Similarity:  32.1%         Mismatches:        60
Query Match:            22.0%         Indels:            16
DB:                     61            Gaps:               6

US-10-758-902-9 (1-149) x US-10-893-584-154 (1-1834)
```

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 80
US-10-089-058-124
; Sequence 124, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP325
US-10-089-058-124

Alignment Scores:
Pred. No.:              1.46e-15      Length:          1837
Score:                  169.00        Matches:           51
Percent Similarity:     52.2%         Conservative:      32
Best Local Similarity:  32.1%         Mismatches:        60
Query Match:            22.0%         Indels:            16
DB:                     39            Gaps:               6

US-10-758-902-9 (1-149) x US-10-089-058-124 (1-1837)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
```

```
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                          :::           :::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||              ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||           |||           |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 81
US-10-089-058A-124
; Sequence 124, Application US/10089058A
; GENERAL INFORMATION:
; APPLICANT: Braun, Curtis
; APPLICANT: Borgford, Thor
; APPLICANT: Purac, Admir
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: E. coli
US-10-089-058A-124

Alignment Scores:

Pred. No.:	1.46e-15	Length:	1837
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058A-124 (1-1837)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                          :::           :::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||              ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||       |||   ||||||   |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||           |||           |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 82
US-10-893-584-266
; Sequence 266, Application US/10893584
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-266

Alignment Scores:

Pred. No.:	1.46e-15	Length:	1837
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	61	Gaps:	6

US-10-758-902-9 (1-149) x US-10-893-584-266 (1-1837)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                          :::           :::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||              ::::::
```

```
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 83
US-10-089-058-117
; Sequence 117, Application US/10089058
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP 324
US-10-089-058-117

Alignment Scores:

Pred. No.:	1.46e-15	Length:	1843
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058-117 (1-1843)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 84
US-10-089-058A-117
; Sequence 117, Application US/10089058A
; GENERAL INFORMATION:
; APPLICANT: Braun, Curtis
; APPLICANT: Borgford, Thor
; APPLICANT: Purac, Admir
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: E. coli
US-10-089-058A-117

Alignment Scores:

Pred. No.:	1.46e-15	Length:	1843
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058A-117 (1-1843)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
RESULT 85
US-10-893-584-259
; Sequence 259, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 259
;   LENGTH: 1843
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-259

Alignment Scores:
Pred. No.:                1.46e-15        Length:         1843
Score:                    169.00          Matches:        51
Percent Similarity:       52.2%           Conservative:   32
Best Local Similarity:    32.1%           Mismatches:     60
Query Match:              22.0%           Indels:         16
DB:                       61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-259 (1-1843)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||       ::::::|||             |||           |||       ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||       |||       |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 86
US-10-089-058-110
; Sequence 110, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
;   LENGTH: 1849
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP323
US-10-089-058-110

Alignment Scores:
Pred. No.:                1.47e-15        Length:         1849
Score:                    169.00          Matches:        51
Percent Similarity:       52.2%           Conservative:   32
Best Local Similarity:    32.1%           Mismatches:     60
Query Match:              22.0%           Indels:         16
DB:                       39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058-110 (1-1849)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||       ::::::|||             |||           |||       ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||     |||     |||     |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::|||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||       |||       |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 87
US-10-089-058A-110
; Sequence 110, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
```

```
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
;   LENGTH: 1849
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-110

Alignment Scores:
Pred. No.:              1.47e-15        Length:         1849
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058A-110 (1-1849)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||  ||||||  |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 88
US-10-893-584-252
; Sequence 252, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 252
;   LENGTH: 1849
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-252

Alignment Scores:
Pred. No.:              1.47e-15        Length:         1849
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-252 (1-1849)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
              |||   :::   ||||||      |||  ||||||  |||      |||  |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                |||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 89
US-10-089-058-5
; Sequence 5, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: pAP301
US-10-089-058-5

Alignment Scores:
Pred. No.:              1.48e-15        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058-5 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::             ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 90
US-10-089-058-47
; Sequence 47, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP309
US-10-089-058-47

Alignment Scores:
Pred. No.:              1.48e-15        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058-47 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::             ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   |||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 91
US-10-089-058-75
; Sequence 75, Application US/10089058
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP316
US-10-089-058-75

Alignment Scores:
Pred. No.:              1.48e-15        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     39              Gaps:           6

US-10-758-902-9 (1-149) x US-10-089-058-75 (1-1855)
```

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||              ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::              |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 92
US-10-089-058-82
; Sequence 82, Application US/10089058
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP318
US-10-089-058-82

Alignment Scores:

Pred. No.:	1.48e-15	Length:	1855
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058-82 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||              ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::              |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 93
US-10-089-058A-5
; Sequence 5, Application US/10089058A
; GENERAL INFORMATION:
; APPLICANT: Braun, Curtis
; APPLICANT: Borgford, Thor
; APPLICANT: Purac, Admir
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: E. coli
US-10-089-058A-5

Alignment Scores:

Pred. No.:	1.48e-15	Length:	1855
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058A-5 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
```

```
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 94
US-10-089-058A-47
; Sequence 47, Application US/10089058A
; GENERAL INFORMATION:
; APPLICANT: Braun, Curtis
; APPLICANT: Borgford, Thor
; APPLICANT: Purac, Admir
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: E. coli
US-10-089-058A-47

Alignment Scores:

Pred. No.:	1.48e-15	Length:	1855
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058A-47 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 95
US-10-089-058A-75
; Sequence 75, Application US/10089058A
; GENERAL INFORMATION:
; APPLICANT: Braun, Curtis
; APPLICANT: Borgford, Thor
; APPLICANT: Purac, Admir
; TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
; FILE REFERENCE: 10447-22
; CURRENT APPLICATION NUMBER: US/10/089,058A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: E. coli
US-10-089-058A-75

Alignment Scores:

Pred. No.:	1.48e-15	Length:	1855
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	39	Gaps:	6

US-10-758-902-9 (1-149) x US-10-089-058A-75 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18

Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37

Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55

Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75

Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92

Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112

Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132

Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147

Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

```
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 96
US-10-089-058A-82
; Sequence 82, Application US/10089058A
; GENERAL INFORMATION:
;  APPLICANT: Braun, Curtis
;  APPLICANT:  Borgford, Thor
;  APPLICANT:  Purac, Admir
;  TITLE OF INVENTION: Improved Ricin-Like Toxins for Treatment of Cancer
;  FILE REFERENCE: 10447-22
;  CURRENT APPLICATION NUMBER: US/10/089,058A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-089-058A-82

Alignment Scores:
Pred. No.:              1.48e-15       Length:          1855
Score:                  169.00         Matches:         51
Percent Similarity:     52.2%          Conservative:    32
Best Local Similarity:  32.1%          Mismatches:      60
Query Match:            22.0%          Indels:          16
DB:                     39             Gaps:            6

US-10-758-902-9 (1-149) x US-10-089-058A-82 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||      ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 97
US-10-893-584-147
; Sequence 147, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 147
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-147

Alignment Scores:
Pred. No.:              1.48e-15       Length:          1855
Score:                  169.00         Matches:         51
Percent Similarity:     52.2%          Conservative:    32
Best Local Similarity:  32.1%          Mismatches:      60
Query Match:            22.0%          Indels:          16
DB:                     61             Gaps:            6

US-10-758-902-9 (1-149) x US-10-893-584-147 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||:::   |||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||      ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 98
US-10-893-584-189
; Sequence 189, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
```

```
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-189

Alignment Scores:
Pred. No.:              1.48e-15        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-189 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::|||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 99
US-10-893-584-217
; Sequence 217, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-217

Alignment Scores:
Pred. No.:              1.48e-15        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-217 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      :::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           ::::::||||||:::|||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                    :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||         |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 100
US-10-893-584-224
; Sequence 224, Application US/10893584
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
```

```
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-893-584-224

Alignment Scores:
Pred. No.:              1.48e-15        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     61              Gaps:           6

US-10-758-902-9 (1-149) x US-10-893-584-224 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||            |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                          :::   |||   |||            ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591


Search completed: September 18, 2006, 20:23:34
Job time : 7871.06 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 17:57:26 ; Search time 615.978 Seconds
(without alignments)
693.279 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2651964 seqs, 955356087 residues

Total number of hits satisfying chosen parameters: 5303928

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10758902/runat_18092006_162716_11719/app_query.fasta_1
-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10758902_@CGN_1_1_342_@runat_18092006_162716_11719 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pna/US11_NEW_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pna/US11_NEW_COMB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	183.5	23.9	886	6	US-10-280-725D-3	Sequence 3, Appli
2	169	22.0	1807	8	US-11-414-227-54	Sequence 54, Appl
3	169	22.0	1810	8	US-11-414-227-26	Sequence 26, Appl
4	169	22.0	1813	8	US-11-414-227-103	Sequence 103, App
5	169	22.0	1819	8	US-11-414-227-96	Sequence 96, Appl
6	169	22.0	1822	8	US-11-414-227-33	Sequence 33, Appl
7	169	22.0	1822	8	US-11-414-227-40	Sequence 40, Appl
8	169	22.0	1825	8	US-11-414-227-89	Sequence 89, Appl
9	169	22.0	1828	8	US-11-414-227-68	Sequence 68, Appl
10	169	22.0	1831	8	US-11-414-227-19	Sequence 19, Appl
11	169	22.0	1831	8	US-11-414-227-61	Sequence 61, Appl
12	169	22.0	1834	8	US-11-414-227-12	Sequence 12, Appl
13	169	22.0	1837	8	US-11-414-227-124	Sequence 124, App
14	169	22.0	1843	8	US-11-414-227-117	Sequence 117, App
15	169	22.0	1849	8	US-11-414-227-110	Sequence 110, App
16	169	22.0	1855	8	US-11-414-227-5	Sequence 5, Appli
17	169	22.0	1855	8	US-11-414-227-47	Sequence 47, Appl
18	169	22.0	1855	8	US-11-414-227-75	Sequence 75, Appl
19	169	22.0	1855	8	US-11-414-227-82	Sequence 82, Appl
20	104.5	13.6	765	8	US-11-361-977A-66	Sequence 66, Appl
21	104.5	13.6	984	8	US-11-361-977A-60	Sequence 60, Appl
22	104.5	13.6	993	8	US-11-361-977A-63	Sequence 63, Appl
23	104.5	13.6	999	8	US-11-361-977A-54	Sequence 54, Appl
24	104.5	13.6	999	8	US-11-361-977A-57	Sequence 57, Appl
25	82.5	10.7	537	8	US-11-434-137-7205	Sequence 7205, Ap
26	82.5	10.7	537	8	US-11-434-184-7205	Sequence 7205, Ap
27	82.5	10.7	537	8	US-11-434-203-7205	Sequence 7205, Ap
28	82.5	10.7	537	8	US-11-434-127-7205	Sequence 7205, Ap
29	82.5	10.7	537	8	US-11-434-199-7205	Sequence 7205, Ap
30	82	10.7	3501	8	US-11-434-137-5139	Sequence 5139, Ap
31	82	10.7	3501	8	US-11-434-184-5139	Sequence 5139, Ap
32	82	10.7	3501	8	US-11-434-203-5139	Sequence 5139, Ap
33	82	10.7	3501	8	US-11-434-127-5139	Sequence 5139, Ap
34	82	10.7	3501	8	US-11-434-199-5139	Sequence 5139, Ap
35	81.5	10.6	1057	8	US-11-253-199-3222	Sequence 3222, Ap
36	81.5	10.6	2495	7	US-11-514-704-3386	Sequence 3386, Ap
37	78.5	10.2	498	8	US-11-434-137-7209	Sequence 7209, Ap
38	78.5	10.2	498	8	US-11-434-184-7209	Sequence 7209, Ap
39	78.5	10.2	498	8	US-11-434-203-7209	Sequence 7209, Ap
40	78.5	10.2	498	8	US-11-434-127-7209	Sequence 7209, Ap
41	78.5	10.2	498	8	US-11-434-199-7209	Sequence 7209, Ap
42	78.5	10.2	531	8	US-11-434-137-7125	Sequence 7125, Ap
43	78.5	10.2	531	8	US-11-434-184-7125	Sequence 7125, Ap
44	78.5	10.2	531	8	US-11-434-203-7125	Sequence 7125, Ap
45	78.5	10.2	531	8	US-11-434-127-7125	Sequence 7125, Ap
46	78.5	10.2	531	8	US-11-434-199-7125	Sequence 7125, Ap
47	78.5	10.2	591	8	US-11-434-137-7203	Sequence 7203, Ap
48	78.5	10.2	591	8	US-11-434-184-7203	Sequence 7203, Ap
49	78.5	10.2	591	8	US-11-434-203-7203	Sequence 7203, Ap
50	78.5	10.2	591	8	US-11-434-127-7203	Sequence 7203, Ap
51	78.5	10.2	591	8	US-11-434-199-7203	Sequence 7203, Ap
52	78.5	10.2	657	8	US-11-434-137-7219	Sequence 7219, Ap
53	78.5	10.2	657	8	US-11-434-184-7219	Sequence 7219, Ap
54	78.5	10.2	657	8	US-11-434-203-7219	Sequence 7219, Ap
55	78.5	10.2	657	8	US-11-434-127-7219	Sequence 7219, Ap
56	78.5	10.2	657	8	US-11-434-199-7219	Sequence 7219, Ap
57	78.5	10.2	702	8	US-11-434-137-6971	Sequence 6971, Ap
58	78.5	10.2	702	8	US-11-434-137-10773	Sequence 10773, A
59	78.5	10.2	702	8	US-11-434-184-6971	Sequence 6971, Ap
60	78.5	10.2	702	8	US-11-434-184-10773	Sequence 10773, A
61	78.5	10.2	702	8	US-11-434-203-6971	Sequence 6971, Ap
62	78.5	10.2	702	8	US-11-434-203-10773	Sequence 10773, A
63	78.5	10.2	702	8	US-11-434-127-6971	Sequence 6971, Ap
64	78.5	10.2	702	8	US-11-434-127-10773	Sequence 10773, A
65	78.5	10.2	702	8	US-11-434-199-6971	Sequence 6971, Ap
66	78.5	10.2	702	8	US-11-434-199-10773	Sequence 10773, A
67	78.5	10.2	774	8	US-11-434-137-6969	Sequence 6969, Ap
68	78.5	10.2	774	8	US-11-434-184-6969	Sequence 6969, Ap
69	78.5	10.2	774	8	US-11-434-203-6969	Sequence 6969, Ap
70	78.5	10.2	774	8	US-11-434-127-6969	Sequence 6969, Ap
71	78.5	10.2	774	8	US-11-434-199-6969	Sequence 6969, Ap
72	78.5	10.2	1176	8	US-11-434-137-757	Sequence 757, App
73	78.5	10.2	1176	8	US-11-434-184-757	Sequence 757, App
74	78.5	10.2	1176	8	US-11-434-203-757	Sequence 757, App
75	78.5	10.2	1176	8	US-11-434-127-757	Sequence 757, App
76	78.5	10.2	1176	8	US-11-434-199-757	Sequence 757, App
77	78.5	10.2	1362	8	US-11-434-137-9591	Sequence 9591, Ap
78	78.5	10.2	1362	8	US-11-434-184-9591	Sequence 9591, Ap
79	78.5	10.2	1362	8	US-11-434-203-9591	Sequence 9591, Ap
80	78.5	10.2	1362	8	US-11-434-127-9591	Sequence 9591, Ap
81	78.5	10.2	1362	8	US-11-434-199-9591	Sequence 9591, Ap

82	78.5	10.2	1401	8	US-11-434-137-763	Sequence 763, App
83	78.5	10.2	1401	8	US-11-434-184-763	Sequence 763, App
84	78.5	10.2	1401	8	US-11-434-203-763	Sequence 763, App
85	78.5	10.2	1401	8	US-11-434-127-763	Sequence 763, App
86	78.5	10.2	1401	8	US-11-434-199-763	Sequence 763, App
87	78.5	10.2	4167	8	US-11-434-137-9593	Sequence 9593, Ap
88	78.5	10.2	4167	8	US-11-434-184-9593	Sequence 9593, Ap
89	78.5	10.2	4167	8	US-11-434-203-9593	Sequence 9593, Ap
90	78.5	10.2	4167	8	US-11-434-127-9593	Sequence 9593, Ap
91	78.5	10.2	4167	8	US-11-434-199-9593	Sequence 9593, Ap
92	78.5	10.2	2160266	8	US-11-434-137-10967	Sequence 10967, A
93	78.5	10.2	2160266	8	US-11-434-184-10967	Sequence 10967, A
94	78.5	10.2	2160266	8	US-11-434-203-10967	Sequence 10967, A
95	78.5	10.2	2160266	8	US-11-434-127-10967	Sequence 10967, A
96	78.5	10.2	2160266	8	US-11-434-199-10967	Sequence 10967, A
c 97	77	10.0	3309400	6	US-10-805-394A-1	Sequence 1, Appli
98	76.5	10.0	726	8	US-11-434-137-7201	Sequence 7201, Ap
99	76.5	10.0	726	8	US-11-434-184-7201	Sequence 7201, Ap
100	76.5	10.0	726	8	US-11-434-203-7201	Sequence 7201, Ap

ALIGNMENTS

RESULT 1
US-10-280-725D-3
; Sequence 3, Application US/10280725D
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Recombinant Viral Nucleic Acids
; FILE REFERENCE: LSBC-0109-US02
; CURRENT APPLICATION NUMBER: US/10/280,725D
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/557,941
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 08/484,341
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600,244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641,617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737,899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739,143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310,881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160,766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160,771
; PRIOR FILING DATE: 1988-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 886
; TYPE: DNA
; ORGANISM: Trichosanthes kirilowii
; FEATURE:
; NAME/KEY: exon
; LOCATION: (8)..(877)
US-10-280-725D-3

Alignment Scores:

Pred. No.:	1.28e-13	Length:	886
Score:	183.50	Matches:	44
Percent Similarity:	53.5%	Conservative:	32
Best Local Similarity:	31.0%	Mismatches:	61
Query Match:	23.9%	Indels:	5
DB:	6	Gaps:	2

US-10-758-902-9 (1-149) x US-10-280-725D-3 (1-886)

```
Qy          4 ValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIleGlnAspLeu 21
              |||||||||   |||       |||             |||      ||||||   :::|||
Db         80 GTTAGCTTCCGTTTATCAGGTGCAACAAGCAGTTCCTATGGAGTTTTCATTTCAAATCTG 139

Qy         22 ArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuProValThrLeuGlnThrIle 41
              |||      |||              :::     :::|||:::          ::::::
Db        140 AGAAAAGCTCTTCCAAATGAAAGGAAACTGTACGATATCCCTCTGTTACGTTCCTCTCTT 199

Qy         42 AlaAspAspLysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLys 61
                  :::|||:::   |||:::   :::|||       :::   :::|||:::
Db        200 CCAGGTTCTCAACGCTACGCATTGATCCATCTCACAAATTACGCCGATGAAACCATTTCA 259

Qy         62 ValAlaIleAspValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLys 81
              ||||||||||||||||||:::||||||:::::||||||:::             |||
Db        260 GTGGCCATAGACGTAACGAACGTCTATATTATGGGATATCGC---------GCTGGCGAT 310

Qy         82 AspArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGly 101
                     |||   :::         |||   |||         :::|||
Db        311 ACATCCTATTTTTTCAACGAGGCTTCTGCAACAGAAGCTGCAAAATATGTATTCAAAGAC 370

Qy        102 ValThrAsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAla 121
                  :::||||||||   :::   |||:::|||::::::|||       ||||||
Db        371 GCTATGCGAAAAGTTACGCTTCCATATTCTGGCAATTACGAAAGGCTTCAAACTGCTGCG 430

Qy        122 LysValAspArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAla 141
                    |||:::::::::   ||||||:::       |||:::   :::|||
Db        431 GGCAAAATAAGGGAAAATATTCCGCTTGGACTCCCAGCTTTGGACAGTGCCATTACCACT 490

Qy        142 IleTrp 143
              ::::::
Db        491 TTGTTT 496
```

RESULT 2
US-11-414-227-54
; Sequence 54, Application US/11414227
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
; FILE REFERENCE: 10447-48
; CURRENT APPLICATION NUMBER: US/11/414,227
; CURRENT FILING DATE: 2006-05-01
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP 313
US-11-414-227-54

Alignment Scores:

Pred. No.:	2.12e-11	Length:	1807
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-11-414-227-54 (1-1807)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||             |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186
```

```
Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 3
US-11-414-227-26
; Sequence 26, Application US/11414227
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
; FILE REFERENCE: 10447-48
; CURRENT APPLICATION NUMBER: US/11/414,227
; CURRENT FILING DATE: 2006-05-01
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 1810
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP304
US-11-414-227-26

Alignment Scores:

Pred. No.:	2.12e-11	Length:	1810
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-11-414-227-26 (1-1810)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 4
US-11-414-227-103
; Sequence 103, Application US/11414227
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
; FILE REFERENCE: 10447-48
; CURRENT APPLICATION NUMBER: US/11/414,227
; CURRENT FILING DATE: 2006-05-01
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 1813
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP322
US-11-414-227-103

Alignment Scores:

Pred. No.:	2.13e-11	Length:	1813
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-11-414-227-103 (1-1813)

```
Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306
```

```
Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               :::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                  |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||           |||           |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 5
US-11-414-227-96
; Sequence 96, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
;   LENGTH: 1819
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP321
US-11-414-227-96

Alignment Scores:
Pred. No.:              2.14e-11        Length:         1819
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-96 (1-1819)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||            |||            |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               :::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                  |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||           |||           |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 6
US-11-414-227-33
; Sequence 33, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP305
US-11-414-227-33

Alignment Scores:
Pred. No.:              2.14e-11        Length:         1822
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-33 (1-1822)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||            |||            |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::           ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               :::::::   :::|||   :::|||:::|||||||||:::   |||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                  |||   :::   ||||||      |||   ||||||   |||       |||   |||
Db         367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414
```

```
Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::             |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 7
US-11-414-227-40
; Sequence 40, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1822
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP308
US-11-414-227-40

Alignment Scores:
Pred. No.:                2.14e-11        Length:          1822
Score:                    169.00          Matches:         51
Percent Similarity:       52.2%           Conservative:    32
Best Local Similarity:    32.1%           Mismatches:      60
Query Match:              22.0%           Indels:          16
DB:                       8               Gaps:            6

US-10-758-902-9 (1-149) x US-11-414-227-40 (1-1822)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||           |||          |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                   :::            ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db         367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy         133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                   ||||||   :::|||   |||::::::             |||   ||||||
Db         535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 8
US-11-414-227-89
; Sequence 89, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
;   LENGTH: 1825
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP320
US-11-414-227-89

Alignment Scores:
Pred. No.:                2.15e-11        Length:          1825
Score:                    169.00          Matches:         51
Percent Similarity:       52.2%           Conservative:    32
Best Local Similarity:    32.1%           Mismatches:      60
Query Match:              22.0%           Indels:          16
DB:                       8               Gaps:            6

US-10-758-902-9 (1-149) x US-11-414-227-89 (1-1825)

Qy           1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
               |||      ::::::|||           |||          |||      ||||||
Db         127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy          19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
               :::   :::|||      |||      |||      |||      ::::::||||||
Db         187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy          38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                   :::            ::::::||||||:::||||||:::::::::
Db         247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy          56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
               ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db         307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy          76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db         367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy          93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
               |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db         415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
               :::|||   :::|||         |||         |||:::::::::|||||||||
Db         475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534
```

```
Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 9
US-11-414-227-68
; Sequence 68, Application US/11414227
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
; FILE REFERENCE: 10447-48
; CURRENT APPLICATION NUMBER: US/11/414,227
; CURRENT FILING DATE: 2006-05-01
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1828
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP315
US-11-414-227-68

Alignment Scores:

Pred. No.:	2.15e-11	Length:	1828
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-11-414-227-68 (1-1828)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla-----TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 10
US-11-414-227-19
; Sequence 19, Application US/11414227
; GENERAL INFORMATION:
; APPLICANT: BRAUN, Curtis
; APPLICANT: PURAC, Admir
; APPLICANT: BORGFORD, Thor
; TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
; FILE REFERENCE: 10447-48
; CURRENT APPLICATION NUMBER: US/11/414,227
; CURRENT FILING DATE: 2006-05-01
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/197,409
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/157,807
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP303
US-11-414-227-19

Alignment Scores:

Pred. No.:	2.16e-11	Length:	1831
Score:	169.00	Matches:	51
Percent Similarity:	52.2%	Conservative:	32
Best Local Similarity:	32.1%	Mismatches:	60
Query Match:	22.0%	Indels:	16
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-11-414-227-19 (1-1831)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 11
US-11-414-227-61
; Sequence 61, Application US/11414227

```
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1831
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP314
US-11-414-227-61

Alignment Scores:
Pred. No.:              2.16e-11        Length:         1831
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-61 (1-1831)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      ||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 12
US-11-414-227-12
; Sequence 12, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 1834
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP302
US-11-414-227-12

Alignment Scores:
Pred. No.:              2.16e-11        Length:         1834
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-12 (1-1834)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||            |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||           ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::           |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 13
US-11-414-227-124
; Sequence 124, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
```

```
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP325
US-11-414-227-124

Alignment Scores:
Pred. No.:              2.16e-11        Length:         1837
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-124 (1-1837)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||       |||       |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           :::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||      |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 14
US-11-414-227-117
; Sequence 117, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
;   LENGTH: 1843
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP 324
US-11-414-227-117

Alignment Scores:
Pred. No.:              2.17e-11        Length:         1843
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-117 (1-1843)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||       |||       |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                    :::           :::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                       :::   |||   |||             ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                |||   :::   ||||||      |||   ||||||      |||       |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp-----------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::             |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 15
US-11-414-227-110
; Sequence 110, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 110
;   LENGTH: 1849
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP323
US-11-414-227-110

Alignment Scores:
Pred. No.:              2.18e-11        Length:         1849
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-110 (1-1849)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::          ::::::|||||:::|||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 16
US-11-414-227-5
; Sequence 5, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP301
US-11-414-227-5

Alignment Scores:
Pred. No.:              2.19e-11        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-5 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||          |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::          ::::::|||||:::|||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 -----------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                  ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 17
US-11-414-227-47
; Sequence 47, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP309
US-11-414-227-47
```

```
Alignment Scores:
Pred. No.:              2.19e-11        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-47 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 18
US-11-414-227-75
; Sequence 75, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP316
US-11-414-227-75

Alignment Scores:
Pred. No.:              2.19e-11        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-414-227-75 (1-1855)

Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||           |||           |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                        :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   :::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||            ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                    ||||||   :::|||   |||::::::            |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591

RESULT 19
US-11-414-227-82
; Sequence 82, Application US/11414227
; GENERAL INFORMATION:
;  APPLICANT: BRAUN, Curtis
;  APPLICANT:  PURAC, Admir
;  APPLICANT:  BORGFORD, Thor
;  TITLE OF INVENTION: IMPROVED RICIN-LIKE TOXINS FOR TREATMENT OF CANCER
;  FILE REFERENCE: 10447-48
;  CURRENT APPLICATION NUMBER: US/11/414,227
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/197,409
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 60/157,807
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pAP318
US-11-414-227-82

Alignment Scores:
Pred. No.:              2.19e-11        Length:         1855
Score:                  169.00          Matches:        51
Percent Similarity:     52.2%           Conservative:   32
Best Local Similarity:  32.1%           Mismatches:     60
Query Match:            22.0%           Indels:         16
DB:                     8               Gaps:           6
```

US-10-758-902-9 (1-149) x US-11-414-227-82 (1-1855)

```
Qy          1 TyrAsnThrValSerPheAsnLeuGlyGluAla------TyrGluTyrProThrPheIle 18
              |||      ::::::|||             |||          |||      ||||||
Db        127 TACCCAATTATAAACTTTACCACAGCGGGTGCCACTGTGCAAAGCTACACAAACTTTATC 186

Qy         19 GlnAspLeuArgAsnGluLeuAlaLysGlyThrProVal---CysGlnLeuProValThr 37
              :::   :::|||      |||      |||      |||      ::::::||||||
Db        187 AGAGCTGTTCGCGGTCGTTTAACAACTGGAGCTGATGTGAGACATGAAATACCAGTGTTG 246

Qy         38 LeuGlnThrIleAla------AspAspLysArgPheValLeuValAspIleThrThrThr 55
                  :::            ::::::||||||:::||||||:::::::::
Db        247 CCAAACAGAGTTGGTTTGCCTATAAACCAACGGTTTATTTTAGTTGAACTCTCAAATCAT 306

Qy         56 SerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyrGln 75
              ::::::   :::|||   ::::|||:::||||||||:::   ||||||||||||||:::
Db        307 GCAGAGCTTTCTGTTACATTAGCGCTGGATGTCACCAATGCATATGTGGTCGGCTACCGT 366

Qy         76 AspLysTrpAspGlyLysAspArgAlaValPheLeu---------AspLysValProThr 92
                        :::   |||   |||              ::::::
Db        367 ------------GCTGGAAATAGCGCATATTTCTTTCATCCTGACAATCAGGAAGATGCA 414

Qy         93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                 |||   :::   ||||||      |||   ||||||   |||      |||   |||
Db        415 GAAGCAATCACTCATCTTTTCACTGATGTTCAAAATCGATATACATTCGCCTTTGGTGGT 474

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeuGlyVal 132
              :::|||   :::|||          |||          |||:::::::::|||||||||
Db        475 AATTATGATAGACTTGAACAACTTGCTGGTAATCTGAGAGAAAATATCGAGTTGGGAAAT 534

Qy        133 TyrLysLeuGluPheSerIleGluAlaIleTrp------------GlyLysThrGln 147
                |||||   :::|||   |||::::::              |||   ||||||
Db        535 GGTCCACTAGAGGAGGCTATCTCAGCGCTTTATTATTACAGTACTGGTGGCACTCAG 591
```

RESULT 20
US-11-361-977A-66
; Sequence 66, Application US/11361977A
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 17080-002005/601F
; CURRENT APPLICATION NUMBER: US/11/361,977A
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Construct encoding
; OTHER INFORMATION: Methionine-Saporin fusion protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(765)
US-11-361-977A-66

Alignment Scores:

Pred. No.:	0.00108	Length:	765
Score:	104.50	Matches:	35
Percent Similarity:	46.3%	Conservative:	33
Best Local Similarity:	23.8%	Mismatches:	58
Query Match:	13.6%	Indels:	21
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-11-361-977A-66 (1-765)

```
Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
              |||   :::|||   :::|||:::      :::||||||   :::
Db         40 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 99

Qy         28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                       ||||||   :::      :::
Db        100 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG--------------CCGAGCAAA 144

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
              ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
Db        145 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 201

Qy         65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                    ::::::|||||||||   |||          |||      :::
Db        202 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 261

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
                 |||      ::::::   :::      ::::::   |||||||||
Db        262 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 321

Qy        103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              |||      |||:::      |||   :::          ||||||   :::
Db        322 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 381

Qy        121 AlaLysVal---------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
              |||::::::                ||||||:::|||   ||||||:::      |||
Db        382 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 441

Qy        136 GluPheSerIleGluAlaIle 142
                  |||:::||||||:::
Db        442 AGCACGAGCATGGAAGCGGTC 462
```

RESULT 21
US-11-361-977A-60
; Sequence 60, Application US/11361977A
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 17080-002005/601F
; CURRENT APPLICATION NUMBER: US/11/361,977A
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
; OTHER INFORMATION: toxin fusion protein SDF-1-Beta-AM-SAPORIN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-11-361-977A-60

Alignment Scores:

Pred. No.:	0.00148	Length:	984
Score:	104.50	Matches:	35
Percent Similarity:	46.3%	Conservative:	33
Best Local Similarity:	23.8%	Mismatches:	58
Query Match:	13.6%	Indels:	21
DB:	8	Gaps:	6

US-10-758-902-9 (1-149) x US-11-361-977A-60 (1-984)

```
Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
              |||   :::|||   :::|||:::      :::||||||   :::
Db        259 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 318

Qy         28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                       ||||||   :::      :::
Db        319 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG--------------CCGAGCAAA 363

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
              ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
```

```
Db        364 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 420

Qy         65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                 ::::::||||||||  |||     |||       :::
Db        421 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 480

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
                 |||     ::::::  :::     ::::::  |||||||||
Db        481 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 540

Qy        103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                 |||     |||:::     |||   :::         ||||||   :::
Db        541 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 600

Qy        121 AlaLysVal--------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
                 |||::::::                  ||||||:::|||   ||||||:::     |||
Db        601 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 660

Qy        136 GluPheSerIleGluAlaIle 142
                 |||:::||||||:::
Db        661 AGCACGAGCATGGAAGCGGTC 681

RESULT 22
US-11-361-977A-63
; Sequence 63, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 993
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(993)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
;   OTHER INFORMATION: toxin fusion protein EOTAXIN-AM-SAPORIN
US-11-361-977A-63

Alignment Scores:
Pred. No.:              0.00149       Length:          993
Score:                  104.50        Matches:         35
Percent Similarity:     46.3%         Conservative:    33
Best Local Similarity:  23.8%         Mismatches:      58
Query Match:            13.6%         Indels:          21
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-11-361-977A-63 (1-993)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
                 |||   :::|||   :::|||:::     :::||||||   :::
Db        268 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 327

Qy         28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                      ||||||   :::     :::
Db        328 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG--------------CCGAGCAAA 372

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
                 ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
Db        373 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 429

Qy         65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                 ::::::||||||||  |||     |||       :::
Db        430 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 489

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
                 |||     ::::::  :::     ::::::  |||||||||
Db        490 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 549

Qy        103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                 |||     |||:::     |||   :::         ||||||   :::
Db        550 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 609

Qy        121 AlaLysVal--------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
                 |||::::::                  ||||||:::|||   ||||||:::     |||
Db        610 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 669

Qy        136 GluPheSerIleGluAlaIle 142
                 |||:::||||||:::
Db        670 AGCACGAGCATGGAAGCGGTC 690

RESULT 23
US-11-361-977A-54
; Sequence 54, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
;   LENGTH: 999
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(999)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
;   OTHER INFORMATION: toxin fussion protein MCP1-AM-SAPORIN
US-11-361-977A-54

Alignment Scores:
Pred. No.:              0.0015        Length:          999
Score:                  104.50        Matches:         35
Percent Similarity:     46.3%         Conservative:    33
Best Local Similarity:  23.8%         Mismatches:      58
Query Match:            13.6%         Indels:          21
DB:                     8             Gaps:            6

US-10-758-902-9 (1-149) x US-11-361-977A-54 (1-999)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
                 |||   :::|||   :::|||:::     :::||||||   :::
Db        274 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 333

Qy         28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                      ||||||   :::     :::
Db        334 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG--------------CCGAGCAAA 378

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
                 ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
Db        379 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 435

Qy         65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                 ::::::||||||||  |||     |||       :::
Db        436 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 495

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuProGlyVal 102
                 |||     ::::::  :::     ::::::  |||||||||
Db        496 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 555

Qy        103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
                 |||     |||:::     |||   :::         ||||||   :::
```

```
Db        556 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 615

Qy        121 AlaLysVal--------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
              |||::::::                |||||::|||   ||||||:::      |||
Db        616 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 675

Qy        136 GluPheSerIleGluAlaIle 142
                  |||:::||||||:::
Db        676 AGCACGAGCATGGAAGCGGTC 696

RESULT 24
US-11-361-977A-57
; Sequence 57, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
;   LENGTH: 999
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(999)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
;   OTHER INFORMATION: toxin Fusion Protein MCP3-AM-SAPORIN
US-11-361-977A-57

Alignment Scores:
Pred. No.:              0.0015          Length:         999
Score:                  104.50          Matches:        35
Percent Similarity:     46.3%           Conservative:   33
Best Local Similarity:  23.8%           Mismatches:     58
Query Match:            13.6%           Indels:         21
DB:                     8               Gaps:           6

US-10-758-902-9 (1-149) x US-11-361-977A-57 (1-999)

Qy         11 AlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys--------- 27
              |||   :::|||   :::|||:::      :::|||||   :::
Db        274 GCCGGCCAATATAGCAGCTTCGTGGATAAGATTCGTAACAACGTAAAAGATCCGAATCTG 333

Qy         28 ---------GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp 44
                      ||||||   :::      :::
Db        334 AAATACGGTGGTACTGATATTGCGGTCATCGGTCCG--------------CCGAGCAAA 378

Qy         45 LysArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIle 64
              ::::::|||:::   ::::::         :::|||:::   ||||||   :::   :::
Db        379 GAAAAGTTCCTGCGCATTAACTTT---CAAAGCTCCCGTGGCACTGTTTCTCTGGGCCTG 435

Qy         65 AspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAspGlyLysAsp 82
                    ::::::|||||||||   |||         |||      :::
Db        436 AAGCGCGATAACCTGTATGTTGTTGCCTATCTGGCGATGGATAATACGAACGTGAACCGC 495

Qy         83 ArgAlaValPheLeuAspLysValProThrValAlaThrSerLysLeuPheProGlyVal 102
                  |||      ::::::   :::      ::::::   |||||||||
Db        496 GCCTACTACTTTCGTAGCGAGATTACGAGCGCGGAATCCACTGCTCTGTTCCCGGAGGCG 555

Qy        103 Thr------AsnArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAla 120
              |||      |||:::      |||   :::         ||||||   :::
Db        556 ACCACTGCAAACCAAAAAGCACTGGAATATACGGAAGATTACCAGTCCATCGAGAAGAAC 615

Qy        121 AlaLysVal--------------AspArgLysAspLeuGluLeuGlyValTyrLysLeu 135
              |||::::::                |||||::|||   ||||||:::      |||
Db        616 GCGCAGATCACCCAGGGCGATCAATCCCGCAAAGAACTGGGTCTGGGTATTGATCTGCTG 675

Qy        136 GluPheSerIleGluAlaIle 142
                  |||:::||||||:::
Db        676 AGCACGAGCATGGAAGCGGTC 696

RESULT 25
US-11-434-137-7205
; Sequence 7205, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7205
;   LENGTH: 537
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(537)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-137-7205

Alignment Scores:
Pred. No.:              0.426           Length:         537
Score:                  82.50           Matches:        33
Percent Similarity:     43.9%           Conservative:   14
Best Local Similarity:  30.8%           Mismatches:     57
Query Match:            10.7%           Indels:         3
DB:                     8               Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-137-7205 (1-537)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                    |||:::|||                |||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||  |||                  ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuProGlyValThrAsn 104
                 :::   |||   |||             |||             |||   :::
Db        346 AATGTAGGTAAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426
```

```
RESULT 26
US-11-434-184-7205
; Sequence 7205, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7205
;   LENGTH: 537
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(537)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-184-7205

Alignment Scores:
Pred. No.:              0.426          Length:         537
Score:                  82.50          Matches:        33
Percent Similarity:     43.9%          Conservative:   14
Best Local Similarity:  30.8%          Mismatches:     57
Query Match:            10.7%          Indels:         3
DB:                     8              Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-184-7205 (1-537)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          ||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
              :::   |||   |||              |||          |||   :::
Db        346 AATGTAGGTAAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 27
US-11-434-203-7205
; Sequence 7205, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7205
;   LENGTH: 537
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(537)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-203-7205

Alignment Scores:
Pred. No.:              0.426          Length:         537
Score:                  82.50          Matches:        33
Percent Similarity:     43.9%          Conservative:   14
Best Local Similarity:  30.8%          Mismatches:     57
Query Match:            10.7%          Indels:         3
DB:                     8              Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-203-7205 (1-537)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          ||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
              :::   |||   |||              |||          |||   :::
Db        346 AATGTAGGTAAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 28
US-11-434-127-7205
; Sequence 7205, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
```

```
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7205
;   LENGTH: 537
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(537)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-127-7205

Alignment Scores:
Pred. No.:                0.426          Length:          537
Score:                    82.50          Matches:         33
Percent Similarity:       43.9%          Conservative:    14
Best Local Similarity:    30.8%          Mismatches:      57
Query Match:              10.7%          Indels:          3
DB:                       8              Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-127-7205 (1-537)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||              ||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   |||   |||           |||          |||   :::
Db        346 AATGTAGGTAAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 29
US-11-434-199-7205
; Sequence 7205, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7205
;   LENGTH: 537
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(537)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-199-7205

Alignment Scores:
Pred. No.:                0.426          Length:          537
Score:                    82.50          Matches:         33
Percent Similarity:       43.9%          Conservative:    14
Best Local Similarity:    30.8%          Mismatches:      57
Query Match:              10.7%          Indels:          3
DB:                       8              Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-199-7205 (1-537)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||              ||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   |||   |||           |||          |||   :::
Db        346 AATGTAGGTAAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 30
US-11-434-137-5139
; Sequence 5139, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
```

```
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5139
;    LENGTH: 3501
;    TYPE: DNA
;    ORGANISM: Streptococcus pyogenes
US-11-434-137-5139

Alignment Scores:
Pred. No.:                5.03          Length:          3501
Score:                    82.00         Matches:         30
Percent Similarity:       41.8%         Conservative:    11
Best Local Similarity:    30.6%         Mismatches:      35
Query Match:              10.7%         Indels:          22
DB:                       8             Gaps:            4

US-10-758-902-9 (1-149) x US-11-434-137-5139 (1-3501)

Qy          33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
               ||||||         |||||||||      |||||||||:::      |||   |||:::
Db         721 CAATTAGAAAAGGCTCTACAAACAGCACAAGATGATAAAAAATCTTATTTAGAAGATGTA 780

Qy          53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                     ||||||        |||         |||:::           :::
Db         781 TTAGCTGTTTCAAAAAACGGTTTTAAACATAAG---GATATCCGTAAATTTCAATCATTA 837

Qy          73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
                  |||:::   :::|||                          ||||||   :::|||
Db         838 TTTTATGAAAAAGAGTGGTCA-----------------TTATTAGATTATATTCCT--- 876

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                                                 :::   |||       |||
Db         877 ----------------------------------AAGGGAACGCCAATCTTTTTTGAT 900

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeu 130
                  :::|||||||||||||:::      |||      |||   |||||||||:::
Db         901 GATTTTCAAAAACTAGTTGAT------AAAAATGCAAGATTTGATTTAGAGATT 948

RESULT 31
US-11-434-184-5139
; Sequence 5139, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5139
;    LENGTH: 3501
;    TYPE: DNA
;    ORGANISM: Streptococcus pyogenes
US-11-434-184-5139

Alignment Scores:
Pred. No.:                5.03          Length:          3501
Score:                    82.00         Matches:         30
Percent Similarity:       41.8%         Conservative:    11
Best Local Similarity:    30.6%         Mismatches:      35
Query Match:              10.7%         Indels:          22
DB:                       8             Gaps:            4

US-10-758-902-9 (1-149) x US-11-434-184-5139 (1-3501)

Qy          33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
               ||||||         |||||||||      |||||||||:::      |||   |||:::
Db         721 CAATTAGAAAAGGCTCTACAAACAGCACAAGATGATAAAAAATCTTATTTAGAAGATGTA 780

Qy          53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                     ||||||        |||         |||:::           :::
Db         781 TTAGCTGTTTCAAAAAACGGTTTTAAACATAAG---GATATCCGTAAATTTCAATCATTA 837

Qy          73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
                  |||:::   :::|||                          ||||||   :::|||
Db         838 TTTTATGAAAAAGAGTGGTCA-----------------TTATTAGATTATATTCCT--- 876

Qy          93 ValAlaThrSerLysLeuProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                                                 :::   |||       |||
Db         877 ----------------------------------AAGGGAACGCCAATCTTTTTTGAT 900

Qy         113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeu 130
                  :::|||||||||||||:::      |||      |||   |||||||||:::
Db         901 GATTTTCAAAAACTAGTTGAT------AAAAATGCAAGATTTGATTTAGAGATT 948

RESULT 32
US-11-434-203-5139
; Sequence 5139, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5139
;    LENGTH: 3501
;    TYPE: DNA
;    ORGANISM: Streptococcus pyogenes
US-11-434-203-5139

Alignment Scores:
Pred. No.:                5.03          Length:          3501
Score:                    82.00         Matches:         30
Percent Similarity:       41.8%         Conservative:    11
Best Local Similarity:    30.6%         Mismatches:      35
Query Match:              10.7%         Indels:          22
DB:                       8             Gaps:            4

US-10-758-902-9 (1-149) x US-11-434-203-5139 (1-3501)
```

```
Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
              ||||||  |||||||||  |||||||||:::   |||  |||:::
Db        721 CAATTAGAAAAGGCTCTACAAACAGCACAAGATGATAAAAAATCTTATTTAGAAGATGTA 780

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                  ||||||     |||     |||:::          :::
Db        781 TTAGCTGTTTCAAAAAACGGTTTTAAACATAAG---GATATCCGTAAATTTCAATCATTA 837

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
                ||:::  :::|||                  |||||  :::|||
Db        838 TTTTATGAAAAAGAGTGGTCA----------------TTATTAGATTATATTCCT--- 876

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                                                :::  |||     |||
Db        877 ----------------------------------AAGGGAACGCCAATCTTTTTTGAT 900

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeu 130
                :::|||||||||||:::     |||     |||  |||||||||:::
Db        901 GATTTTCAAAAACTAGTTGAT------AAAAATGCAAGATTTGATTTAGAGATT 948
```

RESULT 33
US-11-434-127-5139
; Sequence 5139, Application US/11434127
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,127
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5139
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-11-434-127-5139

Alignment Scores:

Pred. No.:	5.03	Length:	3501
Score:	82.00	Matches:	30
Percent Similarity:	41.8%	Conservative:	11
Best Local Similarity:	30.6%	Mismatches:	35
Query Match:	10.7%	Indels:	22
DB:	8	Gaps:	4

US-10-758-902-9 (1-149) x US-11-434-127-5139 (1-3501)

```
Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
              ||||||  |||||||||  |||||||||:::   |||  |||:::
Db        721 CAATTAGAAAAGGCTCTACAAACAGCACAAGATGATAAAAAATCTTATTTAGAAGATGTA 780

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                  ||||||     |||     |||:::          :::
Db        781 TTAGCTGTTTCAAAAAACGGTTTTAAACATAAG---GATATCCGTAAATTTCAATCATTA 837

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
                ||:::  :::|||                  |||||  :::|||
Db        838 TTTTATGAAAAAGAGTGGTCA----------------TTATTAGATTATATTCCT--- 876
```

```
Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                                                :::  |||     |||
Db        877 ----------------------------------AAGGGAACGCCAATCTTTTTTGAT 900

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeu 130
                :::|||||||||||:::     |||     |||  |||||||||:::
Db        901 GATTTTCAAAAACTAGTTGAT------AAAAATGCAAGATTTGATTTAGAGATT 948
```

RESULT 34
US-11-434-199-5139
; Sequence 5139, Application US/11434199
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,199
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5139
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-11-434-199-5139

Alignment Scores:

Pred. No.:	5.03	Length:	3501
Score:	82.00	Matches:	30
Percent Similarity:	41.8%	Conservative:	11
Best Local Similarity:	30.6%	Mismatches:	35
Query Match:	10.7%	Indels:	22
DB:	8	Gaps:	4

US-10-758-902-9 (1-149) x US-11-434-199-5139 (1-3501)

```
Qy         33 GlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeuValAspIle 52
              ||||||  |||||||||  |||||||||:::   |||  |||:::
Db        721 CAATTAGAAAAGGCTCTACAAACAGCACAAGATGATAAAAAATCTTATTTAGAAGATGTA 780

Qy         53 ThrThrThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValVal 72
                  ||||||     |||     |||:::          :::
Db        781 TTAGCTGTTTCAAAAAACGGTTTTAAACATAAG---GATATCCGTAAATTTCAATCATTA 837

Qy         73 GlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAspLysValProThr 92
                ||:::  :::|||                  |||||  :::|||
Db        838 TTTTATGAAAAAGAGTGGTCA----------------TTATTAGATTATATTCCT--- 876

Qy         93 ValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThrPheAspGly 112
                                                :::  |||     |||
Db        877 ----------------------------------AAGGGAACGCCAATCTTTTTTGAT 900

Qy        113 SerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGluLeu 130
                :::|||||||||||:::     |||     |||  |||||||||:::
Db        901 GATTTTCAAAAACTAGTTGAT------AAAAATGCAAGATTTGATTTAGAGATT 948
```

RESULT 35
US-11-253-199-3222
; Sequence 3222, Application US/11253199

```
; GENERAL INFORMATION:
;  APPLICANT: Budworth, Paul R.
;  APPLICANT:  Moughamer, Todd G.
;  APPLICANT:  Briggs, Steven P.
;  APPLICANT:  Cooper, Bret
;  APPLICANT:  Glazebrook, Jane
;  APPLICANT:  Goff, Stephen A.
;  APPLICANT:  Katagiri, Fumiyaki
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Provart, Nicholas
;  APPLICANT:  Ricke, Darrell
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: RICE PROMOTERS FOR REGULATION OF PLANT EXPRESSION
;  FILE REFERENCE: 60111 US/CIP
;  CURRENT APPLICATION NUMBER: US/11/253,199
;  CURRENT FILING DATE:  2005-10-18
;  PRIOR APPLICATION NUMBER: 10/260,238
;  PRIOR FILING DATE: 2002-09-26
;  PRIOR APPLICATION NUMBER: 60/325,448
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/325,277
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/370,620
;  PRIOR FILING DATE: 2002-04-04
;  NUMBER OF SEQ ID NOS: 6097
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3222
;   LENGTH: 1057
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-11-253-199-3222

Alignment Scores:
Pred. No.:              1.32          Length:        1057
Score:                  81.50         Matches:       35
Percent Similarity:     41.7%         Conservative:  25
Best Local Similarity:  24.3%         Mismatches:    61
Query Match:            10.6%         Indels:        23
DB:                     8             Gaps:          7

US-10-758-902-9 (1-149) x US-11-253-199-3222 (1-1057)

Qy          8 LeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLys 27
              ||||||:::|||   |||           :::|||   |||:::   ||:::
Db        361 CTCGGCAAGGCGACAGAGAAGGAT------CTGCAGCAGTTGAAGGCCGAGATCATGGAT 414

Qy         28 GlyThrProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAsp------Lys 45
              |||          ||||||           |||      ::::::      |||
Db        415 GGCCTACAGTCCGTGCAGCTCAACGCTGAACACAGTACCTCCGTTGAGGAGGAGGTAAAG 474

Qy         46 ArgPheValLeu------ValAspIleThrThrThrSerLysLysThrValLysValAla 63
              |||            :::|||                        ||||||
Db        475 AGGATCAAGGCCGAACATATTGATCGCAACGCCATCATCCACGGCAGAGTGAAGGGGAAA 534

Qy         64 IleAspValThrAspValTyrValValGlyTyr------GlnAspLysTrpAsp------ 79
              ::::::::|||      :::      ||||||      :::   ||||||:::
Db        535 CTCAACATCACCAGAGCATTCGGGGCTGGCTACCTGAAGGAGCCAAAGTGGAACAGTATG 594

Qy         80 ----------------------------GlyLysAspArgAlaValPheLeuAspLys 89
                                         ||||||||          :::::::::
Db        595 TTGTTAGCGTGCTTCAAGATTGATTACATCGGCAAGGAC------CCCTACATCAATTGC 648

Qy         90 ValProThrValAlaThrSerLysLeuPheProGlyValThrAsnArgValThrLeuThr 109
              :::|||::::::         ::::::   |||               :::   |||:::
Db        649 ATCCCATCACTGCACCACCACCGTATCGGTCCAAAC---GACAAGTTCCTGGTGTTGTCG 705

Qy        110 PheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArgLysAspLeuGlu 129
              ||||||  ||||||         |||         ||||||      ::::::
Db        706 TCCGATGGGCTCTATCAGTATTTCACCAACAAAGAGGTGGTTGATGAGGTAGAGATGTTC 765

Qy        130 LeuGlyValTyr 133
              |||
Db        766 ACAGCTGCGTAT 777
```

```
RESULT 36
US-11-514-704-3386
; Sequence 3386, Application US/11514704
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  Wu, Kunsheng
;  APPLICANT:  Dasgupta, Santanu
;  APPLICANT:  Cherian, Shoba
;  APPLICANT:  Jayaprakash, Targolli L
;  TITLE OF INVENTION: Zea mays Ribulose Bisphosphate Carboxylase
;  TITLE OF INVENTION:  Activase Promoter
;  FILE REFERENCE: 38-21(53660)C
;  CURRENT APPLICATION NUMBER: US/11/514,704
;  CURRENT FILING DATE:  2006-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3386
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-514-704-3386

Alignment Scores:
Pred. No.:              3.83          Length:        2495
Score:                  81.50         Matches:       38
Percent Similarity:     44.2%         Conservative:  15
Best Local Similarity:  31.7%         Mismatches:    38
Query Match:            10.6%         Indels:        29
DB:                     7             Gaps:          8

US-10-758-902-9 (1-149) x US-11-514-704-3386 (1-2495)

Qy         16 ThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThrProValCysGlnLeuPro 35
              ||||||||||||:::::|||   ||||||          |||   |||   |||
Db        680 ACTTTCATCCAGGAGATTCGCCGTGAGCTCGGT---GACACAAGCGTGATGCAGGAGGCG 736

Qy         36 ValThrLeuGlnThrIleAlaAspAspLysArgPheVal---LeuValAspIleThrThr 54
                 |||           |||         |||      ||||||   |||
Db        737 TTCCAGCTCCCGCCTCAGACGGACACCCCGAGCTTTCAGGACCTCGTGCTGATCGCCGGC 796

Qy         55 ThrSerLysLysThrValLysValAlaIleAspValThrAspValTyrValValGlyTyr 74
                 |||      |||:::::::::      |||      ::::::|||||||||||:::
Db        797 GAGAGCACCGCCACCCTGCGGCTGCGTACCGAC------AACCTCTACGTCGTCGGCTTC 850

Qy         75 GlnAsp---------LysTrp-----------------AspGlyLysAspArgAlaVal 85
              ::::::          :::|||                 ||||||
Db        851 CGCAACCAAGCCGGCCGGTGGTTCGAGTTCCGGCACGAGGACGGC--------------- 895

Qy         86 PheLeuAspLysValProThrValAlaThrSerLysLeuProGlyValThrAsnArg 105
                           ||||||:::                 ||||||   |||
Db        896 ------GGACTTCCTCCGACCATA-----------------CCAGGGGCGACG------ 925

Qy        106 ValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAspArg 125
                 |||   |||   |||||||||           :::   |||   ::::::|||
Db        926 ---ATGCTGCACTTCAGCGGGAGCTACGTGGGCACCAACAGTCTAGCTCCGCTAAATCGT 982

RESULT 37
US-11-434-137-7209
; Sequence 7209, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
```

```
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7209
;   LENGTH: 498
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(498)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-137-7209
```

Alignment Scores:			
Pred. No.:	1.25	Length:	498
Score:	78.50	Matches:	32
Percent Similarity:	43.9%	Conservative:	15
Best Local Similarity:	29.9%	Mismatches:	57
Query Match:	10.2%	Indels:	3
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-434-137-7209 (1-498)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::        |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||         |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426
```

```
RESULT 38
US-11-434-184-7209
; Sequence 7209, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7209
;   LENGTH: 498
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(498)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-184-7209
```

Alignment Scores:			
Pred. No.:	1.25	Length:	498
Score:	78.50	Matches:	32
Percent Similarity:	43.9%	Conservative:	15
Best Local Similarity:	29.9%	Mismatches:	57
Query Match:	10.2%	Indels:	3
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-434-184-7209 (1-498)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::        |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||         |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426
```

```
RESULT 39
US-11-434-203-7209
; Sequence 7209, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
```

```
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7209
;   LENGTH: 498
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(498)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-203-7209

Alignment Scores:
Pred. No.:              1.25          Length:         498
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-203-7209 (1-498)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||     :::   ||||||         |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||         |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 40
US-11-434-127-7209
; Sequence 7209, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7209
;   LENGTH: 498
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(498)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-127-7209

Alignment Scores:
Pred. No.:              1.25          Length:         498
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-127-7209 (1-498)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||     :::   ||||||         |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||         |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 41
US-11-434-199-7209
; Sequence 7209, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7209
;   LENGTH: 498
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(498)
```

```
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-199-7209

Alignment Scores:
Pred. No.:              1.25          Length:        498
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-199-7209 (1-498)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::           |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||               ||||||  ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::        |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 42
US-11-434-137-7125
; Sequence 7125, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7125
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(531)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-137-7125

Alignment Scores:
Pred. No.:              1.35          Length:        531
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-137-7125 (1-531)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::           |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||               ||||||  ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::        |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 43
US-11-434-184-7125
; Sequence 7125, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7125
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(531)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-184-7125

Alignment Scores:
Pred. No.:              1.35          Length:        531
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
```

```
Query Match:          10.2%      Indels:      3
DB:                   8          Gaps:        3

US-10-758-902-9 (1-149) x US-11-434-184-7125 (1-531)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 44
US-11-434-203-7125
; Sequence 7125, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7125
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(531)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-203-7125

Alignment Scores:
Pred. No.:            1.35       Length:      531
Score:                78.50      Matches:     32
Percent Similarity:   43.9%      Conservative: 15
Best Local Similarity: 29.9%     Mismatches:  57
Query Match:          10.2%      Indels:      3
DB:                   8          Gaps:        3

US-10-758-902-9 (1-149) x US-11-434-203-7125 (1-531)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 45
US-11-434-127-7125
; Sequence 7125, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7125
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(531)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-127-7125

Alignment Scores:
Pred. No.:            1.35       Length:      531
Score:                78.50      Matches:     32
Percent Similarity:   43.9%      Conservative: 15
Best Local Similarity: 29.9%     Mismatches:  57
Query Match:          10.2%      Indels:      3
DB:                   8          Gaps:        3

US-10-758-902-9 (1-149) x US-11-434-127-7125 (1-531)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165
```

```
Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||             |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 46
US-11-434-199-7125
; Sequence 7125, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7125
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(531)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-199-7125

Alignment Scores:
Pred. No.:              1.35          Length:         531
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-199-7125 (1-531)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::|||||||      :::           |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||             |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 47
US-11-434-137-7203
; Sequence 7203, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7203
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(591)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-137-7203

Alignment Scores:
Pred. No.:              1.54          Length:         591
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-137-7203 (1-591)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::|||||||      :::           |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285
```

```
Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
Db        406 GGTACAACAGTAGCCTTTGAA 426
```

RESULT 48
US-11-434-184-7203
; Sequence 7203, Application US/11434184
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,184
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7203
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(591)
; OTHER INFORMATION: n = a, c, g, or t
US-11-434-184-7203

Alignment Scores:

Pred. No.:	1.54	Length:	591
Score:	78.50	Matches:	32
Percent Similarity:	43.9%	Conservative:	15
Best Local Similarity:	29.9%	Mismatches:	57
Query Match:	10.2%	Indels:	3
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-434-184-7203 (1-591)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
Db        406 GGTACAACAGTAGCCTTTGAA 426
```

RESULT 49
US-11-434-203-7203
; Sequence 7203, Application US/11434203
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,203
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7203
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(591)
; OTHER INFORMATION: n = a, c, g, or t
US-11-434-203-7203

Alignment Scores:

Pred. No.:	1.54	Length:	591
Score:	78.50	Matches:	32
Percent Similarity:	43.9%	Conservative:	15
Best Local Similarity:	29.9%	Mismatches:	57
Query Match:	10.2%	Indels:	3
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-434-203-7203 (1-591)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405
```

```
Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 50
US-11-434-127-7203
; Sequence 7203, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7203
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(591)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-127-7203

Alignment Scores:
Pred. No.:              1.54          Length:         591
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-127-7203 (1-591)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::|||||||      :::           |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
              |||:::|||           ||||||  ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 51
US-11-434-199-7203
; Sequence 7203, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7203
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(591)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-199-7203

Alignment Scores:
Pred. No.:              1.54          Length:         591
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-199-7203 (1-591)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::|||||||      :::           |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
              |||:::|||           ||||||  ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 52
US-11-434-137-7219
; Sequence 7219, Application US/11434137
```

```
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7219
;   LENGTH: 657
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(657)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-137-7219

Alignment Scores:
Pred. No.:              1.76        Length:         657
Score:                  78.50       Matches:        32
Percent Similarity:     43.9%       Conservative:   15
Best Local Similarity:  29.9%       Mismatches:     57
Query Match:            10.2%       Indels:         3
DB:                     8           Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-137-7219 (1-657)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db         73 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 129

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        130 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 189

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db        190 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 249

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        250 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 309

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuProGlyValThrAsn 104
                 :::   :::  |||           |||       |||   :::
Db        310 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 369

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        370 GGTACAACAGTAGCCTTTGAA 390

RESULT 53
US-11-434-184-7219
; Sequence 7219, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7219
;   LENGTH: 657
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(657)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-184-7219

Alignment Scores:
Pred. No.:              1.76        Length:         657
Score:                  78.50       Matches:        32
Percent Similarity:     43.9%       Conservative:   15
Best Local Similarity:  29.9%       Mismatches:     57
Query Match:            10.2%       Indels:         3
DB:                     8           Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-184-7219 (1-657)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db         73 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 129

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        130 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 189

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db        190 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 249

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        250 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 309

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuProGlyValThrAsn 104
                 :::   :::  |||           |||       |||   :::
Db        310 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 369

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        370 GGTACAACAGTAGCCTTTGAA 390

RESULT 54
US-11-434-203-7219
; Sequence 7219, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
```

```
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7219
;   LENGTH: 657
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(657)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-203-7219

Alignment Scores:
Pred. No.:              1.76          Length:        657
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-203-7219 (1-657)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||     :::          |||   :::|||      :::|||
Db         73 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 129

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        130 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 189

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||          ||||||   ||||||   |||   :::
Db        190 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 249

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||              ::::::         ||||||||:::   |||
Db        250 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 309

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||          |||          |||   :::
Db        310 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 369

Qy        105 ArgValThrLeuThrPheAsp 111
                |||:::   |||:::
Db        370 GGTACAACAGTAGCCTTTGAA 390

RESULT 55
US-11-434-127-7219
; Sequence 7219, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7219
;   LENGTH: 657
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(657)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-127-7219

Alignment Scores:
Pred. No.:              1.76          Length:        657
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-127-7219 (1-657)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||     :::          |||   :::|||      :::|||
Db         73 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 129

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        130 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 189

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||          ||||||   ||||||   |||   :::
Db        190 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 249

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||              ::::::         ||||||||:::   |||
Db        250 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 309

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||          |||          |||   :::
Db        310 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 369

Qy        105 ArgValThrLeuThrPheAsp 111
                |||:::   |||:::
Db.       370 GGTACAACAGTAGCCTTTGAA 390

RESULT 56
US-11-434-199-7219
; Sequence 7219, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
```

```
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7219
;   LENGTH: 657
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(657)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-199-7219

Alignment Scores:
Pred. No.:              1.76          Length:         657
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-199-7219 (1-657)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db         73 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 129

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        130 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 189

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   |||||   |||   :::
Db        190 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 249

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||             ::::::         |||||||:::   |||
Db        250 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 309

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||           |||          |||   :::
Db        310 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 369

Qy        105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db        370 GGTACAACAGTAGCCTTTGAA 390

RESULT 57
US-11-434-137-6971
; Sequence 6971, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6971
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(702)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-137-6971

Alignment Scores:
Pred. No.:              1.91          Length:         702
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-137-6971 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   |||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||             ::::::         |||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||           |||          |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 58
US-11-434-137-10773
; Sequence 10773, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10773
;   LENGTH: 702
```

```
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-10773

Alignment Scores:
Pred. No.:              1.91          Length:        702
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-137-10773 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||            |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 59
US-11-434-184-6971
; Sequence 6971, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6971
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(702)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-184-6971

Alignment Scores:
Pred. No.:              1.91          Length:        702
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-184-6971 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||            |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 60
US-11-434-184-10773
; Sequence 10773, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10773
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-10773

Alignment Scores:
Pred. No.:              1.91          Length:        702
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3
```

```
US-10-758-902-9 (1-149) x US-11-434-184-10773 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::           |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::        ||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||         |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 61
US-11-434-203-6971
; Sequence 6971, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6971
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(702)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-203-6971

Alignment Scores:
Pred. No.:              1.91          Length:         702
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-203-6971 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::           |||   :::|||      :::|||

Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::        ||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||         |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 62
US-11-434-203-10773
; Sequence 10773, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10773
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-10773

Alignment Scores:
Pred. No.:              1.91          Length:         702
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-203-10773 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::           |||   :::|||      :::|||

Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||   |||   :::
```

```
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||              |||             |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 63
US-11-434-127-6971
; Sequence 6971, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6971
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(702)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-127-6971

Alignment Scores:
Pred. No.:              1.91          Length:         702
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-127-6971 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
              |||:::|||                 ||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||              |||             |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 64
US-11-434-127-10773
; Sequence 10773, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10773
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-10773

Alignment Scores:
Pred. No.:              1.91          Length:         702
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-127-10773 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
              |||:::|||                 ||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||              |||             |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
```

```
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 65
US-11-434-199-6971
; Sequence 6971, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6971
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(702)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-199-6971

Alignment Scores:
Pred. No.:              1.91          Length:         702
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-199-6971 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   |||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::        |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 66
US-11-434-199-10773
; Sequence 10773, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10773
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-10773

Alignment Scores:
Pred. No.:              1.91          Length:         702
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-199-10773 (1-702)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   |||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::        |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 67
US-11-434-137-6969
; Sequence 6969, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
```

```
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6969
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-6969

Alignment Scores:
Pred. No.:              2.15          Length:        774
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-137-6969 (1-774)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db         61 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 117

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        118 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 177

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||             ||||||  ||||||  |||   :::
Db        178 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 237

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::       |||||||||:::   |||
Db        238 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 297

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||         |||           |||   :::
Db        298 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 357

Qy        105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db        358 GGTACAACAGTAGCCTTTGAA 378

RESULT 68
US-11-434-184-6969
; Sequence 6969, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6969
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-6969

Alignment Scores:
Pred. No.:              2.15          Length:        774
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-184-6969 (1-774)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db         61 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 117

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        118 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 177

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||             ||||||  ||||||  |||   :::
Db        178 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 237

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::       |||||||||:::   |||
Db        238 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 297

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||         |||           |||   :::
Db        298 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 357

Qy        105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db        358 GGTACAACAGTAGCCTTTGAA 378

RESULT 69
US-11-434-203-6969
; Sequence 6969, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6969
```

```
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-6969

Alignment Scores:
Pred. No.:              2.15          Length:         774
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-203-6969 (1-774)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::           |||   :::|||      :::|||
Db         61 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 117

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        118 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 177

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db        178 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 237

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::         |||||||||:::   |||
Db        238 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 297

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        298 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 357

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        358 GGTACAACAGTAGCCTTTGAA 378

RESULT 70
US-11-434-127-6969
; Sequence 6969, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6969
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-6969

Alignment Scores:
Pred. No.:              2.15          Length:         774
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-127-6969 (1-774)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::           |||   :::|||      :::|||
Db         61 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 117

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        118 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 177

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db        178 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 237

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::         |||||||||:::   |||
Db        238 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 297

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        298 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 357

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        358 GGTACAACAGTAGCCTTTGAA 378

RESULT 71
US-11-434-199-6969
; Sequence 6969, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6969
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-6969

Alignment Scores:
Pred. No.:              2.15          Length:         774
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-199-6969 (1-774)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
```

```
              |||:::||||||      :::            |||   :::|||      :::|||
Db         61 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 117

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        118 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 177

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||            ||||||  ||||||  |||   :::
Db        178 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 237

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        238 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 297

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        298 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 357

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        358 GGTACAACAGTAGCCTTTGAA 378

RESULT 72
US-11-434-137-757
; Sequence 757, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 757
;   LENGTH: 1176
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-757

Alignment Scores:
Pred. No.:              3.62          Length:         1176
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-137-757 (1-1176)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
```

```
                 |||:::|||            ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 73
US-11-434-184-757
; Sequence 757, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 757
;   LENGTH: 1176
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-757

Alignment Scores:
Pred. No.:              3.62          Length:         1176
Score:                  78.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.2%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-184-757 (1-1176)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||            ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
```

```
                ::: ::: ||| ||| ||| :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                  |||::: |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 74
US-11-434-203-757
; Sequence 757, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 757
;   LENGTH: 1176
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-757

Alignment Scores:
Pred. No.:              3.62          Length:          1176
Score:                  78.50         Matches:         32
Percent Similarity:     43.9%         Conservative:    15
Best Local Similarity:  29.9%         Mismatches:      57
Query Match:            10.2%         Indels:          3
DB:                     8             Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-203-757 (1-1176)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||     :::          |||  :::|||     :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||     :::  ||||||       |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||               ||||||  ||||||  |||  :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||  |||                :::::       |||||||||:::  |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::  :::  |||          |||          |||  :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                  |||::: |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 75
US-11-434-127-757
; Sequence 757, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 757
;   LENGTH: 1176
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-757

Alignment Scores:
Pred. No.:              3.62          Length:          1176
Score:                  78.50         Matches:         32
Percent Similarity:     43.9%         Conservative:    15
Best Local Similarity:  29.9%         Mismatches:      57
Query Match:            10.2%         Indels:          3
DB:                     8             Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-127-757 (1-1176)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||     :::          |||  :::|||     :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||     :::  ||||||       |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||               ||||||  ||||||  |||  :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||  |||                :::::       |||||||||:::  |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::  :::  |||          |||          |||  :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                  |||::: |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 76
US-11-434-199-757
; Sequence 757, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
```

```
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 757
;   LENGTH: 1176
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-757

Alignment Scores:
Pred. No.:                3.62          Length:        1176
Score:                    78.50         Matches:       32
Percent Similarity:       43.9%         Conservative:  15
Best Local Similarity:    29.9%         Mismatches:    57
Query Match:              10.2%         Indels:        3
DB:                       8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-199-757 (1-1176)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                |||:::|||                 ||||||  ||||||  |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::        |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
              :::   :::   |||             |||         |||   :::
Db        346 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 77
US-11-434-137-9591
; Sequence 9591, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9591
;   LENGTH: 1362
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1362)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-137-9591

Alignment Scores:
Pred. No.:                4.34          Length:        1362
Score:                    78.50         Matches:       32
Percent Similarity:       43.9%         Conservative:  15
Best Local Similarity:    29.9%         Mismatches:    57
Query Match:              10.2%         Indels:        3
DB:                       8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-137-9591 (1-1362)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                |||:::|||                 ||||||  ||||||  |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::        |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
              :::   :::   |||             |||         |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047

RESULT 78
US-11-434-184-9591
; Sequence 9591, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
```

; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9591
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1362)
; OTHER INFORMATION: n = a, c, g, or t
US-11-434-184-9591

Alignment Scores:

Pred. No.:	4.34	Length:	1362
Score:	78.50	Matches:	32
Percent Similarity:	43.9%	Conservative:	15
Best Local Similarity:	29.9%	Mismatches:	57
Query Match:	10.2%	Indels:	3
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-434-184-9591 (1-1362)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||   ||||||   |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::  |||           |||           |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047
```

RESULT 79
US-11-434-203-9591
; Sequence 9591, Application US/11434203
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,203
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9591
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1362)
; OTHER INFORMATION: n = a, c, g, or t
US-11-434-203-9591

Alignment Scores:

Pred. No.:	4.34	Length:	1362
Score:	78.50	Matches:	32
Percent Similarity:	43.9%	Conservative:	15
Best Local Similarity:	29.9%	Mismatches:	57
Query Match:	10.2%	Indels:	3
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-434-203-9591 (1-1362)

```
Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||   ||||||   |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::  |||           |||           |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                    |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047
```

RESULT 80
US-11-434-127-9591
; Sequence 9591, Application US/11434127
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,127
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9591
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1362)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-127-9591

Alignment Scores:
Pred. No.:              4.34          Length:        1362
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-127-9591 (1-1362)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||       :::   ||||||          |||       |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                |||:::|||                ||||||  ||||||   |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                    ::::::        |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||           |||         |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047

RESULT 81
US-11-434-199-9591
; Sequence 9591, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9591
;   LENGTH: 1362
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1362)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-199-9591

Alignment Scores:
Pred. No.:              4.34          Length:        1362
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
DB:                     8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-199-9591 (1-1362)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::            |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||       :::   ||||||          |||       |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                |||:::|||                ||||||  ||||||   |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                    ::::::        |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||           |||         |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047

RESULT 82
US-11-434-137-763
; Sequence 763, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 763
;   LENGTH: 1401
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-763

Alignment Scores:
Pred. No.:              4.49          Length:        1401
Score:                  78.50         Matches:       32
Percent Similarity:     43.9%         Conservative:  15
Best Local Similarity:  29.9%         Mismatches:    57
Query Match:            10.2%         Indels:        3
```

```
DB:                    8             Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-137-763 (1-1401)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        769 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 825

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||     :::   ||||||         |||       |||
Db        826 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 885

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db        886 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 945

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                   ::::::         |||||||||:::   |||
Db        946 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 1005

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||             |||             |||   :::
Db       1006 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1065

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db       1066 GGTACAACAGTAGCCTTTGAA 1086

RESULT 83
US-11-434-184-763
; Sequence 763, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 763
;   LENGTH: 1401
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-763

Alignment Scores:
Pred. No.:              4.49          Length:          1401
Score:                  78.50         Matches:         32
Percent Similarity:     43.9%         Conservative:    15
Best Local Similarity:  29.9%         Mismatches:      57
Query Match:            10.2%         Indels:          3
DB:                     8             Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-184-763 (1-1401)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        769 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 825

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||     :::   ||||||         |||       |||
Db        826 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 885

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db        886 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 945

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                   ::::::         |||||||||:::   |||
Db        946 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 1005

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||             |||             |||   :::
Db       1006 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1065

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db       1066 GGTACAACAGTAGCCTTTGAA 1086

RESULT 84
US-11-434-203-763
; Sequence 763, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 763
;   LENGTH: 1401
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-763

Alignment Scores:
Pred. No.:              4.49          Length:          1401
Score:                  78.50         Matches:         32
Percent Similarity:     43.9%         Conservative:    15
Best Local Similarity:  29.9%         Mismatches:      57
Query Match:            10.2%         Indels:          3
DB:                     8             Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-203-763 (1-1401)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        769 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 825

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||     :::   ||||||         |||       |||
Db        826 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 885

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db        886 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 945
```

```
Qy          66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
               |||   |||                 :::::: .       |||||||||:::   |||
Db         946 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 1005

Qy          86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        1006 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1065

Qy         105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db        1066 GGTACAACAGTAGCCTTTGAA 1086
```

RESULT 85
US-11-434-127-763
; Sequence 763, Application US/11434127
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,127
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 763
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-11-434-127-763

Alignment Scores:

Pred. No.:	4.49	Length:	1401
Score:	78.50	Matches:	32
Percent Similarity:	43.9%	Conservative:	15
Best Local Similarity:	29.9%	Mismatches:	57
Query Match:	10.2%	Indels:	3
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-434-127-763 (1-1401)

```
Qy           7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
               |||:::||||||      :::          |||   :::|||      :::|||
Db         769 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 825

Qy          27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
               |||||||||   |||      :::   ||||||          |||      |||
Db         826 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 885

Qy          46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db         886 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 945

Qy          66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
               |||   |||                 ::::::          |||||||||:::   |||
Db         946 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 1005

Qy          86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        1006 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1065

Qy         105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db        1066 GGTACAACAGTAGCCTTTGAA 1086
```

RESULT 86
US-11-434-199-763
; Sequence 763, Application US/11434199
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,199
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 763
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-11-434-199-763

Alignment Scores:

Pred. No.:	4.49	Length:	1401
Score:	78.50	Matches:	32
Percent Similarity:	43.9%	Conservative:	15
Best Local Similarity:	29.9%	Mismatches:	57
Query Match:	10.2%	Indels:	3
DB:	8	Gaps:	3

US-10-758-902-9 (1-149) x US-11-434-199-763 (1-1401)

```
Qy           7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
               |||:::||||||      :::          |||   :::|||      :::|||
Db         769 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 825

Qy          27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
               |||||||||   |||      :::   ||||||          |||      |||
Db         826 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 885

Qy          46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||  ||||||  |||   :::
Db         886 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 945

Qy          66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
               |||   |||                 ::::::          |||||||||:::   |||
Db         946 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 1005

Qy          86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||           |||           |||   :::
Db        1006 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1065

Qy         105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db        1066 GGTACAACAGTAGCCTTTGAA 1086
```

RESULT 87
US-11-434-137-9593
; Sequence 9593, Application US/11434137
; GENERAL INFORMATION:

```
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9593
;   LENGTH: 4167
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-9593

Alignment Scores:
Pred. No.:                17.3          Length:          4167
Score:                    78.50         Matches:         32
Percent Similarity:       43.9%         Conservative:    15
Best Local Similarity:    29.9%         Mismatches:      57
Query Match:              10.2%         Indels:          3
DB:                       8             Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-137-9593 (1-4167)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   |||||   |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||            |||            |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047

RESULT 88
US-11-434-184-9593
; Sequence 9593, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9593
;   LENGTH: 4167
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-9593

Alignment Scores:
Pred. No.:                17.3          Length:          4167
Score:                    78.50         Matches:         32
Percent Similarity:       43.9%         Conservative:    15
Best Local Similarity:    29.9%         Mismatches:      57
Query Match:              10.2%         Indels:          3
DB:                       8             Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-184-9593 (1-4167)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   |||||   |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||            |||            |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047

RESULT 89
US-11-434-203-9593
; Sequence 9593, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
```

```
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9593
;   LENGTH: 4167
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-9593

Alignment Scores:
Pred. No.:                17.3          Length:          4167
Score:                    78.50         Matches:         32
Percent Similarity:       43.9%         Conservative:    15
Best Local Similarity:    29.9%         Mismatches:      57
Query Match:              10.2%         Indels:          3
DB:                       8             Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-203-9593 (1-4167)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::           |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||  ||||||   |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::         |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||            |||            |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047

RESULT 90
US-11-434-127-9593
; Sequence 9593, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9593
;   LENGTH: 4167
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-9593

Alignment Scores:
Pred. No.:                17.3          Length:          4167
Score:                    78.50         Matches:         32
Percent Similarity:       43.9%         Conservative:    15
Best Local Similarity:    29.9%         Mismatches:      57
Query Match:              10.2%         Indels:          3
DB:                       8             Gaps:            3

US-10-758-902-9 (1-149) x US-11-434-127-9593 (1-4167)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::           |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||  ||||||   |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::         |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||            |||            |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047

RESULT 91
US-11-434-199-9593
; Sequence 9593, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9593
;   LENGTH: 4167
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-9593

Alignment Scores:
Pred. No.:                17.3          Length:          4167
Score:                    78.50         Matches:         32
Percent Similarity:       43.9%         Conservative:    15
Best Local Similarity:    29.9%         Mismatches:      57
```

```
Query Match:            10.2%          Indels:        3
DB:                     8              Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-199-9593 (1-4167)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        730 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 786

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db        787 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 846

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db        847 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 906

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        907 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 966

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||            |||            |||   :::
Db        967 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 1026

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db       1027 GGTACAACAGTAGCCTTTGAA 1047

RESULT 92
US-11-434-137-10967
; Sequence 10967, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10967
;   LENGTH: 2160266
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-10967

Alignment Scores:
Pred. No.:              3.99e+04       Length:        2160266
Score:                  78.50          Matches:       32
Percent Similarity:     43.9%          Conservative:  15
Best Local Similarity:  29.9%          Mismatches:    57
Query Match:            10.2%          Indels:        3
DB:                     8              Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-137-10967 (1-2160266)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db     419450 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 419506

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db     419507 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 419566

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db     419567 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 419626

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db     419627 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 419686

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||            |||            |||   :::
Db     419687 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 419746

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db     419747 GGTACAACAGTAGCCTTTGAA 419767

RESULT 93
US-11-434-184-10967
; Sequence 10967, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10967
;   LENGTH: 2160266
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-10967

Alignment Scores:
Pred. No.:              3.99e+04       Length:        2160266
Score:                  78.50          Matches:       32
Percent Similarity:     43.9%          Conservative:  15
Best Local Similarity:  29.9%          Mismatches:    57
Query Match:            10.2%          Indels:        3
DB:                     8              Gaps:          3

US-10-758-902-9 (1-149) x US-11-434-184-10967 (1-2160266)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db     419450 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 419506

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||      |||
Db     419507 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 419566

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                |||||   ||||||   |||   :::
Db     419567 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 419626
```

```
Qy          66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
               |||   |||                 ::::::         |||||||||:::   |||
Db      419627 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 419686

Qy          86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                  :::   :::   |||             |||             |||   :::
Db      419687 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 419746

Qy         105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db      419747 GGTACAACAGTAGCCTTTGAA 419767

RESULT 94
US-11-434-203-10967
; Sequence 10967, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10967
;   LENGTH: 2160266
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-10967

Alignment Scores:
Pred. No.:              3.99e+04        Length:         2160266
Score:                  78.50           Matches:        32
Percent Similarity:     43.9%           Conservative:   15
Best Local Similarity:  29.9%           Mismatches:     57
Query Match:            10.2%           Indels:         3
DB:                     8               Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-203-10967 (1-2160266)

Qy           7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
               |||:::||||||      :::             |||   :::|||      :::|||
Db      419450 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 419506

Qy          27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
               |||||||||   |||       :::   ||||||          |||       |||
Db      419507 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 419566

Qy          46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                  |||:::|||                 ||||||   ||||||   |||   :::
Db      419567 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 419626

Qy          66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
               |||   |||                 ::::::         |||||||||:::   |||
Db      419627 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 419686

Qy          86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                  :::   :::   |||             |||             |||   :::
Db      419687 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 419746

Qy         105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db      419747 GGTACAACAGTAGCCTTTGAA 419767

RESULT 95
US-11-434-127-10967
; Sequence 10967, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10967
;   LENGTH: 2160266
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-10967

Alignment Scores:
Pred. No.:              3.99e+04        Length:         2160266
Score:                  78.50           Matches:        32
Percent Similarity:     43.9%           Conservative:   15
Best Local Similarity:  29.9%           Mismatches:     57
Query Match:            10.2%           Indels:         3
DB:                     8               Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-127-10967 (1-2160266)

Qy           7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
               |||:::||||||      :::             |||   :::|||      :::|||
Db      419450 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 419506

Qy          27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
               |||||||||   |||       :::   ||||||          |||       |||
Db      419507 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 419566

Qy          46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                  |||:::|||                 ||||||   ||||||   |||   :::
Db      419567 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 419626

Qy          66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
               |||   |||                 ::::::         |||||||||:::   |||
Db      419627 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 419686

Qy          86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                  :::   :::   |||             |||             |||   :::
Db      419687 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 419746

Qy         105 ArgValThrLeuThrPheAsp 111
                  |||:::   |||:::
Db      419747 GGTACAACAGTAGCCTTTGAA 419767

RESULT 96
US-11-434-199-10967
; Sequence 10967, Application US/11434199
```

```
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10967
;   LENGTH: 2160266
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-10967

Alignment Scores:
Pred. No.:              3.99e+04        Length:         2160266
Score:                  78.50           Matches:        32
Percent Similarity:     43.9%           Conservative:   15
Best Local Similarity:  29.9%           Mismatches:     57
Query Match:            10.2%           Indels:         3
DB:                     8               Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-199-10967 (1-2160266)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db     419450 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 419506

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||       |||
Db     419507 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 419566

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                |||:::|||             ||||||   ||||||   |||   :::
Db     419567 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 419626

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                  ::::::         |||||||||:::   |||
Db     419627 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 419686

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                 :::   :::   |||             |||             |||   :::
Db     419687 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 419746

Qy        105 ArgValThrLeuThrPheAsp 111
                |||:::   |||:::
Db     419747 GGTACAACAGTAGCCTTTGAA 419767

RESULT 97
US-10-805-394A-1/c
; Sequence 1, Application US/10805394A
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/10/805,394A
;  CURRENT FILING DATE:  2004-03-22
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
;   LENGTH: 3309400
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-10-805-394A-1

Alignment Scores:
Pred. No.:              1.04e+05        Length:         3309400
Score:                  77.00           Matches:        39
Percent Similarity:     42.4%           Conservative:   20
Best Local Similarity:  28.1%           Mismatches:     58
Query Match:            10.0%           Indels:         22
DB:                     6               Gaps:           6

US-10-758-902-9 (1-149) x US-10-805-394A-1 (1-3309400)

Qy         10 GluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAlaLysGlyThr 29
              ||||||   |||   |||       :::                   :::   :::|||
Db     958866 GAGGCTGTCGAGCTGCCCGGCAGGGTC-----------------GTCCGTCGCGGCGAC 958825

Qy         30 ProValCysGlnLeuProValThrLeuGlnThrIleAlaAspAspLysArgPheValLeu 49
                 |||       ||||||          |||   |||   |||:::|||
Db     958824 AAGGTGCGGGTGCTGCCTCCGCGAGGGGGGACAAAGGCAGGTGACCAACGGCTG------ 958771

Qy         50 ValAspIleThrThrThrSerLysLysThrValLysVal---AlaIleAspValThrAsp 68
                                        :::|||   ::::::      :::|||
Db     958770 --------------------TGGCGGACAACTCGGATCGAGTGCGTCGACGGGCAGCGT 958732

Qy         69 ValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaValPheLeuAsp 88
              |||     :::         |||       :::   :::   |||||||||      |||
Db     958731 GTGGCTCATCTCGCGGAGCTCGACGTCGAAGAACCCGAGACTCGGGCAGTGCTTGCCGAC 958672

Qy         89 LysValProThrValAla------ThrSerLysLeuProGlyVal------ThrAsn 104
                 |||       ||||||          :::::::::||||||:::      |||
Db     958671 GACGTGGTGGTCGTCGCGGAGTTCCGGGATCGCATCTACCCCGGCCTGGTGGAGACAGGC 958612

Qy        105 ArgValThrLeuThrPheAspGlySerTyrGlnLysLeuValAsnAlaAlaLysValAsp 124
                ||||||             |||      :::      :::|||||||||
Db     958611 AGGGTTGAGCGGGGCGGCGACAAGCCGTTCCACACGGTCGTCAACGCTGAGAACTACCAC 958552

Qy        125 ArgLysAspLeuGluLeuGlyValTyrLysLeuGluPheSerIleGluAlaIleTrp 143
                  ||||||:::      |||             ||||||:::||||||:::
Db     958551 GCG------CTGGAGATGCTGACCTATACGCACCGGCATTCCATCGACGCCATCTAC 958501

RESULT 98
US-11-434-137-7201
; Sequence 7201, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
```

```
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7201
;   LENGTH: 726
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(726)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-137-7201

Alignment Scores:
Pred. No.:              3.56          Length:         726
Score:                  76.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.0%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-137-7201 (1-726)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||               ||||||  ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||           |||           |||   :::
Db        346 AATGTATGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 99
US-11-434-184-7201
; Sequence 7201, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7201
;   LENGTH: 726
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(726)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-184-7201

Alignment Scores:
Pred. No.:              3.56          Length:         726
Score:                  76.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.0%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-184-7201 (1-726)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::             |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||          |||       |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||               ||||||  ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::          |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                :::   :::   |||           |||           |||   :::
Db        346 AATGTATGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426

RESULT 100
US-11-434-203-7201
; Sequence 7201, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
```

```
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7201
;   LENGTH: 726
;   TYPE: DNA
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(726)
;   OTHER INFORMATION: n = a, c, g, or t
US-11-434-203-7201

Alignment Scores:
Pred. No.:              3.56          Length:         726
Score:                  76.50         Matches:        32
Percent Similarity:     43.9%         Conservative:   15
Best Local Similarity:  29.9%         Mismatches:     57
Query Match:            10.0%         Indels:         3
DB:                     8             Gaps:           3

US-10-758-902-9 (1-149) x US-11-434-203-7201 (1-726)

Qy          7 AsnLeuGlyGluAlaTyrGluTyrProThrPheIleGlnAspLeuArgAsnGluLeuAla 26
              |||:::||||||      :::          |||   :::|||      :::|||
Db        109 AATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTA---CCAGATCTTCCG 165

Qy         27 LysGlyThrProValCys---GlnLeuProValThrLeuGlnThrIleAlaAspAspLys 45
              |||||||||   |||      :::   ||||||         |||      |||
Db        166 AAAGGTACAACAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCA 225

Qy         46 ArgPheValLeuValAspIleThrThrThrSerLysLysThrValLysValAlaIleAsp 65
                 |||:::|||                 ||||||   ||||||   |||   :::
Db        226 GCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAG 285

Qy         66 ValThrAspValTyrValValGlyTyrGlnAspLysTrpAspGlyLysAspArgAlaVal 85
              |||   |||                 ::::::         |||||||||:::   |||
Db        286 GTTGTCGATCCACGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTC 345

Qy         86 PheLeuAspLysValProThrValAlaThrSer---LysLeuPheProGlyValThrAsn 104
                ::   :::   |||             |||             |||   :::
Db        346 AATGTATGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAA 405

Qy        105 ArgValThrLeuThrPheAsp 111
                 |||:::   |||:::
Db        406 GGTACAACAGTAGCCTTTGAA 426


Search completed: September 18, 2006, 21:10:27
Job time : 2098.98 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:14:17 ; Search time 37.4581 Seconds
(without alignments)
348.177 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	768	100.0	149	2	US-09-445-160B-9	Sequence 9, Appli
2	221.5	28.8	250	1	US-07-901-707-8	Sequence 8, Appli
3	221.5	28.8	250	1	US-07-988-430-8	Sequence 8, Appli
4	221.5	28.8	250	1	US-08-425-336-8	Sequence 8, Appli
5	221.5	28.8	250	1	US-08-488-113B-8	Sequence 8, Appli
6	221.5	28.8	250	1	US-08-477-484B-8	Sequence 8, Appli
7	221.5	28.8	250	1	US-08-646-360-8	Sequence 8, Appli
8	221.5	28.8	250	2	US-08-839-765-8	Sequence 8, Appli
9	221.5	28.8	250	2	US-09-136-389-8	Sequence 8, Appli
10	221.5	28.8	250	2	US-09-610-838-8	Sequence 8, Appli
11	221.5	28.8	250	2	US-09-711-485-8	Sequence 8, Appli
12	221.5	28.8	250	5	PCT-US92-09487-8	Sequence 8, Appli
13	220.5	28.7	263	1	US-07-901-707-4	Sequence 4, Appli
14	220.5	28.7	263	1	US-07-988-430-4	Sequence 4, Appli
15	220.5	28.7	263	1	US-08-425-336-4	Sequence 4, Appli
16	220.5	28.7	263	1	US-08-488-113B-4	Sequence 4, Appli
17	220.5	28.7	263	1	US-08-477-484B-4	Sequence 4, Appli
18	220.5	28.7	263	1	US-08-646-360-4	Sequence 4, Appli
19	220.5	28.7	263	2	US-08-839-765-4	Sequence 4, Appli
20	220.5	28.7	263	2	US-09-136-389-4	Sequence 4, Appli
21	220.5	28.7	263	2	US-09-610-838-4	Sequence 4, Appli
22	220.5	28.7	263	2	US-09-711-485-4	Sequence 4, Appli
23	220.5	28.7	263	2	US-09-645-603B-1	Sequence 1, Appli
24	220.5	28.7	263	5	PCT-US92-09487-4	Sequence 4, Appli
25	220.5	28.7	286	1	US-08-324-301-13	Sequence 13, Appl
26	217.5	28.3	250	1	US-08-378-761A-76	Sequence 76, Appl
27	217.5	28.3	250	1	US-08-485-286-76	Sequence 76, Appl
28	211.5	27.5	250	1	US-07-854-845B-8	Sequence 8, Appli
29	190.5	24.8	282	1	US-08-324-301-15	Sequence 15, Appl
30	183.5	23.9	247	1	US-08-488-113B-6	Sequence 6, Appli
31	183.5	23.9	247	1	US-08-477-484B-6	Sequence 6, Appli
32	183.5	23.9	247	1	US-08-646-360-6	Sequence 6, Appli
33	183.5	23.9	247	2	US-08-839-765-6	Sequence 6, Appli
34	183.5	23.9	247	2	US-09-136-389-6	Sequence 6, Appli
35	183.5	23.9	247	2	US-09-610-838-6	Sequence 6, Appli
36	183.5	23.9	247	2	US-09-711-485-6	Sequence 6, Appli
37	183.5	23.9	267	1	US-08-378-761A-74	Sequence 74, Appl
38	183.5	23.9	267	1	US-08-485-286-74	Sequence 74, Appl
39	183.5	23.9	289	1	US-07-923-692C-4	Sequence 4, Appli
40	183.5	23.9	289	1	US-08-184-237-4	Sequence 4, Appli
41	183.5	23.9	289	1	US-08-482-920-4	Sequence 4, Appli
42	183.5	23.9	289	2	US-08-484-341-4	Sequence 4, Appli
43	183.5	23.9	289	2	US-08-483-502-4	Sequence 4, Appli
44	183.5	23.9	289	2	US-09-726-651A-4	Sequence 4, Appli
45	179.5	23.4	248	2	US-08-902-486-7	Sequence 7, Appli
46	179.5	23.4	254	2	US-09-601-667C-37	Sequence 37, Appl
47	179.5	23.4	256	2	US-09-601-667C-5	Sequence 5, Appli
48	179.5	23.4	256	2	US-09-601-667C-38	Sequence 38, Appl
49	179.5	23.4	290	1	US-08-245-754A-2	Sequence 2, Appli
50	179.5	23.4	290	1	US-08-597-731-2	Sequence 2, Appli
51	179.5	23.4	496	2	US-08-902-486-15	Sequence 15, Appl
52	179	23.3	253	2	US-09-601-667C-39	Sequence 39, Appl
53	176.5	23.0	253	2	US-08-776-059-31	Sequence 31, Appl
54	176.5	23.0	531	2	US-09-601-667C-4	Sequence 4, Appli
55	176.5	23.0	564	2	US-08-776-059-35	Sequence 35, Appl
56	176	22.9	255	2	US-09-601-667C-2	Sequence 2, Appli
57	176	22.9	533	2	US-09-601-667C-1	Sequence 1, Appli
58	174.5	22.7	263	1	US-07-901-707-7	Sequence 7, Appli
59	174.5	22.7	263	1	US-07-988-430-7	Sequence 7, Appli
60	174.5	22.7	263	1	US-08-425-336-7	Sequence 7, Appli
61	174.5	22.7	263	1	US-08-488-113B-7	Sequence 7, Appli
62	174.5	22.7	263	1	US-08-477-484B-7	Sequence 7, Appli
63	174.5	22.7	263	1	US-08-646-360-7	Sequence 7, Appli
64	174.5	22.7	263	2	US-08-839-765-7	Sequence 7, Appli
65	174.5	22.7	263	2	US-09-136-389-7	Sequence 7, Appli
66	174.5	22.7	263	2	US-09-610-838-7	Sequence 7, Appli
67	174.5	22.7	263	2	US-09-711-485-7	Sequence 7, Appli
68	174.5	22.7	263	5	PCT-US92-09487-7	Sequence 7, Appli
69	174.5	22.7	279	2	US-09-627-165E-16	Sequence 16, Appl
70	172.5	22.5	256	2	US-09-601-667C-41	Sequence 41, Appl
71	172.5	22.5	534	2	US-09-601-667C-40	Sequence 40, Appl
72	171.5	22.3	254	2	US-09-627-165E-4	Sequence 4, Appli
73	169.5	22.1	235	2	US-08-776-059-39	Sequence 39, Appl
74	169	22.0	198	2	US-10-083-336A-3	Sequence 3, Appli
75	169	22.0	198	2	US-10-083-336A-7	Sequence 7, Appli
76	169	22.0	199	2	US-10-083-336A-5	Sequence 5, Appli
77	169	22.0	200	2	US-10-083-336A-10	Sequence 10, Appl
78	169	22.0	267	1	US-07-901-707-1	Sequence 1, Appli
79	169	22.0	267	1	US-07-988-430-1	Sequence 1, Appli
80	169	22.0	267	1	US-08-218-303-16	Sequence 16, Appl
81	169	22.0	267	1	US-08-425-336-1	Sequence 1, Appli
82	169	22.0	267	1	US-08-488-113B-1	Sequence 1, Appli
83	169	22.0	267	1	US-08-477-484B-1	Sequence 1, Appli
84	169	22.0	267	1	US-08-646-360-1	Sequence 1, Appli
85	169	22.0	267	1	US-08-338-793D-61	Sequence 61, Appl
86	169	22.0	267	2	US-08-839-765-1	Sequence 1, Appli
87	169	22.0	267	2	US-09-136-389-1	Sequence 1, Appli
88	169	22.0	267	2	US-09-610-838-1	Sequence 1, Appli
89	169	22.0	267	2	US-09-538-873-1	Sequence 1, Appli
90	169	22.0	267	2	US-09-711-485-1	Sequence 1, Appli
91	169	22.0	267	2	US-10-282-935-1	Sequence 1, Appli
92	169	22.0	267	5	PCT-US92-09487-1	Sequence 1, Appli
93	169	22.0	268	1	US-08-356-786-8	Sequence 8, Appli
94	169	22.0	290	1	US-08-378-761A-27	Sequence 27, Appl
95	169	22.0	290	1	US-08-485-286-27	Sequence 27, Appl
96	169	22.0	290	7	5248606-4	Patent No. 5248606
97	169	22.0	534	1	US-08-356-786-10	Sequence 10, Appl
98	169	22.0	576	2	US-10-083-336A-1	Sequence 1, Appli
99	168.5	21.9	254	2	US-09-627-165E-2	Sequence 2, Appli

100 167 21.7 250 1 US-08-378-761A-80 Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-09-445-160B-9
; Sequence 9, Application US/09445160B
; Patent No. 6680296
; GENERAL INFORMATION:
; APPLICANT: Stirpe, Fiorenza
; APPLICANT: Bolognesi, Andrea
; TITLE OF INVENTION: Type 1 Ribosome Inactivating Protein
; FILE REFERENCE: Stirpe
; CURRENT APPLICATION NUMBER: US/09/445,160B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/NL98/00336
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: EP 97201725.5
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 9
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Bougainvillea spectrabilis
; NAME/KEY:
; LOCATION: 143
; OTHER INFORMATION: Trp uncertain
; PUBLICATION INFORMATION:
US-09-445-160B-9

Query Match 100.0%; Score 768; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.6e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |||||||||||||||||||||||||||||
Db        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
```

RESULT 2
US-07-901-707-8
; Sequence 8, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,707
; FILING DATE: 19920619
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5376546and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27129/30910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-5750
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-901-707-8

Query Match 28.8%; Score 221.5; DB 1; Length 250;
Best Local Similarity 37.2%; Pred. No. 3e-17;
Matches 54; Conservative 27; Mismatches 55; Indels 9; Gaps 4;

```
Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148
```

RESULT 3
US-07-988-430-8
; Sequence 8, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,430
;      FILING DATE:  19921209
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5416202and, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-988-430-8

  Query Match             28.8%;  Score 221.5;  DB 1;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                 : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 4
US-08-425-336-8
; Sequence 8, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-425-336-8

  Query Match             28.8%;  Score 221.5;  DB 1;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                 : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 5
US-08-488-113B-8
; Sequence 8, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-8

  Query Match             28.8%;  Score 221.5;  DB 1;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 6
US-08-477-484B-8
; Sequence 8, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-8

  Query Match             28.8%;  Score 221.5;  DB 1;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 7
US-08-646-360-8
; Sequence 8, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-360-8

  Query Match             28.8%;  Score 221.5;  DB 1;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                 : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 8
US-08-839-765-8
; Sequence 8, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-8

  Query Match             28.8%;  Score 221.5;  DB 2;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                 : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 9
US-09-136-389-8
; Sequence 8, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
```

```
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-8

  Query Match             28.8%;  Score 221.5;  DB 2;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 10
US-09-610-838-8
; Sequence 8, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/610,838
;      FILING DATE:  06-JUL-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:  18-AUG-1998
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-610-838-8

  Query Match             28.8%;  Score 221.5;  DB 2;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 11
US-09-711-485-8
; Sequence 8, Application US/09711485
; Patent No. 6649742
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
```

```
;       COUNTRY:  USA
;       ZIP:  60661
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/711,485
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/839,765
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  250 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-711-485-8

  Query Match             28.8%;  Score 221.5;  DB 2;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|   |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                 : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 12
PCT-US92-09487-8
; Sequence 8, Application PC/TUS9209487
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/09487
;      FILING DATE:  19921104
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US92-09487-8

  Query Match             28.8%;  Score 221.5;  DB 5;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 3e-17;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|   |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                 : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 13
US-07-901-707-4
; Sequence 4, Application US/07901707
; Patent No. 5376546
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Composition and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
```

```
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60603
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/901,707
;       FILING DATE:  19920619
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  No. 5376546and, Greta E.
;       REGISTRATION NUMBER:  35,302
;       REFERENCE/DOCKET NUMBER:  27129/30910
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 346-5750
;       TELEFAX:  (312) 984-5750
;       TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  263 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-07-901-707-4

  Query Match             28.7%;  Score 220.5;  DB 1;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 14
US-07-988-430-4
; Sequence 4, Application US/07988430
; Patent No. 5416202
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,430
;      FILING DATE:  19921209
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5416202and, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-988-430-4

  Query Match             28.7%;  Score 220.5;  DB 1;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 15
US-08-425-336-4
; Sequence 4, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-425-336-4

  Query Match             28.7%;  Score 220.5;  DB 1;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |     |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 16
US-08-488-113B-4
; Sequence 4, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-4

  Query Match             28.7%;  Score 220.5;  DB 1;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |     |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 17
US-08-477-484B-4
; Sequence 4, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  263 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-477-484B-4

  Query Match             28.7%;  Score 220.5;  DB 1;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      | :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                . |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 18
US-08-646-360-4
; Sequence 4, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;       FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-360-4

  Query Match             28.7%;  Score 220.5;  DB 1;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      | :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 19
US-08-839-765-4
; Sequence 4, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-4

  Query Match             28.7%;  Score 220.5;  DB 2;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 20
US-09-136-389-4
; Sequence 4, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-4

  Query Match             28.7%;  Score 220.5;  DB 2;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 21
US-09-610-838-4
; Sequence 4, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/610,838
;       FILING DATE:  06-JUL-2000
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/136,389
;       FILING DATE:  18-AUG-1998
;       APPLICATION NUMBER:  08/646,360
;       FILING DATE:  13-MAY-1996
;       APPLICATION NUMBER:  PCT/US94/05348
;       FILING DATE:  12-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  200-70.P4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  263 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-610-838-4

  Query Match             28.7%;  Score 220.5;  DB 2;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                 |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 22
US-09-711-485-4
; Sequence 4, Application US/09711485
; Patent No. 6649742
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/711,485
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/839,765
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-711-485-4

  Query Match             28.7%;  Score 220.5;  DB 2;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                 |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 23
US-09-645-603B-1
; Sequence 1, Application US/09645603B
; Patent No. 6652861
; GENERAL INFORMATION:
;  APPLICANT: LEE-HUANG, Sylvia
;  TITLE OF INVENTION: Anti-HIV and Anti-tumor Peptides and Truncated Polypeptides of
;  TITLE OF INVENTION:  map30 and gap31
;  FILE REFERENCE: LEE-HUANG 4A
;  CURRENT APPLICATION NUMBER: US/09/645,603B
;  CURRENT FILING DATE:  2000-08-25
;  PRIOR APPLICATION NUMBER: US 60/150,885
;  PRIOR FILING DATE: 1999-08-26
```

```
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 263
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-09-645-603B-1

  Query Match             28.7%;  Score 220.5;  DB 2;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|     |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                   |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 24
PCT-US92-09487-4
; Sequence 4, Application PC/TUS9209487
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/09487
;      FILING DATE:  19921104
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US92-09487-4

  Query Match             28.7%;  Score 220.5;  DB 5;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 4.2e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|     |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                   |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 25
US-08-324-301-13
; Sequence 13, Application US/08324301
; Patent No. 5597569
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    APPLICANT:  Gawlak, Susan L.
;    APPLICANT:  Marquardt, Hans
;    TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;    TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONICA DIOICA
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,301
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/141,891
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0109A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-728-4800
;      TELEFAX:  206-727-3601
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  286 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Momordica charantia
US-08-324-301-13

  Query Match             28.7%;  Score 220.5;  DB 1;  Length 286;
  Best Local Similarity   36.6%;  Pred. No. 4.8e-17;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;
```

```
Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db         25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         85 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 139

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        140 HKIRENIDLGLPALSSAITTLF 161


RESULT 26
US-08-378-761A-76
; Sequence 76, Application US/08378761A
; Patent No. 5635384
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761A
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  76:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-761A-76

  Query Match             28.3%;  Score 217.5;  DB 1;  Length 250;
  Best Local Similarity   36.6%;  Pred. No. 8.8e-17;
  Matches   53;  Conservative   27;  Mismatches   56;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::   |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVVDKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                 : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 27
US-08-485-286-76
; Sequence 76, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,286
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/378761
;      FILING DATE:  26-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  76:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-485-286-76

  Query Match             28.3%;  Score 217.5;  DB 1;  Length 250;
  Best Local Similarity   36.6%;  Pred. No. 8.8e-17;
  Matches   53;  Conservative   27;  Mismatches   56;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::   |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVVDKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                 : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 28
US-07-854-845B-8
; Sequence 8, Application US/07854845B
; Patent No. 5340732
;  GENERAL INFORMATION:
;    APPLICANT:  HABUKA, No. 5340732iyuki
;    APPLICANT:  MIYANO, Masashi
;    APPLICANT:  MATSUMOTO, Takashi
;    APPLICANT:  NOMA, Masana
```

```
;    TITLE OF INVENTION:  ANTIVIRAL PROTEIN
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH, & BIRCH
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22042
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/854,845B
;      FILING DATE:  20-MAR-1992
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy Jr., Gerald M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  42-194P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-205-8000
;      TELEFAX:  703-205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  Mirabilis jalapa
US-07-854-845B-8

  Query Match             27.5%;  Score 211.5;  DB 1;  Length 250;
  Best Local Similarity   36.6%;  Pred. No. 4.3e-16;
  Matches   53;  Conservative   27;  Mismatches   56;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |        |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTE----QSTIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                 : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 29
US-08-324-301-15
; Sequence 15, Application US/08324301
; Patent No. 5597569
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    APPLICANT:  Gawlak, Susan L.
;    APPLICANT:  Marquardt, Hans
;    TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;    TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONICA DIOICA
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,301
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/141,891
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0109A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-728-4800
;      TELEFAX:  206-727-3601
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  282 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
;      TISSUE TYPE:  leaf
US-08-324-301-15

  Query Match             24.8%;  Score 190.5;  DB 1;  Length 282;
  Best Local Similarity   39.1%;  Pred. No. 1.3e-13;
  Matches   50;  Conservative   24;  Mismatches   47;  Indels    7;  Gaps    4;

Qy         14 YPTFIQDLRNELAKGTP-VCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVV 72
              | |||::|| :|  ||| |  :||      |   || || :|  : ::| ||:|| :||||
Db         36 YKTFIRNLRTKLTVGTPRVYDIPVLRNAAAGLARFQLVTLTNYNGESVTVALDVVNVYVV 95

Qy         73 GYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA-KVDRKDLELG 131
                |:      : | ||    | | : || |: | | | : |:|  |  || :: |:::|||
Db         96 AYR----AGNTAYFLADASTEANNVLFAGI-NHVRLPYGGNYDGLETAAGRISRENIELG 150

Qy        132 VYKLEFSI 139
                 ::  :|
Db        151 FSEISSAI 158


RESULT 30
US-08-488-113B-6
; Sequence 6, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-6

  Query Match             23.9%;  Score 183.5;  DB 1;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 7.1e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 31
US-08-477-484B-6
; Sequence 6, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-6

  Query Match             23.9%;  Score 183.5;  DB 1;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 7.1e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 32
US-08-646-360-6
; Sequence 6, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/646,360
;       FILING DATE:  13-MAY-1996
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/05348
;       FILING DATE:  12-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  200-70.P4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  247 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-646-360-6

  Query Match             23.9%;  Score 183.5;  DB 1;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 7.1e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 33
US-08-839-765-6
; Sequence 6, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-6

  Query Match             23.9%;  Score 183.5;  DB 2;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 7.1e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 34
US-09-136-389-6
; Sequence 6, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
```

```
;       COUNTRY:  USA
;       ZIP:  60661
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/136,389
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/646,360
;       FILING DATE:  13-MAY-1996
;       APPLICATION NUMBER:  PCT/US94/05348
;       FILING DATE:  12-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  200-70.P4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  247 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-136-389-6

  Query Match             23.9%;  Score 183.5;  DB 2;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 7.1e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                 |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 35
US-09-610-838-6
; Sequence 6, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;       STREET:  500 West Madison Street, 34th floor
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60661
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/610,838
;       FILING DATE:  06-JUL-2000
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/136,389
;       FILING DATE:  18-AUG-1998
;       APPLICATION NUMBER:  08/646,360
;       FILING DATE:  13-MAY-1996
;       APPLICATION NUMBER:  PCT/US94/05348
;       FILING DATE:  12-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  200-70.P4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  247 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-610-838-6

  Query Match             23.9%;  Score 183.5;  DB 2;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 7.1e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                 |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 36
US-09-711-485-6
; Sequence 6, Application US/09711485
; Patent No. 6649742
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
```

```
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/711,485
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/839,765
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-711-485-6

  Query Match             23.9%;  Score 183.5;  DB 2;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 7.1e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 37
US-08-378-761A-74
; Sequence 74, Application US/08378761A
; Patent No. 5635384
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761A
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  74:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-761A-74

  Query Match             23.9%;  Score 183.5;  DB 1;  Length 267;
  Best Local Similarity   31.0%;  Pred. No. 7.9e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db          3 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 62

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         63 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 119

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        120 GKIRENIPLGLPALDSAITTLF 141


RESULT 38
US-08-485-286-74
; Sequence 74, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
```

; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-286-74

Query Match 23.9%; Score 183.5; DB 1; Length 267;
Best Local Similarity 31.0%; Pred. No. 7.9e-13;
Matches 44; Conservative 32; Mismatches 61; Indels 5; Gaps 2;

```
Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     : :|:  ::   :|: |: :|  : :|:
Db          3 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 62

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         63 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 119

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        120 GKIRENIPLGLPALDSAITTLF 141
```

RESULT 39
US-07-923-692C-4
; Sequence 4, Application US/07923692C
; Patent No. 5316931
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William 0.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CAL
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,692C
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,244
; FILING DATE: 22-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 641,617
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 310,881
; FILING DATE: 17-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,766
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,771
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 347,637
; FILING DATE: 05-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 363,138
; FILING DATE: 08-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 219,279
; FILING DATE: 15-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: BIOG-20121
; REFERENCE/DOCKET NUMBER: USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-433-4150
; TELEFAX: 415-433-8716
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-923-692C-4

Query Match 23.9%; Score 183.5; DB 1; Length 289;
Best Local Similarity 31.0%; Pred. No. 8.9e-13;
Matches 44; Conservative 32; Mismatches 61; Indels 5; Gaps 2;

```
Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     : :|:  ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163
```

RESULT 40
US-08-184-237-4
; Sequence 4, Application US/08184237
; Patent No. 5589367
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William 0.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS

```
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Limbach & Limbach
;      STREET:  2001 Ferry Building
;      CITY:  San Francisco
;      STATE:  CAL
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent in Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,237
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 923,692
;      FILING DATE:  31-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  BIOG-20121  USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-433-4150
;      TELEFAX:  415-433-8716
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  289 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-184-237-4

  Query Match             23.9%;  Score 183.5;  DB 1;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 8.9e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163
```

```
RESULT 41
US-08-482-920-4
; Sequence 4, Application US/08482920
; Patent No. 5866785
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent in Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,920
;      FILING DATE:  07-JUNE-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 184,237
;      FILING DATE:  19-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  8129-112
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  289 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-482-920-4

  Query Match             23.9%;  Score 183.5;  DB 1;  Length 289;
```

```
  Best Local Similarity   31.0%;  Pred. No. 8.9e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 42
US-08-484-341-4
; Sequence 4, Application US/08484341
;   GENERAL INFORMATION:
;        APPLICANT: Donson, Jon
;                   Dawson, William 0.
;                   Grantham, George L.
;                   Turpen, Thomas H.
;                   Turpen, Ann Myers
;                   Garger, Stephen J.
;                   Grill, Laurence K.
;        TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Limbach & Limbach
;             STREET: 2001 Ferry Building
;             CITY: San Francisco
;             STATE: CAL
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Patent in Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/484,341
;             FILING DATE: 07-Jun-1995
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/184,237
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 600,244
;             FILING DATE: 22-OCT-1990
;             APPLICATION NUMBER: US 641,617
;             FILING DATE: 16-JAN-1991
;             APPLICATION NUMBER: US 310,881
;             FILING DATE: 17-FEB-1989
;             APPLICATION NUMBER: US 160,766
;             FILING DATE: 26-FEB-1988
;             APPLICATION NUMBER: US 160,771
;             FILING DATE: 26-FEB-1988
;             APPLICATION NUMBER: US 347,637
;             FILING DATE: 05-MAY-1989
;             APPLICATION NUMBER: US 363,138
;             FILING DATE: 08-JUN-1989
;             APPLICATION NUMBER: US 219,279
;             FILING DATE: 15-JUL-1988
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Halluin, Albert P.
;             REGISTRATION NUMBER: 28,957
;             REFERENCE/DOCKET NUMBER: BIOG-20121  USA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-433-4150
;             TELEFAX: 415-433-8716
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 289 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-484-341-4

  Query Match             23.9%;  Score 183.5;  DB 2;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 8.9e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 43
US-08-483-502-4
; Sequence 4, Application US/08483502
; Patent No. 6284492
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Venable, Baetjer, Howard & Civiletti
;      STREET:  1201 New York Avenue N.W., Suite 1000
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,502
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/739,143
;      FILING DATE:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ihnen, Jeffrey L.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  18604-090574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-962-4810
;      TELEFAX:  202-962-8300
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  289 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-483-502-4

  Query Match             23.9%;  Score 183.5;  DB 2;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 8.9e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 44
US-09-726-651A-4
; Sequence 4, Application US/09726651A
; Patent No. 6448046
; GENERAL INFORMATION:
;  APPLICANT: Donson, Jon
;  APPLICANT:  DAWSON, William O.
;  APPLICANT:  GRANTHAM, GEORGE L.
;  APPLICANT:  TURPEN, Thomas H.
;  APPLICANT:  TURPEN, Ann M.
;  APPLICANT:  GARGER, Stephen J.
;  APPLICANT:  GRILL, Laurence K.
;  TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
;  FILE REFERENCE: 008010023CNUS01
;  CURRENT APPLICATION NUMBER: US/09/726,651A
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: 08/483,502
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/184,237
;  PRIOR FILING DATE: 1994-01-19
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Chinese Cucumber alpha-trichosanthin
US-09-726-651A-4

  Query Match             23.9%;  Score 183.5;  DB 2;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 8.9e-13;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 45
US-08-902-486-7
; Sequence 7, Application US/08902486
; Patent No. 6140075
;  GENERAL INFORMATION:
;    APPLICANT:  Russel, David R.
;    APPLICANT:  Fuller, James T.
;    TITLE OF INVENTION:  METHOD FOR PRODUCING ANTIBODIES AND
;    TITLE OF INVENTION:  PROTEIN TOXINS IN PLANT CELLS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/902,486
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  670513.90261
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  248 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-902-486-7

  Query Match             23.4%;  Score 179.5;  DB 2;  Length 248;
  Best Local Similarity   30.8%;  Pred. No. 2.1e-12;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::|| |      |  :|:   :|:    |: |: :|  : :|:
Db          3 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 62

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         63 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 118

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
                |   |::: ||:  |: :|  ::
```

```
Db        119 AGKIRENIPLGLPALDSAITTLY 141


RESULT 46
US-09-601-667C-37
; Sequence 37, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 37
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1
US-09-601-667C-37

  Query Match             23.4%;  Score 179.5;  DB 2;  Length 254;
  Best Local Similarity   37.6%;  Pred. No. 2.1e-12;
  Matches   50;  Conservative   26;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db .       16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSVTAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:||| |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        130 LGIDQLIQSVTAL 142


RESULT 47
US-09-601-667C-5
; Sequence 5, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 5
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Lectin A2
US-09-601-667C-5

  Query Match             23.4%;  Score 179.5;  DB 2;  Length 256;
  Best Local Similarity   36.6%;  Pred. No. 2.2e-12;
  Matches   49;  Conservative   27;  Mismatches   49;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSITAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||      |:: ||   |  | : || | | :| :| | ||| |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFTGSYTDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 PLGIEQLIQSVSAL 144


RESULT 48
US-09-601-667C-38
; Sequence 38, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 38
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-09-601-667C-38

  Query Match             23.4%;  Score 179.5;  DB 2;  Length 256;
  Best Local Similarity   36.6%;  Pred. No. 2.2e-12;
  Matches   49;  Conservative   27;  Mismatches   49;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSITAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||      |:: ||   |  | : || | | :| :| | ||| |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFTGSYTDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 PLGIEQLIQSVSAL 144


RESULT 49
US-08-245-754A-2
; Sequence 2, Application US/08245754A
; Patent No. 5541110
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    TITLE OF INVENTION:  Cloning and Expression of a Gene
;    TITLE OF INVENTION:  Encoding Bryodin 1 From Bryonia dioica
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Aveune
;      CITY:  Seattle
;      STATE:  Washington
```

```
;       COUNTRY:  USA
;       ZIP:  98121
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/245,754A
;       FILING DATE:  06-MAY-1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poor, Brian W.
;       REGISTRATION NUMBER:  32,928
;       REFERENCE/DOCKET NUMBER:  ON0124
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 728-4800
;       TELEFAX:  (206) 727-3601
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  290 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FRAGMENT TYPE:  N-terminal
;     ORIGINAL SOURCE:
;       ORGANISM:  Bryonia dioica
US-08-245-754A-2

  Query Match             23.4%;  Score 179.5;  DB 1;  Length 290;
  Best Local Similarity   30.8%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db         25 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||        | : | ::      :| :|     :||| : |:|::|  |
Db         85 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 140

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        141 AGKIRENIPLGLPALDSAITTLY 163


RESULT 50
US-08-597-731-2
; Sequence 2, Application US/08597731
; Patent No. 5932447
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    TITLE OF INVENTION:  Cloning and Expression of a Gene
;    TITLE OF INVENTION:  Encoding Bryodin 1 From Bryonia dioica
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Aveune
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/597,731
;      FILING DATE:  07-FEB-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/245,754
;      FILING DATE:  06-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0124
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 728-4800
;      TELEFAX:  (206) 727-3601
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  290 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Bryonia dioica
US-08-597-731-2

  Query Match             23.4%;  Score 179.5;  DB 1;  Length 290;
  Best Local Similarity   30.8%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db         25 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||        | : | ::      :| :|     :||| : |:|::|  |
Db         85 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 140

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        141 AGKIRENIPLGLPALDSAITTLY 163


RESULT 51
US-08-902-486-15
; Sequence 15, Application US/08902486
; Patent No. 6140075
;  GENERAL INFORMATION:
;    APPLICANT:  Russel, David R.
;    APPLICANT:  Fuller, James T.
;    TITLE OF INVENTION:  METHOD FOR PRODUCING ANTIBODIES AND
;    TITLE OF INVENTION:  PROTEIN TOXINS IN PLANT CELLS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/902,486
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  670513.90261
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 496 amino acids
;      TYPE:  amino acid
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-902-486-15

  Query Match             23.4%;  Score 179.5;  DB 2;  Length 496;
  Best Local Similarity   30.8%;  Pred. No. 5.5e-12;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db          3 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 62

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         63 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 118

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
                 |   |::: ||:  |: :|  ::
Db        119 AGKIRENIPLGLPALDSAITTLY 141


RESULT 52
US-09-601-667C-39
; Sequence 39, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 39
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1 (matched)
US-09-601-667C-39

  Query Match             23.3%;  Score 179;  DB 2;  Length 253;
  Best Local Similarity   36.8%;  Pred. No. 2.4e-12;
  Matches   49;  Conservative   27;  Mismatches   47;  Indels   10;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSVTAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:||| |   |    : :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYA--GHRQIP 128

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        129 LGIDQLIQSVTAL 141


RESULT 53
US-08-776-059-31
; Sequence 31, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
;  APPLICANT: LENTZEN, Hans
;  APPLICANT: ECK, Jurgen
;  APPLICANT: BAUR, Axel
;  APPLICANT: ZINKE, Holger
;  TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
;  FILE REFERENCE: 674503-2003
;  CURRENT APPLICATION NUMBER: US/08/776,059B
;  CURRENT FILING DATE: 1999-06-19
;  EARLIER APPLICATION NUMBER: PCT/EP96/02273
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 95109949.8
;  EARLIER FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Viscum album
US-08-776-059-31

  Query Match             23.0%;  Score 176.5;  DB 2;  Length 253;
  Best Local Similarity   36.8%;  Pred. No. 4.7e-12;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|      ::  |||||::
Db         17 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 76

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:||| |   |    | :
Db         77 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 130

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 LGIDQLIQSVTAL 143


RESULT 54
US-09-601-667C-4
; Sequence 4, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 4
;   LENGTH: 531
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MLI match
US-09-601-667C-4

  Query Match             23.0%;  Score 176.5;  DB 2;  Length 531;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-11;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|      ::  |||||::
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:||| |   |    | :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
```

```
Db        130 LGIDQLIQSVTAL 142


RESULT 55
US-08-776-059-35
; Sequence 35, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
;  APPLICANT: LENTZEN, Hans
;  APPLICANT: ECK, Jurgen
;  APPLICANT: BAUR, Axel
;  APPLICANT: ZINKE, Holger
;  TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
;  FILE REFERENCE: 674503-2003
;  CURRENT APPLICATION NUMBER: US/08/776,059B
;  CURRENT FILING DATE: 1999-06-19
;  EARLIER APPLICATION NUMBER: PCT/EP96/02273
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 95109949.8
;  EARLIER FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 564
;   TYPE: PRT
;   ORGANISM: Viscum album
US-08-776-059-35

  Query Match             23.0%;  Score 176.5;  DB 2;  Length 564;
  Best Local Similarity   36.8%;  Pred. No. 1.4e-11;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         49 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 108

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:||| |   |   |  :
Db        109 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 162

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        163 LGIDQLIQSVTAL 175


RESULT 56
US-09-601-667C-2
; Sequence 2, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 2
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MLA-chain
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 15
;   OTHER INFORMATION: product= "Xaa is Asp or Glu"
;   OTHER INFORMATION: /label= Xaa1
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 63
;   OTHER INFORMATION: product= "Xaa is Gly or Gln"
;   OTHER INFORMATION: /label= Xaa2
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 66
;   OTHER INFORMATION: product= "Xaa is Ile or Val"
;   OTHER INFORMATION: /label= Xaa3
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 75
;   OTHER INFORMATION: product= "Xaa is Leu or Ala"
;   OTHER INFORMATION: /label= Xaa4
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 107
;   OTHER INFORMATION: product= "Xaa is missing"
;   OTHER INFORMATION: /label= Xaa5
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 113
;   OTHER INFORMATION: product= "Xaa is Asn or Thr"
;   OTHER INFORMATION: /label= Xaa6
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 117
;   OTHER INFORMATION: product= "Xaa is Pro or Thr"
;   OTHER INFORMATION: /label= Xaa7
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 134
;   OTHER INFORMATION: product= "Xaa is Asp or Glu"
;   OTHER INFORMATION: /label= Xaa8
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 141
;   OTHER INFORMATION: product= "Xaa is Ser or Thr"
;   OTHER INFORMATION: /label= Xaa9
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 145
;   OTHER INFORMATION: product= "Xaa is Phe or Tyr"
;   OTHER INFORMATION: /label= Xaa10
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 152
;   OTHER INFORMATION: product= "Xaa is Thr or Ala"
;   OTHER INFORMATION: /label= Xaa11
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 177
;   OTHER INFORMATION: product= "Xaa is Ala or Tyr"
;   OTHER INFORMATION: /label= Xaa12
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 180
;   OTHER INFORMATION: product= "Xaa is Tyr or Asp"
;   OTHER INFORMATION: /label= Xaa13
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 185
;   OTHER INFORMATION: product= "Xaa is Ala or Glu"
;   OTHER INFORMATION: /label= Xaa14
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 191
;   OTHER INFORMATION: product= "Xaa is Val or Met"
;   OTHER INFORMATION: /label= Xaa15
;   FEATURE:
;   NAME/KEY: SITE
```

; LOCATION: 219
; OTHER INFORMATION: product= "Xaa is Ile or Phe"
; OTHER INFORMATION: /label= Xaa16
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 224
; OTHER INFORMATION: product= "Xaa is Pro or Ser"
; OTHER INFORMATION: /label= Xaa17
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 225
; OTHER INFORMATION: product= "Xaa is Pro or Thr"
; OTHER INFORMATION: /label= Xaa18
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 232
; OTHER INFORMATION: product= "Xaa is Thr or Ser"
; OTHER INFORMATION: /label= Xaa19
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 236
; OTHER INFORMATION: product= "Xaa is Asp or Ser"
; OTHER INFORMATION: /label= Xaa20
US-09-601-667C-2

Query Match 22.9%; Score 176; DB 2; Length 255;
Best Local Similarity 36.1%; Pred. No. 5.4e-12;
Matches 48; Conservative 24; Mismatches 53; Indels 8; Gaps 3;

```
Qy          13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
               ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     :   |||||:
Db          16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGXDSXTAAIDVTNX 75

Qy          70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
               ||| ||      |:: ||   |  | : || | |   :| | ||| |   |   |  :
Db          76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRXSSLPFXGSYXDLERYAG-HRDQIP 130

Qy         130 LGVYKLEFSIEAI 142
               ||: :|  |: |:
Db         131 LGIXQLIQSVXAL 143
```

RESULT 57
US-09-601-667C-1
; Sequence 1, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667C
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 1
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 15
; OTHER INFORMATION: product= "Xaa is Asp or Glu"
; OTHER INFORMATION: /label= Xaa1
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 63
; OTHER INFORMATION: product= "Xaa is Gly or Gln"
; OTHER INFORMATION: /label= Xaa2
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 66
; OTHER INFORMATION: product= "Xaa is Ile or Val"
; OTHER INFORMATION: /label= Xaa3
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 75
; OTHER INFORMATION: product= "Xaa is Leu or Ala"
; OTHER INFORMATION: /label= Xaa4
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 107
; OTHER INFORMATION: product= "Xaa is missing"
; OTHER INFORMATION: /label= Xaa5
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 113
; OTHER INFORMATION: product= "Xaa is Asn or Thr"
; OTHER INFORMATION: /label= Xaa6
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 117
; OTHER INFORMATION: product= "Xaa is Pro or Thr"
; OTHER INFORMATION: /label= Xaa7
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 134
; OTHER INFORMATION: product= "Xaa is Asp or Glu"
; OTHER INFORMATION: /label= Xaa8
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 141
; OTHER INFORMATION: product= "Xaa is Ser or Thr"
; OTHER INFORMATION: /label= Xaa9
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 145
; OTHER INFORMATION: product= "Xaa is Phe or Tyr"
; OTHER INFORMATION: /label= Xaa10
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 152
; OTHER INFORMATION: product= "Xaa is Thr or Ala"
; OTHER INFORMATION: /label= Xaa11
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 177
; OTHER INFORMATION: product= "Xaa is Ala or Tyr"
; OTHER INFORMATION: /label= Xaa12
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 180
; OTHER INFORMATION: product= "Xaa is Tyr or Asp"
; OTHER INFORMATION: /label= Xaa13
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 185
; OTHER INFORMATION: product= "Xaa is Ala or Glu"
; OTHER INFORMATION: /label= Xaa14
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 191
; OTHER INFORMATION: product= "Xaa is Val or Met"
; OTHER INFORMATION: /label= Xaa15
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 219
; OTHER INFORMATION: product= "Xaa is Ile or Phe"
; OTHER INFORMATION: /label= Xaa16

```
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 224
;   OTHER INFORMATION: product= "Xaa is Pro or Ser"
;   OTHER INFORMATION: /label= Xaa17
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 225
;   OTHER INFORMATION: product= "Xaa is Pro or Thr"
;   OTHER INFORMATION: /label= Xaa18
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 232
;   OTHER INFORMATION: product= "Xaa is Thr or Ser"
;   OTHER INFORMATION: /label= Xaa19
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 236
;   OTHER INFORMATION: product= "Xaa is Asp or Ser"
;   OTHER INFORMATION: /label= Xaa20
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 287
;   OTHER INFORMATION: product= "Xaa is Asn or Ser"
;   OTHER INFORMATION: /label= Xaa21
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 290
;   OTHER INFORMATION: product= "Xaa is Cys or Arg"
;   OTHER INFORMATION: /label= Xaa22
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 325
;   OTHER INFORMATION: product= "Xaa is Gly or Asn"
;   OTHER INFORMATION: /label= Xaa23
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 364
;   OTHER INFORMATION: product= "Xaa is Gly or Asp"
;   OTHER INFORMATION: /label= Xaa24
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 426
;   OTHER INFORMATION: product= "Xaa is Gly or Gln"
;   OTHER INFORMATION: /label= Xaa25
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 435
;   OTHER INFORMATION: product= "Xaa is Val or Asp"
;   OTHER INFORMATION: /label= Xaa26
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 439
;   OTHER INFORMATION: product= "Xaa is Gln or Lys"
;   OTHER INFORMATION: /label= Xaa27
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 442
;   OTHER INFORMATION: product= "Xaa is Gly or missing"
;   OTHER INFORMATION: /label= Xaa28
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 443
;   OTHER INFORMATION: product= "Xaa is Arg or Lys"
;   OTHER INFORMATION: /label= Xaa29
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 464
;   OTHER INFORMATION: product= "Xaa is Cys or Ser or Val"
;   OTHER INFORMATION: /label= Xaa30
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 480
;   OTHER INFORMATION: product= "Xaa is Ala or Gly"
;   OTHER INFORMATION: /label= Xaa
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 481
;   OTHER INFORMATION: product= "Xaa is Gly or Ala"
;   OTHER INFORMATION: /label= Xaa32
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 483
;   OTHER INFORMATION: product= "Xaa is Ser or Gly"
;   OTHER INFORMATION: /label= Xaa33
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 484
;   OTHER INFORMATION: product= "Xaa is Gly or Ser"
;   OTHER INFORMATION: /label= Xaa34
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 493
;   OTHER INFORMATION: product= "Xaa is Gly or Tyr"
;   OTHER INFORMATION: /label= Xaa35
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 500

  Query Match             22.9%;  Score 176;  DB 2;  Length 533;
  Best Local Similarity   36.1%;  Pred. No. 1.5e-11;
  Matches   48;  Conservative   24;  Mismatches   53;  Indels    8;  Gaps    3;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     :   |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGXDSXTAAIDVTNX 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | |   :| | |||  |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRXSSLPFXGSYXDLERYAG-HRDQIP 130

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 LGIXQLIQSVXAL 143


RESULT 58
US-07-901-707-7
; Sequence 7, Application US/07901707
; Patent No. 5376546
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Composition and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/901,707
;      FILING DATE:  19920619
;      CLASSIFICATION:  435
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5376546and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27129/30910
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-5750
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-901-707-7

  Query Match             22.7%;  Score 174.5;  DB 1;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |  :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 59
US-07-988-430-7
; Sequence 7, Application US/07988430
; Patent No. 5416202
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,430
;      FILING DATE:  19921209
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5416202and, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-988-430-7

  Query Match             22.7%;  Score 174.5;  DB 1;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |  :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 60
US-08-425-336-7
; Sequence 7, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-425-336-7

  Query Match             22.7%;  Score 174.5;  DB 1;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||:|||| |     |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |  :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 61
US-08-488-113B-7
; Sequence 7, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-7

  Query Match             22.7%;  Score 174.5;  DB 1;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||:|||| |     |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |  :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 62
US-08-477-484B-7
; Sequence 7, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-7

  Query Match             22.7%;  Score 174.5;  DB 1;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |  :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 63
US-08-646-360-7
; Sequence 7, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-360-7

  Query Match             22.7%;  Score 174.5;  DB 1;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |  :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 64
US-08-839-765-7
; Sequence 7, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-7

  Query Match             22.7%;  Score 174.5;  DB 2;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||      |   :    |   :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 65
US-09-136-389-7
; Sequence 7, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-7

  Query Match             22.7%;  Score 174.5;  DB 2;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||      |   :    |   :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 66
US-09-610-838-7
; Sequence 7, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/610,838
;      FILING DATE:  06-JUL-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:  18-AUG-1998
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
```

```
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-610-838-7

  Query Match             22.7%;  Score 174.5;  DB 2;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |   :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 67
US-09-711-485-7
; Sequence 7, Application US/09711485
; Patent No. 6649742
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/711,485
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/839,765
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-711-485-7

  Query Match             22.7%;  Score 174.5;  DB 2;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |   :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 68
PCT-US92-09487-7
; Sequence 7, Application PC/TUS9209487
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/09487
;      FILING DATE:  19921104
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US92-09487-7

  Query Match             22.7%;  Score 174.5;  DB 5;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 8.5e-12;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |   :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 69
US-09-627-165E-16
; Sequence 16, Application US/09627165E
; Patent No. 6846913
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jong-Bae
;  TITLE OF INVENTION: CRUDE EXTRACT FROM Viscum album coloratum, AND PROTEINS
;  TITLE OF INVENTION:  AND LECTINS ISOLATED THEREFROM
;  FILE REFERENCE: Korean Mistletoe Lectin
;  CURRENT APPLICATION NUMBER: US/09/627,165E
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 16
;   LENGTH: 279
;   TYPE: PRT
;   ORGANISM: Viscum album coloratum
US-09-627-165E-16

  Query Match             22.7%;  Score 174.5;  DB 2;  Length 279;
  Best Local Similarity   36.8%;  Pred. No. 9.2e-12;
  Matches   49;  Conservative   25;  Mismatches   50;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db          7 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 66

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  |   || | | | :| | |||  |   |   |  :
Db         67 YVVAYQ----AGDQSYFLRDAPDGAERHLFTG-TTRSSLPFTGSYTDLERYAG-HRDQIP 120

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        121 LGIEELIQSVSAL 133


RESULT 70
US-09-601-667C-41
; Sequence 41, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/09/601,667C
;  CURRENT FILING DATE:  2000-10-06
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 41
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MLA-chain
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Xaa is Asp or Glu
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (63)..(63)
;   OTHER INFORMATION: Xaa is Gly or Gln
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (66)..(66)
;   OTHER INFORMATION: Xaa is Ile or Val
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (75)..(75)
;   OTHER INFORMATION: Xaa is Leu or Ala
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (114)..(114)
;   OTHER INFORMATION: Xaa is Asn or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (118)..(118)
;   OTHER INFORMATION: Xaa is Pro or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (135)..(135)
;   OTHER INFORMATION: Xaa is Asp or Glu
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (142)..(142)
;   OTHER INFORMATION: Xaa is Ser or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (146)..(146)
;   OTHER INFORMATION: Xaa is Phe or Tyr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (153)..(153)
;   OTHER INFORMATION: Xaa is Thr or Ala
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (178)..(178)
```

; OTHER INFORMATION: Xaa is Ala or Tyr
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (181)..(181)
; OTHER INFORMATION: Xaa is Tyr or Asp
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (186)..(186)
; OTHER INFORMATION: Xaa is Ala or Glu
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (192)..(192)
; OTHER INFORMATION: Xaa is Val or Met
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (220)..(220)
; OTHER INFORMATION: Xaa is Ile or Phe
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (225)..(225)
; OTHER INFORMATION: Xaa is Pro or Ser
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (226)..(226)
; OTHER INFORMATION: Xaa is Pro or Thr
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (233)..(233)
; OTHER INFORMATION: Xaa is Thr or Ser
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (237)..(237)
; OTHER INFORMATION: Xaa is Asp or Ser
US-09-601-667C-41

Query Match 22.5%; Score 172.5; DB 2; Length 256;
Best Local Similarity 36.6%; Pred. No. 1.4e-11;
Matches 49; Conservative 25; Mismatches 51; Indels 9; Gaps 4;

```
Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     :   |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGXDSXTAAIDVTNX 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||      |:: ||   |  | : || | | :| :| | |||  |   |   | :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFXGSYXDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
               ||: :|  |: |:
Db        131 PLGIXQLIQSVXAL 144
```

RESULT 71
US-09-601-667C-40
; Sequence 40, Application US/09601667C
; Patent No. 6927207
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/09/601,667C
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 40
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (15)..(15)
; OTHER INFORMATION: Xaa is Asp or Glu
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (63)..(63)
; OTHER INFORMATION: Xaa is Gly or Gln
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (66)..(66)
; OTHER INFORMATION: Xaa is Ile or Val
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (75)..(75)
; OTHER INFORMATION: Xaa is Leu or Ala
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)..(114)
; OTHER INFORMATION: Xaa is Asn or Thr
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (118)..(118)
; OTHER INFORMATION: Xaa is Pro or Thr
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (135)..(135)
; OTHER INFORMATION: Xaa is Asp or Glu
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (142)..(142)
; OTHER INFORMATION: Xaa is Ser or Thr
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (146)..(146)
; OTHER INFORMATION: Xaa is Phe or Tyr
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (153)..(153)
; OTHER INFORMATION: Xaa is Thr or Ala
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (178)..(178)
; OTHER INFORMATION: Xaa is Ala or Tyr
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (181)..(181)
; OTHER INFORMATION: Xaa is Tyr or Asp
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (186)..(186)
; OTHER INFORMATION: Xaa is Ala or Glu
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (192)..(192)
; OTHER INFORMATION: Xaa is Val or Met
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (220)..(220)
; OTHER INFORMATION: Xaa is Ile or Phe
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (225)..(225)
; OTHER INFORMATION: Xaa is Pro or Ser
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (226)..(226)
; OTHER INFORMATION: Xaa is Pro or Thr
; FEATURE:
; NAME/KEY: SITE

```
;   LOCATION: (233)..(233)
;   OTHER INFORMATION: Xaa is Thr or Ser
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (237)..(237)
;   OTHER INFORMATION: Xaa is Asp or Ser
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (288)..(288)
;   OTHER INFORMATION: Xaa is Asn or Ser
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (291)..(291)
;   OTHER INFORMATION: Xaa is Cys or Arg
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (326)..(326)
;   OTHER INFORMATION: Xaa is Gly or Asn
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (365)..(365)
;   OTHER INFORMATION: Xaa is Gly or Asp
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (427)..(427)
;   OTHER INFORMATION: Xaa is Gly or Gln
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (436)..(436)
;   OTHER INFORMATION: Xaa is Val or Asp
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (440)..(440)
;   OTHER INFORMATION: Xaa is Gln or Lys
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (443)..(443)
;   OTHER INFORMATION: Xaa is Gly or missing
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (444)..(444)
;   OTHER INFORMATION: Xaa is Arg or Lys
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (465)..(465)
;   OTHER INFORMATION: Xaa is Cys or Ser or Val
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (481)..(481)
;   OTHER INFORMATION: Xaa is Ala or Gly
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (482)..(482)
;   OTHER INFORMATION: Xaa is Gly or Ala
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (484)..(484)
;   OTHER INFORMATION: Xaa is Ser or Gly
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (485)..(485)
;   OTHER INFORMATION: Xaa is Gly or Ser
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (494)..(494)
;   OTHER INFORMATION: Xaa is Gly or Tyr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (501)..(501)
;   OTHER INFORMATION: Xaa is Asn or Ser or Thr or Lys
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (502)..(502)
;   OTHER INFORMATION: Xaa is Ser or Gly
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (503)..(503)
;   OTHER INFORMATION: Xaa is Leu or Pro
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (504)..(504)
;   OTHER INFORMATION: Xaa is Ala or Met
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (505)..(505)
;   OTHER INFORMATION: Xaa is Met or Val
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (534)..(534)
;   OTHER INFORMATION: Xaa is Pro or Phe
US-09-601-667C-40

  Query Match             22.5%;  Score 172.5;  DB 2;  Length 534;
  Best Local Similarity   36.6%;  Pred. No. 3.9e-11;
  Matches   49;  Conservative   25;  Mismatches   51;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     :   |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGXDSXTAAIDVTNX 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||      |:: ||   |  | : || | | :| :| | |||  |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFXGSYXDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
               ||: :|  |: |:
Db        131 PLGIXQLIQSVXAL 144


RESULT 72
US-09-627-165E-4
; Sequence 4, Application US/09627165E
; Patent No. 6846913
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jong-Bae
;  TITLE OF INVENTION: CRUDE EXTRACT FROM Viscum album coloratum, AND PROTEINS
;  TITLE OF INVENTION:  AND LECTINS ISOLATED THEREFROM
;  FILE REFERENCE: Korean Mistletoe Lectin
;  CURRENT APPLICATION NUMBER: US/09/627,165E
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 4
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Viscum album coloratum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 240
;   OTHER INFORMATION: Xaa = any amino acid
US-09-627-165E-4

  Query Match             22.3%;  Score 171.5;  DB 2;  Length 254;
  Best Local Similarity   35.3%;  Pred. No. 1.8e-11;
  Matches   47;  Conservative   29;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              :|  ||  ||: :: |:   |:|:  |:   ::| :|||||:::     ::  |||||::
Db         16 QYFKFITLLRDHVSSGSLSNQIPLLRQSTVPVSDTQRFVLVELSNQGGDSITAAIDVTNL 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      ::: ||   |  | : || | | | :| |:|||  |   |   |  :
Db         76 YVVAYQ----AGNQSYFLRDAPRGAETYLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
               ||: :|  |: |:
Db        130 LGIDQLIQSVSAL 142
```

```
RESULT 73
US-08-776-059-39
; Sequence 39, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
;  APPLICANT: LENTZEN, Hans
;  APPLICANT: ECK, Jurgen
;  APPLICANT: BAUR, Axel
;  APPLICANT: ZINKE, Holger
;  TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
;  FILE REFERENCE: 674503-2003
;  CURRENT APPLICATION NUMBER: US/08/776,059B
;  CURRENT FILING DATE: 1999-06-19
;  EARLIER APPLICATION NUMBER: PCT/EP96/02273
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 95109949.8
;  EARLIER FILING DATE: 1995-06-26
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Viscum album
US-08-776-059-39

  Query Match             22.1%;  Score 169.5;  DB 2;  Length 235;
  Best Local Similarity   36.4%;  Pred. No. 2.7e-11;
  Matches   47;  Conservative   27;  Mismatches   46;  Indels    9;  Gaps    4;

Qy         17 FIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDVYVVG 73
              ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::|||
Db          3 FITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNLYVVA 62

Qy         74 YQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVY 133
              ||      |:: ||   |  | : || | | | :| |:|||  |   |   |  : ||:
Db         63 YQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIPLGID 116

Qy        134 KLEFSIEAI 142
              :|  |: |:
Db        117 QLIQSVTAL 125


RESULT 74
US-10-083-336A-3
; Sequence 3, Application US/10083336A
; Patent No. 6869787
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 198
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-3

  Query Match             22.0%;  Score 169;  DB 2;  Length 198;
  Best Local Similarity   32.1%;  Pred. No. 2.5e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 75
US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Patent No. 6869787
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 198
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-7

  Query Match             22.0%;  Score 169;  DB 2;  Length 198;
  Best Local Similarity   32.1%;  Pred. No. 2.5e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 76
US-10-083-336A-5
; Sequence 5, Application US/10083336A
; Patent No. 6869787
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 199
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-5

  Query Match             22.0%;  Score 169;  DB 2;  Length 199;
  Best Local Similarity   32.1%;  Pred. No. 2.5e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
```

```
                |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
               :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         67 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 122

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
               :| :|   |   |:::|||   || :| |::    | ||
Db        123 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 161


RESULT 77
US-10-083-336A-10
; Sequence 10, Application US/10083336A
; Patent No. 6869787
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;  LENGTH: 200
;  TYPE: PRT
;  ORGANISM: Ricinus communis
US-10-083-336A-10

  Query Match             22.0%;  Score 169;  DB 2;  Length 200;
  Best Local Similarity   32.1%;  Pred. No. 2.5e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
               :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         67 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 122

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
               :| :|   |   |:::|||   || :| |::    | ||
Db        123 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 161


RESULT 78
US-07-901-707-1
; Sequence 1, Application US/07901707
; Patent No. 5376546
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Composition and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/901,707
;      FILING DATE:  19920619
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5376546and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27129/30910
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-5750
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-901-707-1

  Query Match             22.0%;  Score 169;  DB 1;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
               :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
               :| :|   |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 79
US-07-988-430-1
; Sequence 1, Application US/07988430
; Patent No. 5416202
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,430
;      FILING DATE:  19921209
```

```
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5416202and, Greta E.
;      REGISTRATION NUMBER:  35302
;      REFERENCE/DOCKET NUMBER:  31133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-988-430-1

  Query Match             22.0%;  Score 169;  DB 1;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 80
US-08-218-303-16
; Sequence 16, Application US/08218303
; Patent No. 5547867
;  GENERAL INFORMATION:
;    APPLICANT:  Kara, Bhuphendra V.
;    APPLICANT:  Hockney, Robert C.
;    APPLICANT:  Fitton, John E.
;    TITLE OF INVENTION:  FERMENTATION PROCESS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1615 L Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20036-5601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/218,303
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/841,533
;      FILING DATE:  26-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  PNK/3893/94908/MJW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-218-303-16

  Query Match             22.0%;  Score 169;  DB 1;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 81
US-08-425-336-1
; Sequence 1, Application US/08425336
; Patent No. 5621083
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribsome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/425,336
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,691
;      FILING DATE:  12-MAY-1993
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Thomas C.
;      REGISTRATION NUMBER:  P-36,989
;      REFERENCE/DOCKET NUMBER:  31394
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-425-336-1

  Query Match             22.0%;  Score 169;  DB 1;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 82
US-08-488-113B-1
; Sequence 1, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-1

  Query Match             22.0%;  Score 169;  DB 1;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 83
US-08-477-484B-1
; Sequence 1, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-1

  Query Match             22.0%;  Score 169;  DB 1;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 84
US-08-646-360-1
; Sequence 1, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-360-1

  Query Match             22.0%;  Score 169;  DB 1;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 85
US-08-338-793D-61
; Sequence 61, Application US/08338793D
; Patent No. 5840521
;  GENERAL INFORMATION:
;    APPLICANT:  Barth, Peter Thomas
;    TITLE OF INVENTION:  VECTOR
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN DARBY CUSHMAN
;      ADDRESSEE:  INTELLECTUAL PROPERTY GROUP OF
;      ADDRESSEE:  PILLSBURY MADISON & SUTRO, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
;      COMPUTER:  IBM PC/XT/AT Compatibles
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word or ASCII editors
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/338,793D
;      FILING DATE:  08-No. 5840521-94
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842,081
;      FILING DATE:  26-Feb-92
;      CLASSIFICATION:  435
;      APPLICATION NUMBER:  9104017.0
;      FILING DATE:  26-Feb-91
;      APPLICATION NUMBER:  9109188.4
;      FILING DATE:  29-Apr-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  DJB/9901/215431/TGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  61:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-338-793D-61

  Query Match             22.0%;  Score 169;  DB 1;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 86
US-08-839-765-1
; Sequence 1, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-1

  Query Match             22.0%;  Score 169;  DB 2;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 87
US-09-136-389-1
; Sequence 1, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
```

```
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-1

  Query Match             22.0%;  Score 169;  DB 2;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 88
US-09-610-838-1
; Sequence 1, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/610,838
;      FILING DATE:  06-JUL-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:  18-AUG-1998
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-610-838-1

  Query Match             22.0%;  Score 169;  DB 2;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 89
US-09-538-873-1
; Sequence 1, Application US/09538873
; Patent No. 6566500
; GENERAL INFORMATION:
;  APPLICANT: VITETTA, ELLEN S.
;  APPLICANT: GHETIE, VICTOR F.
;  APPLICANT: SMALLSHAW, JOAN
;  APPLICANT: BALUNA, ROXANA G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
;  TITLE OF INVENTION: SYNDROME (VLS)
;  FILE REFERENCE: UTSD:603
;  CURRENT APPLICATION NUMBER: US/09/538,873
;  CURRENT FILING DATE: 2000-03-30
;  EARLIER APPLICATION NUMBER: 60/126,826
;  EARLIER FILING DATE: 1999-03-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-09-538-873-1

  Query Match             22.0%;  Score 169;  DB 2;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
```

```
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 90
US-09-711-485-1
; Sequence 1, Application US/09711485
; Patent No. 6649742
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/711,485
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/839,765
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-711-485-1

  Query Match             22.0%;  Score 169;  DB 2;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 91
US-10-282-935-1
; Sequence 1, Application US/10282935
; Patent No. 6960652
; GENERAL INFORMATION:
;  APPLICANT: VITETTA, ELLEN S.
;  APPLICANT:  GHETIE, VICTOR F.
;  APPLICANT:  SMALLSHAW, JOAN
;  APPLICANT:  BALUNA, ROXANA G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
;  TITLE OF INVENTION:  PROTEINACEOUS COMPOUNDS
;  FILE REFERENCE: UTSD:884US
;  CURRENT APPLICATION NUMBER: US/10/282,935
;  CURRENT FILING DATE:  2002-10-29
;  PRIOR APPLICATION NUMBER: 09/538,873
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 60/126,826
;  PRIOR FILING DATE: 1999-03-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-10-282-935-1

  Query Match             22.0%;  Score 169;  DB 2;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 92
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
;  GENERAL INFORMATION:
;    APPLICANT:  Bernhard, Susan L.
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Lane, Julie A.
;    APPLICANT:  Lei, Shau-Ping
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
```

```
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60603
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US92/09487
;       FILING DATE:  19921104
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Noland, Greta E.
;       REGISTRATION NUMBER:  35302
;       REFERENCE/DOCKET NUMBER:  31133
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 346-5750
;       TELEFAX:  (312) 984-9740
;       TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  267 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US92-09487-1

  Query Match             22.0%;  Score 169;  DB 5;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 93
US-08-356-786-8
; Sequence 8, Application US/08356786
; Patent No. 5877305
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Protein for Cancer
;    TITLE OF INVENTION:  Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,786
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/831,967
;      FILING DATE:  06-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  268 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-356-786-8

  Query Match             22.0%;  Score 169;  DB 1;  Length 268;
  Best Local Similarity   32.1%;  Pred. No. 3.7e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         67 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 122

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        123 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 161


RESULT 94
US-08-378-761A-27
; Sequence 27, Application US/08378761A
; Patent No. 5635384
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761A
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  290 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-761A-27

  Query Match             22.0%;  Score 169;  DB 1;  Length 290;
  Best Local Similarity   32.1%;  Pred. No. 4.2e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db         30 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 89

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         90 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 145

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        146 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 184


RESULT 95
US-08-485-286-27
; Sequence 27, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,286
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/378761
;      FILING DATE:  26-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  290 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-485-286-27

  Query Match             22.0%;  Score 169;  DB 1;  Length 290;
  Best Local Similarity   32.1%;  Pred. No. 4.2e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db         30 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 89

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         90 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 145

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        146 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 184


RESULT 96
5248606-4
;Patent No. 5248606
;    APPLICANT: WALSH, TERENCE A.;HEY, TIMOTHY D.;MORGAN,
;ALICE E.R.
;    TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
;ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
;    NUMBER OF SEQUENCES: 49
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/535,636
;      FILING DATE: 11-JUN-1990
;SEQ ID NO:4:
;      LENGTH: 290
5248606-4

  Query Match             22.0%;  Score 169;  DB 7;  Length 290;
  Best Local Similarity   32.1%;  Pred. No. 4.2e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db         30 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 89

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         90 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 145

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        146 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 184


RESULT 97
US-08-356-786-10
; Sequence 10, Application US/08356786
; Patent No. 5877305
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Protein for Cancer
;    TITLE OF INVENTION:  Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/356,786
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/831,967
;       FILING DATE:  06-FEB-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pitcher, Edmund R.
;       REGISTRATION NUMBER:  27,829
;       REFERENCE/DOCKET NUMBER:  CRP-053
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 248-7000
;       TELEFAX:  (617) 248-7100
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  534 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-356-786-10

  Query Match             22.0%;  Score 169;  DB 1;  Length 534;
  Best Local Similarity   32.1%;  Pred. No. 9.8e-11;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          9 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 68

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         69 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 124

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        125 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 163


RESULT 98
US-10-083-336A-1
; Sequence 1, Application US/10083336A
; Patent No. 6869787
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-1

  Query Match             22.0%;  Score 169;  DB 2;  Length 576;
  Best Local Similarity   32.1%;  Pred. No. 1.1e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db         41 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 100

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db        101 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 156

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        157 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 195


RESULT 99
US-09-627-165E-2
; Sequence 2, Application US/09627165E
; Patent No. 6846913
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jong-Bae
;  TITLE OF INVENTION: CRUDE EXTRACT FROM Viscum album coloratum, AND PROTEINS
;  TITLE OF INVENTION:  AND LECTINS ISOLATED THEREFROM
;  FILE REFERENCE: Korean Mistletoe Lectin
;  CURRENT APPLICATION NUMBER: US/09/627,165E
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 2
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Viscum album coloratum
;   FEATURE:
;   NAME/KEY: misc_feature
US-09-627-165E-2

  Query Match             21.9%;  Score 168.5;  DB 2;  Length 254;
  Best Local Similarity   36.8%;  Pred. No. 4e-11;
  Matches   49;  Conservative   24;  Mismatches   51;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||       |:: ||   |  |   || | | | :| | |||  |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPDGAERHLFTG-TTRSSLPFTGSYTDLERFAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||  :|  |: |:
Db        130 LGREELIQSVSAL 142


RESULT 100
US-08-378-761A-80
; Sequence 80, Application US/08378761A
; Patent No. 5635384
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761A
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
```

; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-80

Query Match 21.7%; Score 167; DB 1; Length 250;
Best Local Similarity 29.3%; Pred. No. 5.8e-11;
Matches 44; Conservative 34; Mismatches 50; Indels 22; Gaps 4;

```
Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |||:|   ::  |  ||  ||  |     |  :|: | : :   |::|: ::    | :
Db          3 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGASRYILMQLSNYDAKAIT 62

Qy         62 VAIDVTDVYVVGY--------QDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGS 113
              :|||||:||:||         :: | |           :|:  :| | |  ||: : |:
Db         63 MAIDVTNVYIMGYLVNSTSYFANESDAK----------LASQYVFKGST-LVTIPYSGN 110

Qy        114 YQKLVNAAKVDRKDLELGVYKLEFSIEAIW 143
              |::| |||   |: : ||   |: :: :|:
Db        111 YERLQNAAGKIREKIPLGFRALDSALTSIF 140
```

Search completed: September 18, 2006, 19:15:34
Job time : 40.4581 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:30:33 ; Search time 209.765 Seconds
(without alignments)
329.030 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	768	100.0	149	5	US-10-758-902-9	Sequence 9, Appli
2	747	97.3	250	6	US-11-084-080-1	Sequence 1, Appli
3	738	96.1	250	6	US-11-084-080-129	Sequence 129, App
4	727	94.7	250	6	US-11-084-080-14	Sequence 14, Appl
5	726	94.5	250	6	US-11-084-080-13	Sequence 13, Appl
6	726	94.5	750	6	US-11-084-080-16	Sequence 16, Appl
7	726	94.5	750	6	US-11-084-080-20	Sequence 20, Appl
8	726	94.5	750	6	US-11-084-080-22	Sequence 22, Appl
9	726	94.5	750	6	US-11-084-080-24	Sequence 24, Appl
10	726	94.5	759	6	US-11-084-080-28	Sequence 28, Appl
11	721	93.9	250	6	US-11-084-080-11	Sequence 11, Appl
12	721	93.9	250	6	US-11-084-080-12	Sequence 12, Appl
13	221.5	28.8	250	3	US-09-792-793A-36	Sequence 36, Appl
14	221.5	28.8	250	4	US-10-127-890-8	Sequence 8, Appli
15	221.5	28.8	250	4	US-10-375-209A-36	Sequence 36, Appl
16	221.5	28.8	250	5	US-10-717-243-8	Sequence 8, Appli
17	220.5	28.7	263	4	US-10-127-890-4	Sequence 4, Appli
18	220.5	28.7	263	5	US-10-717-243-4	Sequence 4, Appli
19	183.5	23.9	247	3	US-09-792-793A-39	Sequence 39, Appl
20	183.5	23.9	247	4	US-10-127-890-6	Sequence 6, Appli
21	183.5	23.9	247	4	US-10-375-209A-39	Sequence 39, Appl
22	183.5	23.9	247	5	US-10-717-243-6	Sequence 6, Appli
23	183.5	23.9	289	4	US-10-280-679B-4	Sequence 4, Appli
24	183.5	23.9	289	4	US-10-280-725B-4	Sequence 4, Appli
25	180.5	23.5	289	3	US-09-905-247-1	Sequence 1, Appli
26	179.5	23.4	247	3	US-09-792-793A-34	Sequence 34, Appl
27	179.5	23.4	247	4	US-10-375-209A-34	Sequence 34, Appl
28	179.5	23.4	254	6	US-11-042-707-37	Sequence 37, Appl
29	179.5	23.4	256	6	US-11-042-707-5	Sequence 5, Appli
30	179.5	23.4	256	6	US-11-042-707-38	Sequence 38, Appl
31	179.5	23.4	267	5	US-10-517-707A-1	Sequence 1, Appli
32	179	23.3	253	6	US-11-042-707-39	Sequence 39, Appl
33	176.5	23.0	252	3	US-09-347-064-2	Sequence 2, Appli
34	176.5	23.0	252	3	US-09-347-064-8	Sequence 8, Appli
35	176.5	23.0	285	5	US-10-499-297-2	Sequence 2, Appli
36	176.5	23.0	531	6	US-11-042-707-4	Sequence 4, Appli
37	176.5	23.0	647	5	US-10-499-297-6	Sequence 6, Appli
38	176	22.9	255	6	US-11-042-707-2	Sequence 2, Appli
39	176	22.9	533	6	US-11-042-707-1	Sequence 1, Appli
40	174.5	22.7	263	4	US-10-127-890-7	Sequence 7, Appli
41	174.5	22.7	263	5	US-10-717-243-7	Sequence 7, Appli
42	173	22.5	266	5	US-10-800-052-7	Sequence 7, Appli
43	172.5	22.5	256	6	US-11-042-707-41	Sequence 41, Appl
44	172.5	22.5	534	6	US-11-042-707-40	Sequence 40, Appl
45	169	22.0	198	4	US-10-083-336A-3	Sequence 3, Appli
46	169	22.0	198	4	US-10-083-336A-7	Sequence 7, Appli
47	169	22.0	198	5	US-10-923-022-3	Sequence 3, Appli
48	169	22.0	198	5	US-10-923-022-7	Sequence 7, Appli
49	169	22.0	199	4	US-10-083-336A-5	Sequence 5, Appli
50	169	22.0	199	5	US-10-923-022-5	Sequence 5, Appli
51	169	22.0	200	4	US-10-083-336A-10	Sequence 10, Appl
52	169	22.0	200	5	US-10-923-022-10	Sequence 10, Appl
53	169	22.0	267	4	US-10-282-935-1	Sequence 1, Appli
54	169	22.0	267	4	US-10-127-890-1	Sequence 1, Appli
55	169	22.0	267	4	US-10-440-796-1	Sequence 1, Appli
56	169	22.0	267	5	US-10-717-243-1	Sequence 1, Appli
57	169	22.0	268	6	US-11-010-795-24	Sequence 24, Appl
58	169	22.0	576	4	US-10-083-336A-1	Sequence 1, Appli
59	169	22.0	576	5	US-10-923-022-1	Sequence 1, Appli
60	169	22.0	630	5	US-10-893-584-274	Sequence 274, App
61	163.5	21.3	185	4	US-10-083-336A-9	Sequence 9, Appli
62	163.5	21.3	185	5	US-10-923-022-9	Sequence 9, Appli
63	162.5	21.2	251	4	US-10-127-890-101	Sequence 101, App
64	162.5	21.2	251	4	US-10-127-890-110	Sequence 110, App
65	162.5	21.2	251	4	US-10-127-890-111	Sequence 111, App
66	162.5	21.2	251	5	US-10-717-243-101	Sequence 101, App
67	162.5	21.2	251	5	US-10-717-243-110	Sequence 110, App
68	162.5	21.2	251	5	US-10-717-243-111	Sequence 111, App
69	161	21.0	188	4	US-10-083-336A-4	Sequence 4, Appli
70	161	21.0	188	4	US-10-083-336A-8	Sequence 8, Appli
71	161	21.0	188	5	US-10-923-022-4	Sequence 4, Appli
72	161	21.0	188	5	US-10-923-022-8	Sequence 8, Appli
73	161	21.0	189	4	US-10-083-336A-6	Sequence 6, Appli
74	161	21.0	189	5	US-10-923-022-6	Sequence 6, Appli
75	161	21.0	190	4	US-10-083-336A-11	Sequence 11, Appl
76	161	21.0	190	5	US-10-923-022-11	Sequence 11, Appl
77	160.5	20.9	251	4	US-10-127-890-100	Sequence 100, App
78	160.5	20.9	251	5	US-10-717-243-100	Sequence 100, App
79	160	20.8	30	5	US-10-758-902-1	Sequence 1, Appli
80	158.5	20.6	251	4	US-10-127-890-99	Sequence 99, Appl
81	158.5	20.6	251	5	US-10-717-243-99	Sequence 99, Appl
82	156.5	20.4	251	3	US-09-765-527-247	Sequence 247, App
83	156.5	20.4	251	4	US-10-127-890-2	Sequence 2, Appli
84	156.5	20.4	251	4	US-10-127-890-102	Sequence 102, App
85	156.5	20.4	251	4	US-10-127-890-103	Sequence 103, App
86	156.5	20.4	251	4	US-10-127-890-104	Sequence 104, App
87	156.5	20.4	251	4	US-10-127-890-105	Sequence 105, App
88	156.5	20.4	251	4	US-10-127-890-106	Sequence 106, App
89	156.5	20.4	251	4	US-10-127-890-108	Sequence 108, App
90	156.5	20.4	251	4	US-10-127-890-109	Sequence 109, App
91	156.5	20.4	251	5	US-10-717-243-2	Sequence 2, Appli
92	156.5	20.4	251	5	US-10-717-243-102	Sequence 102, App
93	156.5	20.4	251	5	US-10-717-243-103	Sequence 103, App
94	156.5	20.4	251	5	US-10-717-243-104	Sequence 104, App
95	156.5	20.4	251	5	US-10-717-243-105	Sequence 105, App
96	156.5	20.4	251	5	US-10-717-243-106	Sequence 106, App
97	156.5	20.4	251	5	US-10-717-243-108	Sequence 108, App
98	156.5	20.4	251	5	US-10-717-243-109	Sequence 109, App
99	156.5	20.4	316	4	US-10-074-596-1	Sequence 1, Appli
100	156.5	20.4	498	5	US-10-964-195-13	Sequence 13, Appl

ALIGNMENTS

```
RESULT 1
US-10-758-902-9
; Sequence 9, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-9

  Query Match             100.0%;  Score 768;  DB 5;  Length 149;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-76;
  Matches  149;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |||||||||||||||||||||||||||||
Db        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149


RESULT 2
US-11-084-080-1
; Sequence 1, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis Wild
US-11-084-080-1

  Query Match             97.3%;  Score 747;  DB 6;  Length 250;
  Best Local Similarity   98.7%;  Pred. No. 1.9e-73;
  Matches  147;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |||||||||||||||||||||||||||||
Db        121 AKVDRKDLELGVYKLEFSIEAIHGKTING 149


RESULT 3
US-11-084-080-129
; Sequence 129, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-129

  Query Match             96.1%;  Score 738;  DB 6;  Length 250;
  Best Local Similarity   98.0%;  Pred. No. 1.8e-72;
  Matches  146;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVAVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |||||||||||||||||||| ||| ||
Db        121 AKVDRKDLELGVYKLEFSIEAIHGKTING 149


RESULT 4
US-11-084-080-14
; Sequence 14, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-14

  Query Match            94.7%;  Score 727;  DB 6;  Length 250;
  Best Local Similarity  96.6%;  Pred. No. 2.9e-71;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| |||||||||| ||| ||
Db        121 AKADRKALELGVQKLEFSIEAIHGKTING 149


RESULT 5
US-11-084-080-13
; Sequence 13, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-13

  Query Match            94.5%;  Score 726;  DB 6;  Length 250;
  Best Local Similarity  96.6%;  Pred. No. 3.8e-71;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| |||||||||| ||| ||
Db        121 AKADRKALELGVNKLEFSIEAIHGKTING 149


RESULT 6
US-11-084-080-16
; Sequence 16, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-16

  Query Match            94.5%;  Score 726;  DB 6;  Length 750;
  Best Local Similarity  96.6%;  Pred. No. 1.6e-70;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 313

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 373

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| |||||||||| ||| ||
Db        374 AKADRKALELGVNKLEFSIEAIHGKTING 402


RESULT 7
US-11-084-080-20
; Sequence 20, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
```

```
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-20

  Query Match             94.5%;  Score 726;  DB 6;  Length 750;
  Best Local Similarity   96.6%;  Pred. No. 1.6e-70;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 560

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 620

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        621 AKADRKALELGVNKLEFSIEAIHGKTING 649


RESULT 8
US-11-084-080-22
; Sequence 22, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-22

  Query Match             94.5%;  Score 726;  DB 6;  Length 750;
  Best Local Similarity   96.6%;  Pred. No. 1.6e-70;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 82

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 142

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        143 AKADRKALELGVNKLEFSIEAIHGKTING 171


RESULT 9
US-11-084-080-24
; Sequence 24, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-24

  Query Match             94.5%;  Score 726;  DB 6;  Length 750;
  Best Local Similarity   96.6%;  Pred. No. 1.6e-70;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 329

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 389

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        390 AKADRKALELGVNKLEFSIEAIHGKTING 418


RESULT 10
US-11-084-080-28
; Sequence 28, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
```

```
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
;   LENGTH: 759
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-011
US-11-084-080-28

  Query Match             94.5%;  Score 726;  DB 6;  Length 759;
  Best Local Similarity   96.6%;  Pred. No. 1.7e-70;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 322

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 382

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        383 AKADRKALELGVNKLEFSIEAIHGKTING 411


RESULT 11
US-11-084-080-11
; Sequence 11, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (123)..(123)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (127)..(127)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (129)..(129)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (133)..(133)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (152)..(152)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-084-080-11

  Query Match             93.9%;  Score 721;  DB 6;  Length 250;
  Best Local Similarity   96.0%;  Pred. No. 1.3e-70;
  Matches  143;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| | ||| ||||||||| ||| ||
Db        121 AKXDRKXLXLGVXKLEFSIEAIHGKTING 149


RESULT 12
US-11-084-080-12
; Sequence 12, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (123)..(123)
;   OTHER INFORMATION: Xaa can be T or A or Q
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (127)..(127)
;   OTHER INFORMATION: Xaa can be G or A
;   FEATURE:
```

```
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (129)..(129)
;   OTHER INFORMATION: Xaa can be Q or G
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (133)..(133)
;   OTHER INFORMATION: Xaa can be N or D or T or A or R or Q or E or G or H or K or S
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (152)..(152)
;   OTHER INFORMATION: Xaa can be Q or A
US-11-084-080-12

  Query Match             93.9%;  Score 721;  DB 6;  Length 250;
  Best Local Similarity   96.0%;  Pred. No. 1.3e-70;
  Matches  143;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| | ||| |||||||||| ||| ||
Db        121 AKXDRKXLXLGVXKLEFSIEAIHGKTING 149


RESULT 13
US-09-792-793A-36
; Sequence 36, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601D
;  CURRENT APPLICATION NUMBER: US/09/792,793A
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-09-792-793A-36

  Query Match             28.8%;  Score 221.5;  DB 3;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 1.1e-15;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 14
US-10-127-890-8
; Sequence 8, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 250 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-127-890-8

  Query Match             28.8%;  Score 221.5;  DB 4;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 1.1e-15;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |   |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 15
US-10-375-209A-36
; Sequence 36, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601E
;  CURRENT APPLICATION NUMBER: US/10/375,209A
;  CURRENT FILING DATE:  2003-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-10-375-209A-36

  Query Match             28.8%;  Score 221.5;  DB 4;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 1.1e-15;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 16
US-10-717-243-8
; Sequence 8, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 250 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-717-243-8

  Query Match             28.8%;  Score 221.5;  DB 5;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 1.1e-15;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |     :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 17
US-10-127-890-4
; Sequence 4, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
```

```
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 263 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-127-890-4

  Query Match             28.7%;  Score 220.5;  DB 4;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 1.5e-15;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|     |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 18
US-10-717-243-4
; Sequence 4, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 263 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-717-243-4

  Query Match             28.7%;  Score 220.5;  DB 5;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 1.5e-15;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|     |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 19
US-09-792-793A-39
; Sequence 39, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601D
;  CURRENT APPLICATION NUMBER: US/09/792,793A
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthews kirilowii
US-09-792-793A-39

  Query Match             23.9%;  Score 183.5;  DB 3;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 1.6e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |     | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 20
```

```
US-10-127-890-6
; Sequence 6, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;     INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 247 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-890-6

  Query Match             23.9%;  Score 183.5;  DB 4;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 1.6e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| | |    |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140
```

```
RESULT 21
US-10-375-209A-39
; Sequence 39, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601E
;  CURRENT APPLICATION NUMBER: US/10/375,209A
;  CURRENT FILING DATE:  2003-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthews kirilowii
US-10-375-209A-39

  Query Match             23.9%;  Score 183.5;  DB 4;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 1.6e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| | |    |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140
```

```
RESULT 22
US-10-717-243-6
; Sequence 6, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
```

```
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 247 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-717-243-6

  Query Match             23.9%;  Score 183.5;  DB 5;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 1.6e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 23
US-10-280-679B-4
; Sequence 4, Application US/10280679B
; Publication No. US20030150019A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
;  FILE REFERENCE: LSBC-0109-US03
;  CURRENT APPLICATION NUMBER: US/10/280,679B
;  CURRENT FILING DATE:  2000-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Chinese cucumber protein alpha-trichosanthin
US-10-280-679B-4

  Query Match             23.9%;  Score 183.5;  DB 4;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 24
US-10-280-725B-4
; Sequence 4, Application US/10280725B
; Publication No. US20040049025A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Recombinant Viral Nucleic Acids
;  FILE REFERENCE: LSBC-0109-US02
;  CURRENT APPLICATION NUMBER: US/10/280,725B
;  CURRENT FILING DATE:  2002-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Chinese cucumber
US-10-280-725B-4

  Query Match             23.9%;  Score 183.5;  DB 4;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
```

```
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 25
US-09-905-247-1
; Sequence 1, Application US/09905247
; Publication No. US20040197853A1
; GENERAL INFORMATION:
;  APPLICANT: KE, YI-BAO
;  APPLICANT:  NIE, HUI-LING
;  TITLE OF INVENTION: Mutant Trichosanthin
;  FILE REFERENCE: 04399/000J615-US0
;  CURRENT APPLICATION NUMBER: US/09/905,247
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: CN 00119553.0
;  PRIOR FILING DATE: 2000-08-02
;  PRIOR APPLICATION NUMBER: CN 01103102.6
;  PRIOR FILING DATE: 2001-01-18
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Trichosanthes Kirilowii M.
US-09-905-247-1

  Query Match             23.5%;  Score 180.5;  DB 3;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 4.2e-11;
  Matches   44;  Conservative   31;  Mismatches   62;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      |    | |    :|     :||| : |:|::|   ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNGASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 26
US-09-792-793A-34
; Sequence 34, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601D
;  CURRENT APPLICATION NUMBER: US/09/792,793A
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Bryonia dioica
US-09-792-793A-34

  Query Match             23.4%;  Score 179.5;  DB 3;  Length 247;
  Best Local Similarity   30.8%;  Pred. No. 4.4e-11;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||::||  |     |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140


RESULT 27
US-10-375-209A-34
; Sequence 34, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601E
;  CURRENT APPLICATION NUMBER: US/10/375,209A
;  CURRENT FILING DATE:  2003-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Bryonia dioica
US-10-375-209A-34

  Query Match             23.4%;  Score 179.5;  DB 4;  Length 247;
  Best Local Similarity   30.8%;  Pred. No. 4.4e-11;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||::||  |     |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140


RESULT 28
US-11-042-707-37
; Sequence 37, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 37
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1
US-11-042-707-37

  Query Match             23.4%;  Score 179.5;  DB 6;  Length 254;
  Best Local Similarity   37.6%;  Pred. No. 4.6e-11;
```

```
  Matches   50;  Conservative   26;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSVTAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        130 LGIDQLIQSVTAL 142


RESULT 29
US-11-042-707-5
; Sequence 5, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 5
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Lectin A2
US-11-042-707-5

  Query Match             23.4%;  Score 179.5;  DB 6;  Length 256;
  Best Local Similarity   36.6%;  Pred. No. 4.6e-11;
  Matches   49;  Conservative   27;  Mismatches   49;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSITAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||      |:: ||   |  | : || | | :| :| | ||| |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFTGSYTDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 PLGIEQLIQSVSAL 144


RESULT 30
US-11-042-707-38
; Sequence 38, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 38
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-11-042-707-38

  Query Match             23.4%;  Score 179.5;  DB 6;  Length 256;
  Best Local Similarity   36.6%;  Pred. No. 4.6e-11;
  Matches   49;  Conservative   27;  Mismatches   49;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSITAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||      |:: ||   |  | : || | | :| :| | ||| |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFTGSYTDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 PLGIEQLIQSVSAL 144


RESULT 31
US-10-517-707A-1
; Sequence 1, Application US/10517707A
; Publication No. US20060019885A1
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  TITLE OF INVENTION: MODIFIED BRYODIN 1 WITH REDUCED
;  TITLE OF INVENTION:  IMMUNOGENICITY
;  FILE REFERENCE: MER-134
;  CURRENT APPLICATION NUMBER: US/10/517,707A
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: PCT/EP03/06055
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: EP 02012911.0
;  PRIOR FILING DATE: 2002-06-11
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-707A-1

  Query Match             23.4%;  Score 179.5;  DB 5;  Length 267;
  Best Local Similarity   30.8%;  Pred. No. 4.9e-11;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |     |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||        | : | ::       :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140


RESULT 32
US-11-042-707-39
; Sequence 39, Application US/11042707
; Publication No. US20050142183A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 39
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1 (matched)
US-11-042-707-39

  Query Match             23.3%;  Score 179;  DB 6;  Length 253;
  Best Local Similarity   36.8%;  Pred. No. 5.1e-11;
  Matches   49;  Conservative   27;  Mismatches   47;  Indels   10;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSVTAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |    |    : :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYA--GHRQIP 128

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        129 LGIDQLIQSVTAL 141


RESULT 33
US-09-347-064-2
; Sequence 2, Application US/09347064A
; Patent No. US20020045208A1
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064-2

  Query Match             23.0%;  Score 176.5;  DB 3;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 9.6e-11;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         17 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 76

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |    |    : :
Db         77 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 130

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 LGIDQLIQSVTAL 143


RESULT 34
US-09-347-064-8
; Sequence 8, Application US/09347064A
; Patent No. US20020045208A1
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064-8

  Query Match             23.0%;  Score 176.5;  DB 3;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 9.6e-11;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |    |    : :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        130 LGIDQLIQSVTAL 142


RESULT 35
US-10-499-297-2
; Sequence 2, Application US/10499297
; Publication No. US20050221380A1
; GENERAL INFORMATION:
;  APPLICANT: Muthing, Johannes
;  APPLICANT:  Peter-Katalinic, Jasna
;  APPLICANT:  Langer, Martin
;  APPLICANT:  Mockel, Babette
;  APPLICANT:  Eck, Jurgen
;  TITLE OF INVENTION: METHOD FOR DETERMINATION OF THE
;  TITLE OF INVENTION:  RESPONSIVENESS OF AN INDIVIDUAL TO MISTLETOE LECTIN
;  FILE REFERENCE: VOSS-P01-010
;  CURRENT APPLICATION NUMBER: US/10/499,297
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: EP 01130745.1
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 285
```

```
;   TYPE: PRT
;   ORGANISM: Viscum album
US-10-499-297-2

  Query Match             23.0%;  Score 176.5;  DB 5;  Length 285;
  Best Local Similarity   36.8%;  Pred. No. 1.1e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         49 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 108

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   |  :
Db        109 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 162

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        163 LGIDQLIQSVTAL 175


RESULT 36
US-11-042-707-4
; Sequence 4, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 4
;   LENGTH: 531
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: MLI match
US-11-042-707-4

  Query Match             23.0%;  Score 176.5;  DB 6;  Length 531;
  Best Local Similarity   36.8%;  Pred. No. 2.6e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        130 LGIDQLIQSVTAL 142


RESULT 37
US-10-499-297-6
; Sequence 6, Application US/10499297
; Publication No. US20050221380A1
; GENERAL INFORMATION:
;  APPLICANT: Muthing, Johannes
;  APPLICANT:  Peter-Katalinic, Jasna
;  APPLICANT:  Langer, Martin
;  APPLICANT:  Mockel, Babette
;  APPLICANT:  Eck, Jurgen
;  TITLE OF INVENTION: METHOD FOR DETERMINATION OF THE
;  TITLE OF INVENTION:  RESPONSIVENESS OF AN INDIVIDUAL TO MISTLETOE LECTIN
;  FILE REFERENCE: VOSS-P01-010
;  CURRENT APPLICATION NUMBER: US/10/499,297
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: EP 01130745.1
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 647
;   TYPE: PRT
;   ORGANISM: Viscum album
US-10-499-297-6

  Query Match             23.0%;  Score 176.5;  DB 5;  Length 647;
  Best Local Similarity   36.8%;  Pred. No. 3.4e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         66 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 125

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   |  :
Db        126 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 179

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        180 LGIDQLIQSVTAL 192


RESULT 38
US-11-042-707-2
; Sequence 2, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 2
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: MLA-chain
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 15
;   OTHER INFORMATION: product= "Xaa is Asp or Glu"
;   OTHER INFORMATION: /label= Xaa1
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 63
;   OTHER INFORMATION: product= "Xaa is Gly or Gln"
;   OTHER INFORMATION: /label= Xaa2
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 66
;   OTHER INFORMATION: product= "Xaa is Ile or Val"
;   OTHER INFORMATION: /label= Xaa3
;   FEATURE:
```

; NAME/KEY: SITE
; LOCATION: 75
; OTHER INFORMATION: product= "Xaa is Leu or Ala"
; OTHER INFORMATION: /label= Xaa4
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 107
; OTHER INFORMATION: product= "Xaa is missing"
; OTHER INFORMATION: /label= Xaa5
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 113
; OTHER INFORMATION: product= "Xaa is Asn or Thr"
; OTHER INFORMATION: /label= Xaa6
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 117
; OTHER INFORMATION: product= "Xaa is Pro or Thr"
; OTHER INFORMATION: /label= Xaa7
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 134
; OTHER INFORMATION: product= "Xaa is Asp or Glu"
; OTHER INFORMATION: /label= Xaa8
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 141
; OTHER INFORMATION: product= "Xaa is Ser or Thr"
; OTHER INFORMATION: /label= Xaa9
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 145
; OTHER INFORMATION: product= "Xaa is Phe or Tyr"
; OTHER INFORMATION: /label= Xaa10
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 152
; OTHER INFORMATION: product= "Xaa is Thr or Ala"
; OTHER INFORMATION: /label= Xaa11
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 177
; OTHER INFORMATION: product= "Xaa is Ala or Tyr"
; OTHER INFORMATION: /label= Xaa12
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 180
; OTHER INFORMATION: product= "Xaa is Tyr or Asp"
; OTHER INFORMATION: /label= Xaa13
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 185
; OTHER INFORMATION: product= "Xaa is Ala or Glu"
; OTHER INFORMATION: /label= Xaa14
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 191
; OTHER INFORMATION: product= "Xaa is Val or Met"
; OTHER INFORMATION: /label= Xaa15
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 219
; OTHER INFORMATION: product= "Xaa is Ile or Phe"
; OTHER INFORMATION: /label= Xaa16
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 224
; OTHER INFORMATION: product= "Xaa is Pro or Ser"
; OTHER INFORMATION: /label= Xaa17
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 225
; OTHER INFORMATION: product= "Xaa is Pro or Thr"
; OTHER INFORMATION: /label= Xaa18
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 232
; OTHER INFORMATION: product= "Xaa is Thr or Ser"
; OTHER INFORMATION: /label= Xaa19
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 236
; OTHER INFORMATION: product= "Xaa is Asp or Ser"
; OTHER INFORMATION: /label= Xaa20
US-11-042-707-2

Query Match 22.9%; Score 176; DB 6; Length 255;
Best Local Similarity 36.1%; Pred. No. 1.1e-10;
Matches 48; Conservative 24; Mismatches 53; Indels 8; Gaps 3;

```
Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGXDSXTAAIDVTNX 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRXSSLPFXGSYXDLERYAG-HRDQIP 130

Qy        130 LGVYKLEFSIEAI 142
Db        131 LGIXQLIQSVXAL 143
```

RESULT 39
US-11-042-707-1
; Sequence 1, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; APPLICANT: Welters, Peter
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/36636
; CURRENT APPLICATION NUMBER: US/11/042,707
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 1
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mistletoe lectin
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 15
; OTHER INFORMATION: product= "Xaa is Asp or Glu"
; OTHER INFORMATION: /label= Xaa1
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 63
; OTHER INFORMATION: product= "Xaa is Gly or Gln"
; OTHER INFORMATION: /label= Xaa2
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 66
; OTHER INFORMATION: product= "Xaa is Ile or Val"
; OTHER INFORMATION: /label= Xaa3
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 75
; OTHER INFORMATION: product= "Xaa is Leu or Ala"

; OTHER INFORMATION: /label= Xaa4
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 107
; OTHER INFORMATION: product= "Xaa is missing"
; OTHER INFORMATION: /label= Xaa5
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 113
; OTHER INFORMATION: product= "Xaa is Asn or Thr"
; OTHER INFORMATION: /label= Xaa6
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 117
; OTHER INFORMATION: product= "Xaa is Pro or Thr"
; OTHER INFORMATION: /label= Xaa7
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 134
; OTHER INFORMATION: product= "Xaa is Asp or Glu"
; OTHER INFORMATION: /label= Xaa8
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 141
; OTHER INFORMATION: product= "Xaa is Ser or Thr"
; OTHER INFORMATION: /label= Xaa9
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 145
; OTHER INFORMATION: product= "Xaa is Phe or Tyr"
; OTHER INFORMATION: /label= Xaa10
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 152
; OTHER INFORMATION: product= "Xaa is Thr or Ala"
; OTHER INFORMATION: /label= Xaa11
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 177
; OTHER INFORMATION: product= "Xaa is Ala or Tyr"
; OTHER INFORMATION: /label= Xaa12
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 180
; OTHER INFORMATION: product= "Xaa is Tyr or Asp"
; OTHER INFORMATION: /label= Xaa13
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 185
; OTHER INFORMATION: product= "Xaa is Ala or Glu"
; OTHER INFORMATION: /label= Xaa14
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 191
; OTHER INFORMATION: product= "Xaa is Val or Met"
; OTHER INFORMATION: /label= Xaa15
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 219
; OTHER INFORMATION: product= "Xaa is Ile or Phe"
; OTHER INFORMATION: /label= Xaa16
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 224
; OTHER INFORMATION: product= "Xaa is Pro or Ser"
; OTHER INFORMATION: /label= Xaa17
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 225
; OTHER INFORMATION: product= "Xaa is Pro or Thr"
; OTHER INFORMATION: /label= Xaa18
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 232
; OTHER INFORMATION: product= "Xaa is Thr or Ser"
; OTHER INFORMATION: /label= Xaa19
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 236
; OTHER INFORMATION: product= "Xaa is Asp or Ser"
; OTHER INFORMATION: /label= Xaa20
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 287
; OTHER INFORMATION: product= "Xaa is Asn or Ser"
; OTHER INFORMATION: /label= Xaa21
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 290
; OTHER INFORMATION: product= "Xaa is Cys or Arg"
; OTHER INFORMATION: /label= Xaa22
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 325
; OTHER INFORMATION: product= "Xaa is Gly or Asn"
; OTHER INFORMATION: /label= Xaa23
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 364
; OTHER INFORMATION: product= "Xaa is Gly or Asp"
; OTHER INFORMATION: /label= Xaa24
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 426
; OTHER INFORMATION: product= "Xaa is Gly or Gln"
; OTHER INFORMATION: /label= Xaa25
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 435
; OTHER INFORMATION: product= "Xaa is Val or Asp"
; OTHER INFORMATION: /label= Xaa26
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 439
; OTHER INFORMATION: product= "Xaa is Gln or Lys"
; OTHER INFORMATION: /label= Xaa27
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 442
; OTHER INFORMATION: product= "Xaa is Gly or missing"
; OTHER INFORMATION: /label= Xaa28
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 443
; OTHER INFORMATION: product= "Xaa is Arg or Lys"
; OTHER INFORMATION: /label= Xaa29
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 464
; OTHER INFORMATION: product= "Xaa is Cys or Ser or Val"
; OTHER INFORMATION: /label= Xaa30
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 480
; OTHER INFORMATION: product= "Xaa is Ala or Gly"
; OTHER INFORMATION: /label= Xaa
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 481
; OTHER INFORMATION: product= "Xaa is Gly or Ala"
; OTHER INFORMATION: /label= Xaa32
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 483
; OTHER INFORMATION: product= "Xaa is Ser or Gly"
; OTHER INFORMATION: /label= Xaa33

```
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: 484
;    OTHER INFORMATION: product= "Xaa is Gly or Ser"
;    OTHER INFORMATION: /label= Xaa34
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: 493
;    OTHER INFORMATION: product= "Xaa is Gly or Tyr"
;    OTHER INFORMATION: /label= Xaa35
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: 500
```

Query Match 22.9%; Score 176; DB 6; Length 533;
Best Local Similarity 36.1%; Pred. No. 3e-10;
Matches 48; Conservative 24; Mismatches 53; Indels 8; Gaps 3;

```
Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     :   |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGXDSXTAAIDVTNX 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | |   :| | ||| |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRXSSLPFXGSYXDLERYAG-HRDQIP 130

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 LGIXQLIQSVXAL 143
```

```
RESULT 40
US-10-127-890-7
; Sequence 7, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 263 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-127-890-7
```

Query Match 22.7%; Score 174.5; DB 4; Length 263;
Best Local Similarity 30.8%; Pred. No. 1.7e-10;
Matches 44; Conservative 32; Mismatches 58; Indels 9; Gaps 3;

```
Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||:|||| |      |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :   |   :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139
```

```
RESULT 41
US-10-717-243-7
; Sequence 7, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
```

```
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 263 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-717-243-7

  Query Match             22.7%;  Score 174.5;  DB 5;  Length 263;
  Best Local Similarity   30.8%;  Pred. No. 1.7e-10;
  Matches   44;  Conservative   32;  Mismatches   58;  Indels    9;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||:|||| |     |  :|: | :::   |::|: :     ||:
Db          2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT--VATSKLFPGVTNRVTLTFDGSYQKLVN 119
              ||:|||:||::||       |   :    |   :|:  :|     ::|| : |:|::|
Db         62 VAVDVTNVYIMGYL-----ADTTSYFFNEPAAELASQYVFRDARRKITLPYSGNYERLQI 116

Qy        120 AAKVDRKDLELGVYKLEFSIEAI 142
              ||   |: : :|:  |: :|  :
Db        117 AAGKPREKIPIGLPALDSAISTL 139


RESULT 42
US-10-800-052-7
; Sequence 7, Application US/10800052
; Publication No. US20050202561A1
; GENERAL INFORMATION:
;  APPLICANT: Keener, William K
;  TITLE OF INVENTION: Plasmids Encoding Therapeutic Agents
;  FILE REFERENCE: B-221
;  CURRENT APPLICATION NUMBER: US/10/800,052
;  CURRENT FILING DATE:  2004-03-12
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 266
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-800-052-7

  Query Match             22.5%;  Score 173;  DB 5;  Length 266;
  Best Local Similarity   32.7%;  Pred. No. 2.5e-10;
  Matches   52;  Conservative   31;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:|||::
Db          5 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVDLSNH 64

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         65 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 120

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        121 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 159


RESULT 43
US-11-042-707-41
; Sequence 41, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 41
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: MLA-chain
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Xaa is Asp or Glu
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (63)..(63)
;   OTHER INFORMATION: Xaa is Gly or Gln
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (66)..(66)
;   OTHER INFORMATION: Xaa is Ile or Val
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (75)..(75)
;   OTHER INFORMATION: Xaa is Leu or Ala
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (114)..(114)
;   OTHER INFORMATION: Xaa is Asn or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (118)..(118)
;   OTHER INFORMATION: Xaa is Pro or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (135)..(135)
;   OTHER INFORMATION: Xaa is Asp or Glu
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (142)..(142)
;   OTHER INFORMATION: Xaa is Ser or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (146)..(146)
;   OTHER INFORMATION: Xaa is Phe or Tyr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (153)..(153)
;   OTHER INFORMATION: Xaa is Thr or Ala
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (178)..(178)
;   OTHER INFORMATION: Xaa is Ala or Tyr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (181)..(181)
;   OTHER INFORMATION: Xaa is Tyr or Asp
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (186)..(186)
;   OTHER INFORMATION: Xaa is Ala or Glu
;   FEATURE:
;   NAME/KEY: SITE
```

```
;   LOCATION: (192)..(192)
;   OTHER INFORMATION: Xaa is Val or Met
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (220)..(220)
;   OTHER INFORMATION: Xaa is Ile or Phe
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (225)..(225)
;   OTHER INFORMATION: Xaa is Pro or Ser
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (226)..(226)
;   OTHER INFORMATION: Xaa is Pro or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (233)..(233)
;   OTHER INFORMATION: Xaa is Thr or Ser
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (237)..(237)
;   OTHER INFORMATION: Xaa is Asp or Ser
US-11-042-707-41

  Query Match             22.5%;  Score 172.5;  DB 6;  Length 256;
  Best Local Similarity   36.6%;  Pred. No. 2.7e-10;
  Matches   49;  Conservative   25;  Mismatches   51;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||   ||: :: |:   ::|:· |:   ::| :|||||::|     :   |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGXDSXTAAIDVTNX 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||       |:: ||   |  | : || | | :| :| | |||   |    |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFXGSYXDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 PLGIXQLIQSVXAL 144


RESULT 44
US-11-042-707-40
; Sequence 40, Application US/11042707
; Publication No. US20050142183A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 40
;   LENGTH: 534
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Xaa is Asp or Glu
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (63)..(63)
;   OTHER INFORMATION: Xaa is Gly or Gln
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (66)..(66)
;   OTHER INFORMATION: Xaa is Ile or Val
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (75)..(75)
;   OTHER INFORMATION: Xaa is Leu or Ala
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (114)..(114)
;   OTHER INFORMATION: Xaa is Asn or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (118)..(118)
;   OTHER INFORMATION: Xaa is Pro or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (135)..(135)
;   OTHER INFORMATION: Xaa is Asp or Glu
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (142)..(142)
;   OTHER INFORMATION: Xaa is Ser or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (146)..(146)
;   OTHER INFORMATION: Xaa is Phe or Tyr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (153)..(153)
;   OTHER INFORMATION: Xaa is Thr or Ala
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (178)..(178)
;   OTHER INFORMATION: Xaa is Ala or Tyr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (181)..(181)
;   OTHER INFORMATION: Xaa is Tyr or Asp
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (186)..(186)
;   OTHER INFORMATION: Xaa is Ala or Glu
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (192)..(192)
;   OTHER INFORMATION: Xaa is Val or Met
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (220)..(220)
;   OTHER INFORMATION: Xaa is Ile or Phe
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (225)..(225)
;   OTHER INFORMATION: Xaa is Pro or Ser
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (226)..(226)
;   OTHER INFORMATION: Xaa is Pro or Thr
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (233)..(233)
;   OTHER INFORMATION: Xaa is Thr or Ser
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (237)..(237)
;   OTHER INFORMATION: Xaa is Asp or Ser
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (288)..(288)
;   OTHER INFORMATION: Xaa is Asn or Ser
;   FEATURE:
```

; NAME/KEY: SITE
; LOCATION: (291)..(291)
; OTHER INFORMATION: Xaa is Cys or Arg
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (326)..(326)
; OTHER INFORMATION: Xaa is Gly or Asn
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (365)..(365)
; OTHER INFORMATION: Xaa is Gly or Asp
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (427)..(427)
; OTHER INFORMATION: Xaa is Gly or Gln
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (436)..(436)
; OTHER INFORMATION: Xaa is Val or Asp
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (440)..(440)
; OTHER INFORMATION: Xaa is Gln or Lys
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (443)..(443)
; OTHER INFORMATION: Xaa is Gly or missing
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (444)..(444)
; OTHER INFORMATION: Xaa is Arg or Lys
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (465)..(465)
; OTHER INFORMATION: Xaa is Cys or Ser or Val
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (481)..(481)
; OTHER INFORMATION: Xaa is Ala or Gly
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (482)..(482)
; OTHER INFORMATION: Xaa is Gly or Ala
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (484)..(484)
; OTHER INFORMATION: Xaa is Ser or Gly
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (485)..(485)
; OTHER INFORMATION: Xaa is Gly or Ser
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (494)..(494)
; OTHER INFORMATION: Xaa is Gly or Tyr
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (501)..(501)
; OTHER INFORMATION: Xaa is Asn or Ser or Thr or Lys
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (502)..(502)
; OTHER INFORMATION: Xaa is Ser or Gly
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (503)..(503)
; OTHER INFORMATION: Xaa is Leu or Pro
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (504)..(504)
; OTHER INFORMATION: Xaa is Ala or Met
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (505)..(505)
; OTHER INFORMATION: Xaa is Met or Val
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (534)..(534)
; OTHER INFORMATION: Xaa is Pro or Phe
US-11-042-707-40

Query Match 22.5%; Score 172.5; DB 6; Length 534;
Best Local Similarity 36.6%; Pred. No. 7.3e-10;
Matches 49; Conservative 25; Mismatches 51; Indels 9; Gaps 4;

```
Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     :   |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGXDSXTAAIDVTNX 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||       |:: ||   |  | : || | | :| :| | |||  |   |. | :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFXGSYXDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
               ||: :|  |: |:
Db        131 PLGIXQLIQSVXAL 144
```

RESULT 45
US-10-083-336A-3
; Sequence 3, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-3

Query Match 22.0%; Score 169; DB 4; Length 198;
Best Local Similarity 32.1%; Pred. No. 4.7e-10;
Matches 51; Conservative 32; Mismatches 60; Indels 16; Gaps 6;

```
Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160
```

RESULT 46
US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof

```
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 198
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-7

  Query Match             22.0%;  Score 169;  DB 4;  Length 198;
  Best Local Similarity   32.1%;  Pred. No. 4.7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |     |  ||: :|  |  |  | ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 47
US-10-923-022-3
; Sequence 3, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 198
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-3

  Query Match             22.0%;  Score 169;  DB 5;  Length 198;
  Best Local Similarity   32.1%;  Pred. No. 4.7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |     |  ||: :|  |  |  | ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 48
US-10-923-022-7
; Sequence 7, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 198
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-7

  Query Match             22.0%;  Score 169;  DB 5;  Length 198;
  Best Local Similarity   32.1%;  Pred. No. 4.7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |     |  ||: :|  |  |  | ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 49
US-10-083-336A-5
; Sequence 5, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 199
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-5

  Query Match             22.0%;  Score 169;  DB 4;  Length 199;
  Best Local Similarity   32.1%;  Pred. No. 4.7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |     |  ||: :|  |  |  | ::||    :    ::||:||:::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         67 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 122

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        123 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 161
```

```
RESULT 50
US-10-923-022-5
; Sequence 5, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 199
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-5

  Query Match             22.0%;  Score 169;  DB 5;  Length 199;
  Best Local Similarity   32.1%;  Pred. No. 4.7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |     |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         67 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 122

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        123 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 161


RESULT 51
US-10-083-336A-10
; Sequence 10, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 200
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-10

  Query Match             22.0%;  Score 169;  DB 4;  Length 200;
  Best Local Similarity   32.1%;  Pred. No. 4.7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |     |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         67 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 122

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        123 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 161


RESULT 52
US-10-923-022-10
; Sequence 10, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 200
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-10

  Query Match             22.0%;  Score 169;  DB 5;  Length 200;
  Best Local Similarity   32.1%;  Pred. No. 4.7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |     |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         67 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 122

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        123 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 161


RESULT 53
US-10-282-935-1
; Sequence 1, Application US/10282935
; Publication No. US20030143193A1
; GENERAL INFORMATION:
;  APPLICANT: VITETTA, ELLEN S.
;  APPLICANT:  GHETIE, VICTOR F.
;  APPLICANT:  SMALLSHAW, JOAN
;  APPLICANT:  BALUNA, ROXANA G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
;  TITLE OF INVENTION:  PROTEINACEOUS COMPOUNDS
;  FILE REFERENCE: UTSD:884US
;  CURRENT APPLICATION NUMBER: US/10/282,935
;  CURRENT FILING DATE:  2002-10-29
;  PRIOR APPLICATION NUMBER: 09/538,873
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 60/126,826
;  PRIOR FILING DATE: 1999-03-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-10-282-935-1
```

```
  Query Match             22.0%;  Score 169;  DB 4;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 54
US-10-127-890-1
; Sequence 1, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 267 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1

  Query Match             22.0%;  Score 169;  DB 4;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 55
US-10-440-796-1
; Sequence 1, Application US/10440796
; Publication No. US20040009148A1
; GENERAL INFORMATION:
;  APPLICANT: VITETTA, ELLEN S.
;  APPLICANT:  GHETIE, VICTOR F.
;  APPLICANT:  SMALLSHAW, JOAN
;  APPLICANT:  BALUNA, ROXANA G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
;  TITLE OF INVENTION:  SYNDROME (VLS)
;  FILE REFERENCE: UTSD:603
;  CURRENT APPLICATION NUMBER: US/10/440,796
;  CURRENT FILING DATE:  2003-05-19
;  PRIOR APPLICATION NUMBER: US/09/538,873
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 60/126,826
;  PRIOR FILING DATE: 1999-03-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-10-440-796-1

  Query Match             22.0%;  Score 169;  DB 4;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 56
US-10-717-243-1
; Sequence 1, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
```

```
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 169
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/717,243
;            FILING DATE: 18-Nov-2003
;            CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/839,765
;            FILING DATE: 15-APR-1997
;            APPLICATION NUMBER: US 08/425,336
;            FILING DATE: 18-APR-1995
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 267 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-717-243-1

  Query Match             22.0%;  Score 169;  DB 5;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|     |     |  ||: :|  |  |  |  ::||     :     ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::     | : ||  | || |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |    |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 57
US-11-010-795-24
; Sequence 24, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
;  APPLICANT: TUMER, NILGUN E.
;  APPLICANT:  DI, RONG
;  TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
;  TITLE OF INVENTION:  RESISTANT TO TRICHOTHECENE FUNGAL TOXINS
;  FILE REFERENCE: OCIRS 3.0-085
;  CURRENT APPLICATION NUMBER: US/11/010,795
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: 60/529,348
;  PRIOR FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
;   LENGTH: 268
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-11-010-795-24

  Query Match             22.0%;  Score 169;  DB 6;  Length 268;
  Best Local Similarity   32.1%;  Pred. No. 7e-10;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|     |     |  ||: :|  |  |  |  ::||     :     ::||:||:::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::     | : ||  | || |  | |
Db         67 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 122

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |    |:::|||   || :| |::    | ||
Db        123 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 161


RESULT 58
US-10-083-336A-1
; Sequence 1, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-1

  Query Match             22.0%;  Score 169;  DB 4;  Length 576;
  Best Local Similarity   32.1%;  Pred. No. 2e-09;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|     |     |  ||: :|  |  |  |  ::||     :     ::||:||:::
Db         41 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 100

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::     | : ||  | || |  | |
Db        101 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 156

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |    |:::|||   || :| |::    | ||
Db        157 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 195


RESULT 59
US-10-923-022-1
; Sequence 1, Application US/10923022
```

```
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-1

  Query Match            22.0%;  Score 169;  DB 5;  Length 576;
  Best Local Similarity  32.1%;  Pred. No. 2e-09;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db         41 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 100

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db        101 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 156

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        157 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 195


RESULT 60
US-10-893-584-274
; Sequence 274, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
;  APPLICANT: Borgford, Thor
;  APPLICANT:  Braun, Curtis
;  APPLICANT:  Purac, Admir
;  APPLICANT:  Stoll, Dominik
;  TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
;  TITLE OF INVENTION:  Viral or Parasitic Infections
;  FILE REFERENCE: 10447-025
;  CURRENT APPLICATION NUMBER: US/10/893,584
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: US 09/551,151
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/403,752
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 10/089,058
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 274
;   LENGTH: 630
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Ricin-like toxin (TST10054)
US-10-893-584-274

  Query Match            22.0%;  Score 169;  DB 5;  Length 630;
  Best Local Similarity  32.1%;  Pred. No. 2.2e-09;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db         95 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 154

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |
Db        155 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 210

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|   |   |:::|||   || :| |::    | ||
Db        211 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 249


RESULT 61
US-10-083-336A-9
; Sequence 9, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-9

  Query Match            21.3%;  Score 163.5;  DB 4;  Length 185;
  Best Local Similarity  31.0%;  Pred. No. 1.7e-09;
  Matches   49;  Conservative   30;  Mismatches   52;  Indels   27;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAK--GTPVCQLPVTLQTIADDKRFVLVDITTTS 56
              |  ::|    |    |  ||: :|  |    | |:            ::||:||:::  :
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTNRVGLPI-----------NQRFILVELSNHA 53

Qy         57 KKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGS 113
              : :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |:
Db         54 ELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 109

Qy        114 YQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              | :|   |   |:::|||   || :| |::    | ||
Db        110 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 147


RESULT 62
US-10-923-022-9
; Sequence 9, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-9

  Query Match            21.3%;  Score 163.5;  DB 5;  Length 185;
```

```
  Best Local Similarity   31.0%;  Pred. No. 1.7e-09;
  Matches   49;  Conservative   30;  Mismatches   52;  Indels   27;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAK--GTPVCQLPVTLQTIADDKRFVLVDITTTS 56
              |  ::|    |    |  ||: :|  |    | |:           ::||:||:::  :
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTNRVGLPI-----------NQRFILVELSNHA 53

Qy         57 KKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGS 113
              : :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |:
Db         54 ELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 109

Qy        114 YQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              | :|   |   |:::|||   || :| |::    | ||
Db        110 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 147


RESULT 63
US-10-127-890-101
; Sequence 101, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 101:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-127-890-101

  Query Match           21.2%;  Score 162.5;  DB 4;  Length 251;
  Best Local Similarity   35.3%;  Pred. No. 3.3e-09;
  Matches   53;  Conservative   23;  Mismatches   53;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|      : | |:       |:  |||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKADDPGKAFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||      ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              || |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 64
US-10-127-890-110
; Sequence 110, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 110:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-127-890-110
```

```
  Query Match             21.2%;  Score 162.5;  DB 4;  Length 251;
  Best Local Similarity   35.3%;  Pred. No. 3.3e-09;
  Matches   53;  Conservative   23;  Mismatches   53;  Indels   21;  Gaps    8;

Qy          2 NTVSFN-LGEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:  |||  | |||| :
Db          3 DTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKADDPGKAFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::|||||  |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 65
US-10-127-890-111
; Sequence 111, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 111:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 111:

US-10-127-890-111

  Query Match             21.2%;  Score 162.5;  DB 4;  Length 251;
  Best Local Similarity   35.3%;  Pred. No. 3.3e-09;
  Matches   53;  Conservative   23;  Mismatches   53;  Indels   21;  Gaps    8;

Qy          2 NTVSFN-LGEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:  |||  | |||| :
Db          3 DTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKADDPGKAFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::|||||  |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 66
US-10-717-243-101
; Sequence 101, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 101:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
```

```
;       SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-717-243-101

  Query Match             21.2%;  Score 162.5;  DB 5;  Length 251;
  Best Local Similarity   35.3%;  Pred. No. 3.3e-09;
  Matches   53;  Conservative   23;  Mismatches   53;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:  |||  | |||| :
Db          3 DTVSPSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKADDPGKAFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    | |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 67
US-10-717-243-110
; Sequence 110, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 169
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/717,243
;            FILING DATE: 18-Nov-2003
;            CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/839,765
;            FILING DATE: 15-APR-1997
;            APPLICATION NUMBER: US 08/425,336
;            FILING DATE: 18-APR-1995
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 110:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 251 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-717-243-110

  Query Match             21.2%;  Score 162.5;  DB 5;  Length 251;
  Best Local Similarity   35.3%;  Pred. No. 3.3e-09;
  Matches   53;  Conservative   23;  Mismatches   53;  Indels   21;  Gaps    8;

Qy          2 NTVSFN-LGEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:  |||  | |||| :
Db          3 DTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKADDPGKAFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    | |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 68
US-10-717-243-111
; Sequence 111, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 169
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/717,243
;            FILING DATE: 18-Nov-2003
;            CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/839,765
;            FILING DATE: 15-APR-1997
;            APPLICATION NUMBER: US 08/425,336
;            FILING DATE: 18-APR-1995
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 111:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 251 amino acids
;            TYPE: amino acid
```

```
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-717-243-111

  Query Match             21.2%;  Score 162.5;  DB 5;  Length 251;
  Best Local Similarity   35.3%;  Pred. No. 3.3e-09;
  Matches   53;  Conservative   23;  Mismatches   53;  Indels   21;  Gaps    8;

Qy          2 NTVSFN-LGEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:  |||  | |||| :
Db          3 DTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKADDPGKAFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              || |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 69
US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-4

  Query Match             21.0%;  Score 161;  DB 4;  Length 188;
  Best Local Similarity   31.4%;  Pred. No. 3.3e-09;
  Matches   49;  Conservative   30;  Mismatches   57;  Indels   20;  Gaps    5;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKK 58
              |  ::|    |    |  ||: :|  |        ||:       ::||:||:::  ::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-------NQRFILVELSNHAEL 58

Qy         59 TVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
              :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |:|
Db         59 SVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 114

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :|   |   |:::|||   || :| |::    | ||
Db        115 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 150


RESULT 70
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-8

  Query Match             21.0%;  Score 161;  DB 4;  Length 188;
  Best Local Similarity   31.4%;  Pred. No. 3.3e-09;
  Matches   49;  Conservative   30;  Mismatches   57;  Indels   20;  Gaps    5;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKK 58
              |  ::|    |    |  ||: :|  |        ||:       ::||:||:::  ::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-------NQRFILVELSNHAEL 58

Qy         59 TVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
              :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |:|
Db         59 SVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 114

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :|   |   |:::|||   || :| |::    | ||
Db        115 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 150


RESULT 71
US-10-923-022-4
; Sequence 4, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-4

  Query Match             21.0%;  Score 161;  DB 5;  Length 188;
  Best Local Similarity   31.4%;  Pred. No. 3.3e-09;
  Matches   49;  Conservative   30;  Mismatches   57;  Indels   20;  Gaps    5;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKK 58
              |  ::|    |    |  ||: :|  |        ||:       ::||:||:::  ::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-------NQRFILVELSNHAEL 58

Qy         59 TVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
              :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |:|
Db         59 SVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 114

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :|   |   |:::|||   || :| |::    | ||
Db        115 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 150


RESULT 72
US-10-923-022-8
; Sequence 8, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
```

```
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-8

  Query Match             21.0%;  Score 161;  DB 5;  Length 188;
  Best Local Similarity   31.4%;  Pred. No. 3.3e-09;
  Matches   49;  Conservative   30;  Mismatches   57;  Indels   20;  Gaps    5;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKK 58
              |  ::|    |    |  ||: :|  |         ||:       ::||:||:::  ::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-------NQRFILVELSNHAEL 58

Qy         59 TVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
              :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |:|
Db         59 SVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 114

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :|   |   |:::|||   || :| |::    | ||
Db        115 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 150


RESULT 73
US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 189
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-6

  Query Match             21.0%;  Score 161;  DB 4;  Length 189;
  Best Local Similarity   31.4%;  Pred. No. 3.3e-09;
  Matches   49;  Conservative   30;  Mismatches   57;  Indels   20;  Gaps    5;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKK 58
              |  ::|    |    |  ||: :|  |         ||:       ::||:||:::  ::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-------NQRFILVELSNHAEL 59

Qy         59 TVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
              :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |:|
Db         60 SVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 115

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :|   |   |:::|||   || :| |::    | ||
Db        116 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 151


RESULT 74
US-10-923-022-6
; Sequence 6, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 189
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-6

  Query Match             21.0%;  Score 161;  DB 5;  Length 189;
  Best Local Similarity   31.4%;  Pred. No. 3.3e-09;
  Matches   49;  Conservative   30;  Mismatches   57;  Indels   20;  Gaps    5;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKK 58
              |  ::|    |    |  ||: :|  |         ||:       ::||:||:::  ::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-------NQRFILVELSNHAEL 59

Qy         59 TVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
              :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |:|
Db         60 SVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 115

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :|   |   |:::|||   || :| |::    | ||
Db        116 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 151


RESULT 75
US-10-083-336A-11
; Sequence 11, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/083,336A
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 190
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-083-336A-11

  Query Match             21.0%;  Score 161;  DB 4;  Length 190;
  Best Local Similarity   31.4%;  Pred. No. 3.3e-09;
  Matches   49;  Conservative   30;  Mismatches   57;  Indels   20;  Gaps    5;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKK 58
              |  ::|    |    |  ||: :|  |         ||:       ::||:||:::  ::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-------NQRFILVELSNHAEL 59

Qy         59 TVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
              :| :|:|||: |||||:      : | |    ::    | : ||  | || |  | |:|
Db         60 SVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 115

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :|   |   |:::|||   || :| |::    | ||
Db        116 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 151
```

```
RESULT 76
US-10-923-022-11
; Sequence 11, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
;  APPLICANT: Olson, Mark A
;  APPLICANT:  Millard, Charles B
;  APPLICANT:  Byrne, Michael P
;  APPLICANT:  Wannemacher, Robert W
;  TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
;  FILE REFERENCE: P67452US0 (RIID 01-58)
;  CURRENT APPLICATION NUMBER: US/10/923,022
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: US/10/083,336
;  PRIOR FILING DATE: 2002-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 190
;   TYPE: PRT
;   ORGANISM: Ricinus communis
US-10-923-022-11

  Query Match             21.0%;  Score 161;  DB 5;  Length 190;
  Best Local Similarity   31.4%;  Pred. No. 3.3e-09;
  Matches   49;  Conservative   30;  Mismatches   57;  Indels   20;  Gaps    5;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKK 58
              |  ::|    |     |  ||: :|  |          ||:        ::||:||:::  ::
Db          7 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-------NQRFILVELSNHAEL 59

Qy         59 TVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
              :| :|:|||: |||||:      : | |     ::    | : ||  | || |  | |:|
Db         60 SVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 115

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :|    |   |:::|||   || :| |::    | ||
Db        116 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 151


RESULT 77
US-10-127-890-100
; Sequence 100, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 100:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-127-890-100

  Query Match             20.9%;  Score 160.5;  DB 4;  Length 251;
  Best Local Similarity   35.3%;  Pred. No. 5.5e-09;
  Matches   53;  Conservative   23;  Mismatches   53;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:  |||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKADDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||      ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 78
US-10-717-243-100
; Sequence 100, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
```

```
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 100:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-717-243-100

  Query Match             20.9%;  Score 160.5;  DB 5;  Length 251;
  Best Local Similarity   35.3%;  Pred. No. 5.5e-09;
  Matches   53;  Conservative   23;  Mismatches   53;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:  |||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKADDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 79
US-10-758-902-1
; Sequence 1, Application US/10758902
; Publication No. US20040266994A1
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-1

  Query Match             20.8%;  Score 160;  DB 5;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-10;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30
              ||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTP 30


RESULT 80
US-10-127-890-99
; Sequence 99, Application US/10127890
; Publication No. US20030166196A1
;  GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 173
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/127,890
;            FILING DATE: 23-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,360
;            FILING DATE: 13-MAY-1996
;            APPLICATION NUMBER: PCT/US94/05348
;            FILING DATE: 12-MAY-1994
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 99:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 251 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-127-890-99

  Query Match             20.6%;  Score 158.5;  DB 4;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 9.1e-09;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKAFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111
```

```
Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  .|:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 81
US-10-717-243-99
; Sequence 99, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 99:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-717-243-99

  Query Match            20.6%;  Score 158.5;  DB 5;  Length 251;
  Best Local Similarity  34.7%;  Pred. No. 9.1e-09;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKAFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::|||||  |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 82
US-09-765-527-247
; Sequence 247, Application US/09765527
; Patent No. US20020006638A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;        TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;                            Fusion Proteins and BPI-Derived Peptides
;        NUMBER OF SEQUENCES: 265
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;             STREET: 6300 Sears Tower, 233 South Wacker Drive '
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: United States of America
;             ZIP: 60606-6402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/765,527
;             FILING DATE: 18-Jan-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/621,803
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Borun, Michael F.
;             REGISTRATION NUMBER: 25,447
;             REFERENCE/DOCKET NUMBER: 27129/33199
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/474-6300
;             TELEFAX: 312/474-0448
;             TELEX: 25-3856
;   INFORMATION FOR SEQ ID NO: 247:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

  Query Match            20.4%;  Score 156.5;  DB 3;  Length 251;
  Best Local Similarity  34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::|||||  |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 83
US-10-127-890-2
; Sequence 2, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
```

```
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 173
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/127,890
;            FILING DATE: 23-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,360
;            FILING DATE: 13-MAY-1996
;            APPLICATION NUMBER: PCT/US94/05348
;            FILING DATE: 12-MAY-1994
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 251 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-127-890-2

  Query Match             20.4%;  Score 156.5;  DB 4;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 84
US-10-127-890-102
; Sequence 102, Application US/10127890
; Publication No. US20030166196A1
```

```
;   GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 173
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/127,890
;            FILING DATE: 23-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,360
;            FILING DATE: 13-MAY-1996
;            APPLICATION NUMBER: PCT/US94/05348
;            FILING DATE: 12-MAY-1994
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 102:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 251 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-127-890-102

  Query Match             20.4%;  Score 156.5;  DB 4;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 85
US-10-127-890-103
; Sequence 103, Application US/10127890
```

```
; Publication No. US20030166196A1
;  GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 173
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/127,890
;            FILING DATE: 23-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,360
;            FILING DATE: 13-MAY-1996
;            APPLICATION NUMBER: PCT/US94/05348
;            FILING DATE: 12-MAY-1994
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;  INFORMATION FOR SEQ ID NO: 103:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 251 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-127-890-103

  Query Match             20.4%;  Score 156.5;  DB 4;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 86
US-10-127-890-104
```

```
; Sequence 104, Application US/10127890
; Publication No. US20030166196A1
;  GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 173
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/127,890
;            FILING DATE: 23-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,360
;            FILING DATE: 13-MAY-1996
;            APPLICATION NUMBER: PCT/US94/05348
;            FILING DATE: 12-MAY-1994
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;  INFORMATION FOR SEQ ID NO: 104:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 251 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-127-890-104

  Query Match             20.4%;  Score 156.5;  DB 4;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 87
```

```
US-10-127-890-105
; Sequence 105, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 105:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-127-890-105

  Query Match             20.4%;  Score 156.5;  DB 4;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140
```

```
RESULT 88
US-10-127-890-106
; Sequence 106, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 106:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-10-127-890-106

  Query Match             20.4%;  Score 156.5;  DB 4;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFN-LGEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140
```

```
RESULT 89
US-10-127-890-108
; Sequence 108, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 108:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-127-890-108

  Query Match             20.4%;  Score 156.5;  DB 4;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |     |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TCKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              || |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140
```

```
RESULT 90
US-10-127-890-109
; Sequence 109, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 109:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-127-890-109

  Query Match             20.4%;  Score 156.5;  DB 4;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |     |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              || |    |  |:  :||:  |   |: :
```

```
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 91
US-10-717-243-2
; Sequence 2, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;    INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-717-243-2

  Query Match             20.4%;  Score 156.5;  DB 5;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:      |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
```

```
              || |    | |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 92
US-10-717-243-102
; Sequence 102, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;    INFORMATION FOR SEQ ID NO: 102:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-717-243-102

  Query Match             20.4%;  Score 156.5;  DB 5;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:      |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111
```

```
Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 93
US-10-717-243-103
; Sequence 103, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 103:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-717-243-103

  Query Match             20.4%;  Score 156.5;  DB 5;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111


Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 94
US-10-717-243-104
; Sequence 104, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 104:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-717-243-104

  Query Match             20.4%;  Score 156.5;  DB 5;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
```

```
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 95
US-10-717-243-105
; Sequence 105, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 105:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-717-243-105

  Query Match             20.4%;  Score 156.5;  DB 5;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:      |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
```

```
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 96
US-10-717-243-106
; Sequence 106, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 106:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-10-717-243-106

  Query Match             20.4%;  Score 156.5;  DB 5;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFN-LGEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:      |:   ||  | |||| :
Db          3 DTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56
```

```
Qy          53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
               :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db          57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy         113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
               ||  |    |  |:  :||:  |   |: :
Db         112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 97
US-10-717-243-108
; Sequence 108, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 108:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-717-243-108

  Query Match           20.4%;  Score 156.5;  DB 5;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:      |:   ||  | |||| :
Db          3 DTVSPSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TCKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 98
US-10-717-243-109
; Sequence 109, Application US/10717243
; Publication No. US20050054835A1
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 109:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 251 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-717-243-109

  Query Match           20.4%;  Score 156.5;  DB 5;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 1.5e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:      |:   ||  | |||| :
```

```
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    | |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 99
US-10-074-596-1
; Sequence 1, Application US/10074596
; Publication No. US20030176331A1
; GENERAL INFORMATION:
;  APPLICANT: ROSENBLUM, MICHAEL G.
;  APPLICANT:  CHEUNG, LAWRENCE
;  TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
;  TITLE OF INVENTION:  MAKING THEEOF
;  FILE REFERENCE: CLFR:007US
;  CURRENT APPLICATION NUMBER: US/10/074,596
;  CURRENT FILING DATE:  2002-02-12
;  PRIOR APPLICATION NUMBER: 60/268,402
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Gelonium multiflorum
US-10-074-596-1

  Query Match             20.4%;  Score 156.5;  DB 4;  Length 316;
  Best Local Similarity   34.7%;  Pred. No. 2.1e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db         49 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 102

Qy         53 TTTSKKTVKVAIDVTDVYVVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    | |   ||   | :  | | |
Db        103 SNDNGQLAEIAIDVTSVYVVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 157

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        158 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 186


RESULT 100
US-10-964-195-13
; Sequence 13, Application US/10964195
; Publication No. US20050163774A1
; GENERAL INFORMATION:
;  APPLICANT: Rosenblum et al.
;  TITLE OF INVENTION: Immunotoxins Directed Against c-erbB-2 (HER-2/Neu)
;  TITLE OF INVENTION:  Related Surface Antigens
;  FILE REFERENCE: D5425CIP2
;  CURRENT APPLICATION NUMBER: US/10/964,195
;  CURRENT FILING DATE:  2004-10-13
;  PRIOR APPLICATION NUMBER: US/09/320,156
;  PRIOR FILING DATE: 1999-05-26
;  PRIOR APPLICATION NUMBER: 08/404,499
;  PRIOR FILING DATE: 1995-03-17
;  NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 13
;   LENGTH: 498
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Polypeptide encoded by the scFv23-gelonin immunotoxin
US-10-964-195-13

  Query Match             20.4%;  Score 156.5;  DB 5;  Length 498;
  Best Local Similarity   34.7%;  Pred. No. 3.8e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db        249 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 302

Qy         53 TTTSKKTVKVAIDVTDVYVVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    | |   ||   | :  | | |
Db        303 SNDNGQLAEIAIDVTSVYVVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 357

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        358 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 386


Search completed: September 18, 2006, 19:35:33
Job time : 213.265 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:31:32 ; Search time 34.9609 Seconds
(without alignments)
301.092 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 256596 seqs, 70647373 residues

Total number of hits satisfying chosen parameters: 256596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	221.5	28.8	250	7	US-11-361-977A-36	Sequence 36, Appl
2	183.5	23.9	247	7	US-11-361-977A-39	Sequence 39, Appl
3	179.5	23.4	247	7	US-11-361-977A-34	Sequence 34, Appl
4	169	22.0	267	7	US-11-263-537-1	Sequence 1, Appli
5	156.5	20.4	251	7	US-11-345-661-7	Sequence 7, Appli
6	156.5	20.4	316	7	US-11-345-661-21	Sequence 21, Appl
7	156.5	20.4	408	7	US-11-345-661-8	Sequence 8, Appli
8	156.5	20.4	408	7	US-11-345-661-10	Sequence 10, Appl
9	155	20.2	251	7	US-11-263-537-3	Sequence 3, Appli
10	104.5	13.6	254	7	US-11-361-977A-85	Sequence 85, Appl
11	104.5	13.6	275	7	US-11-361-977A-35	Sequence 35, Appl
12	104.5	13.6	327	7	US-11-361-977A-79	Sequence 79, Appl
13	104.5	13.6	330	7	US-11-361-977A-82	Sequence 82, Appl
14	104.5	13.6	332	7	US-11-361-977A-73	Sequence 73, Appl
15	104.5	13.6	332	7	US-11-361-977A-76	Sequence 76, Appl
16	85.5	11.1	277	6	US-10-953-349-30545	Sequence 30545, A
17	85.5	11.1	277	7	US-11-056-355B-61236	Sequence 61236, A
18	85.5	11.1	281	6	US-10-953-349-30544	Sequence 30544, A
19	85.5	11.1	281	7	US-11-056-355B-61235	Sequence 61235, A
20	85.5	11.1	298	6	US-10-953-349-30543	Sequence 30543, A
21	85.5	11.1	298	7	US-11-056-355B-61234	Sequence 61234, A
22	81	10.5	2053	7	US-11-013-711-9	Sequence 9, Appli
23	80.5	10.5	435	7	US-11-316-535A-133	Sequence 133, App
24	80.5	10.5	481	7	US-11-316-535A-157	Sequence 157, App
25	80	10.4	1036	7	US-11-192-046-44	Sequence 44, Appl
26	74.5	9.7	364	7	US-11-056-355B-86437	Sequence 86437, A
27	74.5	9.7	487	6	US-10-953-349-5406	Sequence 5406, Ap
28	74.5	9.7	493	6	US-10-953-349-5405	Sequence 5405, Ap
29	74.5	9.7	510	6	US-10-953-349-5404	Sequence 5404, Ap
30	74.5	9.7	1333	6	US-10-449-902-41289	Sequence 41289, A
31	74	9.6	689	7	US-11-056-355B-97983	Sequence 97983, A
32	74	9.6	689	7	US-11-056-355B-109222	Sequence 109222,
33	74	9.6	699	7	US-11-056-355B-97982	Sequence 97982, A
34	74	9.6	699	7	US-11-056-355B-109221	Sequence 109221,
35	74	9.6	793	7	US-11-056-355B-97981	Sequence 97981, A
36	74	9.6	793	7	US-11-056-355B-109220	Sequence 109220,
37	72.5	9.4	318	7	US-11-330-403-14433	Sequence 14433, A
38	72.5	9.4	1403	6	US-10-505-928-471	Sequence 471, App
39	72	9.4	374	6	US-10-471-571A-706	Sequence 706, App
40	72	9.4	593	6	US-10-449-902-55385	Sequence 55385, A
41	71	9.2	444	7	US-11-174-307B-3704	Sequence 3704, Ap
42	71	9.2	1531	7	US-11-333-747A-44	Sequence 44, Appl
43	70.5	9.2	330	6	US-10-953-349-3286	Sequence 3286, Ap
44	70.5	9.2	347	6	US-10-953-349-3285	Sequence 3285, Ap
45	70.5	9.2	418	6	US-10-449-902-38378	Sequence 38378, A
46	70	9.1	366	6	US-10-449-902-30832	Sequence 30832, A
47	70	9.1	755	6	US-10-449-902-50637	Sequence 50637, A
48	70	9.1	768	7	US-11-056-355B-46135	Sequence 46135, A
49	70	9.1	780	7	US-11-056-355B-86211	Sequence 86211, A
50	70	9.1	839	7	US-11-056-355B-69910	Sequence 69910, A
51	70	9.1	1275	6	US-10-548-463-223	Sequence 223, App
52	69.5	9.0	319	7	US-11-361-977A-38	Sequence 38, Appl
53	69.5	9.0	452	7	US-11-330-403-459	Sequence 459, App
54	69	9.0	282	6	US-10-449-902-56587	Sequence 56587, A
55	69	9.0	393	6	US-10-471-571A-2102	Sequence 2102, Ap
56	69	9.0	1134	6	US-10-833-833-169	Sequence 169, App
57	69	9.0	1290	6	US-10-669-920-835	Sequence 835, App
58	69	9.0	1321	7	US-11-300-928-49	Sequence 49, Appl
59	68	8.9	271	7	US-11-056-355B-17914	Sequence 17914, A
60	68	8.9	339	7	US-11-056-355B-17913	Sequence 17913, A
61	67.5	8.8	247	7	US-11-361-977A-83	Sequence 83, Appl
62	67.5	8.8	249	7	US-11-361-977A-84	Sequence 84, Appl
63	67.5	8.8	293	7	US-11-361-977A-37	Sequence 37, Appl
64	67.5	8.8	320	7	US-11-361-977A-77	Sequence 77, Appl
65	67.5	8.8	322	7	US-11-361-977A-78	Sequence 78, Appl
66	67.5	8.8	323	7	US-11-361-977A-80	Sequence 80, Appl
67	67.5	8.8	325	7	US-11-361-977A-71	Sequence 71, Appl
68	67.5	8.8	325	7	US-11-361-977A-74	Sequence 74, Appl
69	67.5	8.8	325	7	US-11-361-977A-81	Sequence 81, Appl
70	67.5	8.8	327	7	US-11-361-977A-72	Sequence 72, Appl
71	67.5	8.8	327	7	US-11-361-977A-75	Sequence 75, Appl
72	67.5	8.8	338	7	US-11-056-355B-86215	Sequence 86215, A
73	67.5	8.8	478	6	US-10-449-902-48581	Sequence 48581, A
74	67	8.7	437	6	US-10-449-902-55897	Sequence 55897, A
75	66.5	8.7	354	7	US-11-056-355B-22809	Sequence 22809, A
76	66.5	8.7	405	6	US-10-449-902-45576	Sequence 45576, A
77	66.5	8.7	455	7	US-11-330-403-8002	Sequence 8002, Ap
78	66.5	8.7	455	7	US-11-330-403-15293	Sequence 15293, A
79	66.5	8.7	456	7	US-11-056-355B-49172	Sequence 49172, A
80	66.5	8.7	493	7	US-11-056-355B-49171	Sequence 49171, A
81	66.5	8.7	520	7	US-11-056-355B-49170	Sequence 49170, A
82	66.5	8.7	645	6	US-10-449-902-45335	Sequence 45335, A
83	66.5	8.7	967	6	US-10-505-928-795	Sequence 795, App
84	66.5	8.7	967	6	US-10-700-439-143	Sequence 143, App
85	66.5	8.7	967	7	US-11-387-011-2	Sequence 2, Appli
86	66.5	8.7	1428	7	US-11-070-573-11	Sequence 11, Appl
87	66	8.6	180	7	US-11-330-403-5486	Sequence 5486, Ap
88	66	8.6	224	6	US-10-534-238-2	Sequence 2, Appli
89	66	8.6	273	6	US-10-471-571A-3740	Sequence 3740, Ap
90	66	8.6	287	6	US-10-953-349-31921	Sequence 31921, A
91	66	8.6	287	7	US-11-056-355B-64817	Sequence 64817, A
92	66	8.6	311	6	US-10-953-349-31920	Sequence 31920, A
93	66	8.6	311	7	US-11-056-355B-64816	Sequence 64816, A
94	66	8.6	353	6	US-10-953-349-31919	Sequence 31919, A
95	66	8.6	353	7	US-11-056-355B-64815	Sequence 64815, A
96	66	8.6	355	6	US-10-449-902-39182	Sequence 39182, A
97	66	8.6	406	6	US-10-953-349-32766	Sequence 32766, A
98	66	8.6	406	7	US-11-056-355B-67038	Sequence 67038, A

99	66	8.6	462	6	US-10-953-349-32765	Sequence 32765, A
100	66	8.6	462	7	US-11-056-355B-67037	Sequence 67037, A

ALIGNMENTS

RESULT 1
US-11-361-977A-36
; Sequence 36, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 17080-002005/601F
; CURRENT APPLICATION NUMBER: US/11/361,977A
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Momordica charantia
US-11-361-977A-36

Query Match 28.8%; Score 221.5; DB 7; Length 250;
Best Local Similarity 37.2%; Pred. No. 1.3e-14;
Matches 54; Conservative 27; Mismatches 55; Indels 9; Gaps 4;

```
Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148
```

RESULT 2
US-11-361-977A-39
; Sequence 39, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 17080-002005/601F
; CURRENT APPLICATION NUMBER: US/11/361,977A
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Trichosanthews kirilowii
US-11-361-977A-39

Query Match 23.9%; Score 183.5; DB 7; Length 247;
Best Local Similarity 31.0%; Pred. No. 7.9e-11;
Matches 44; Conservative 32; Mismatches 61; Indels 5; Gaps 2;

```
Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140
```

RESULT 3
US-11-361-977A-34
; Sequence 34, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 17080-002005/601F
; CURRENT APPLICATION NUMBER: US/11/361,977A
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Bryonia dioica
US-11-361-977A-34

Query Match 23.4%; Score 179.5; DB 7; Length 247;
Best Local Similarity 30.8%; Pred. No. 2e-10;
Matches 44; Conservative 34; Mismatches 58; Indels 7; Gaps 3;

```
Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||::||  |     |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140
```

RESULT 4
US-11-263-537-1
; Sequence 1, Application US/11263537
; Publication No. US20060100135A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
; FILE REFERENCE: UTSD:884USC1
; CURRENT APPLICATION NUMBER: US/11/263,537
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: 10/282,935
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```
;   OTHER INFORMATION: Peptide
US-11-263-537-1

  Query Match             22.0%;  Score 169;  DB 7;  Length 267;
  Best Local Similarity   32.1%;  Pred. No. 2.4e-09;
  Matches   51;  Conservative   32;  Mismatches   60;  Indels   16;  Gaps    6;

Qy          1 YNTVSFNLGEA--YEYPTFIQDLRNELAKGTPV-CQLPVTLQTIA--DDKRFVLVDITTT 55
              |  ::|    |    |  ||: :|  |  |  |  ::||    :    ::||:||:::
Db          6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL---DKVPTVATSKLFPGVTNRVTLTFDG 112
              :: :| :|:|||: |||||:      : | |    ::    | : ||  | ||| |  | |
Db         66 AELSVTLALDVTNAYVVGYR----AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIW----GKTQ 147
              :| :|    |   |:::|||   || :| |::    | ||
Db        122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQ 160


RESULT 5
US-11-345-661-7
; Sequence 7, Application US/11345661
; Publication No. US20060171919A1
; GENERAL INFORMATION:
;  APPLICANT: Rosenblum, Michael
;  APPLICANT:  Cheung, Lawrence
;  APPLICANT:  Lyu, Mi-Ae
;  TITLE OF INVENTION: Targeted polypeptides
;  FILE REFERENCE: CLFR:059US
;  CURRENT APPLICATION NUMBER: US/11/345,661
;  CURRENT FILING DATE:  2006-02-01
;  PRIOR APPLICATION NUMBER: US 60/649,478
;  PRIOR FILING DATE: 2005-02-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: gelonin plant
US-11-345-661-7

  Query Match             20.4%;  Score 156.5;  DB 7;  Length 251;
  Best Local Similarity   34.7%;  Pred. No. 4e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 6
US-11-345-661-21
; Sequence 21, Application US/11345661
; Publication No. US20060171919A1
; GENERAL INFORMATION:
;  APPLICANT: Rosenblum, Michael
;  APPLICANT:  Cheung, Lawrence
;  APPLICANT:  Lyu, Mi-Ae
;  TITLE OF INVENTION: Targeted polypeptides
;  FILE REFERENCE: CLFR:059US
;  CURRENT APPLICATION NUMBER: US/11/345,661
;  CURRENT FILING DATE:  2006-02-01
;  PRIOR APPLICATION NUMBER: US 60/649,478
;  PRIOR FILING DATE: 2005-02-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Plant
US-11-345-661-21

  Query Match             20.4%;  Score 156.5;  DB 7;  Length 316;
  Best Local Similarity   34.7%;  Pred. No. 5.3e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db         49 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 102

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db        103 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 157

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        158 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 186


RESULT 7
US-11-345-661-8
; Sequence 8, Application US/11345661
; Publication No. US20060171919A1
; GENERAL INFORMATION:
;  APPLICANT: Rosenblum, Michael
;  APPLICANT:  Cheung, Lawrence
;  APPLICANT:  Lyu, Mi-Ae
;  TITLE OF INVENTION: Targeted polypeptides
;  FILE REFERENCE: CLFR:059US
;  CURRENT APPLICATION NUMBER: US/11/345,661
;  CURRENT FILING DATE:  2006-02-01
;  PRIOR APPLICATION NUMBER: US 60/649,478
;  PRIOR FILING DATE: 2005-02-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
;   LENGTH: 408
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: Conjugated Polypeptide
US-11-345-661-8

  Query Match             20.4%;  Score 156.5;  DB 7;  Length 408;
  Best Local Similarity   34.7%;  Pred. No. 7.3e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |  |  |  |: :|| :|     : | |:       |:   ||  | |||| :
Db        160 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 213

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
              :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db        214 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 268

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        269 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 297


RESULT 8
US-11-345-661-10
; Sequence 10, Application US/11345661
; Publication No. US20060171919A1
; GENERAL INFORMATION:
;  APPLICANT: Rosenblum, Michael
;  APPLICANT:  Cheung, Lawrence
```

```
;  APPLICANT:  Lyu, Mi-Ae
;  TITLE OF INVENTION: Targeted polypeptides
;  FILE REFERENCE: CLFR:059US
;  CURRENT APPLICATION NUMBER: US/11/345,661
;  CURRENT FILING DATE:  2006-02-01
;  PRIOR APPLICATION NUMBER: US 60/649,478
;  PRIOR FILING DATE: 2005-02-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
;   LENGTH: 408
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: Conjugated Polypeptide
US-11-345-661-10

  Query Match             20.4%;  Score 156.5;  DB 7;  Length 408;
  Best Local Similarity   34.7%;  Pred. No. 7.3e-08;
  Matches   52;  Conservative   23;  Mismatches   54;  Indels   21;  Gaps    8;

Qy          2 NTVSFNL-GEAY-EYPTFIQDLRNEL-----AKGTPVCQLPVTLQTIADD--KRFVLVDI 52
              :||||:  |   |   |  |: :|| :|     : | |:      |:   ||  | |||| :
Db          3 DTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPL------LRKKCDDPGKCFVLVAL 56

Qy         53 TTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDG 112
               :  : :  ::||||| |||||||     ::|: |    |  |   ||   | :  | | |
Db         57 SNDNGQLAEIAIDVTSVYVVGYQ----VRNRSYFFKDAPDAAYEGLFKN-TIKTRLHFGG 111

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              ||  |    |  |:  :||:  |   |: :
Db        112 SYPSL-EGEKAYRETTDLGIEPLRIGIKKL 140


RESULT 9
US-11-263-537-3
; Sequence 3, Application US/11263537
; Publication No. US20060100135A1
; GENERAL INFORMATION:
;  APPLICANT: VITETTA, ELLEN S.
;  APPLICANT:  GHETIE, VICTOR F.
;  APPLICANT:  SMALLSHAW, JOAN
;  APPLICANT:  BALUNA, ROXANA G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
;  TITLE OF INVENTION:  PROTEINACEOUS COMPOUNDS
;  FILE REFERENCE: UTSD:884USC1
;  CURRENT APPLICATION NUMBER: US/11/263,537
;  CURRENT FILING DATE:  2005-10-31
;  PRIOR APPLICATION NUMBER: 10/282,935
;  PRIOR FILING DATE: 2002-10-29
;  PRIOR APPLICATION NUMBER: 09/538,873
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 60/126,826
;  PRIOR FILING DATE: 1999-03-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Abrus precatorius
US-11-263-537-3

  Query Match             20.2%;  Score 155;  DB 7;  Length 251;
  Best Local Similarity   33.1%;  Pred. No. 5.7e-08;
  Matches   43;  Conservative   25;  Mismatches   50;  Indels   12;  Gaps    4;

Qy         14 YPTFIQDLRNELAKG----TPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              |  ||: ||  |  |      ||   | |||    :  |:: |::: :  ::::| ||||:
Db         17 YKQFIEALRERLRGGLIHDIPVLPDPTTLQ---ERNRYITVELSNSDTESIEVGIDVTNA 73

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              |||  |:       :: ||   |: |:  || | |:: :| | |:|  |    |   |: :
Db         74 YVVAYR----AGTQSYFLRDAPSSASDYLFTG-TDQHSLPFYGTYGDLERWAHQSRQQIP 128

Qy        130 LGVYKLEFSI 139
               ||:  |   |
Db        129 LGLQALTHGI 138


RESULT 10
US-11-361-977A-85
; Sequence 85, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Methionine-Saporin fusion prot
US-11-361-977A-85

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 254;
  Best Local Similarity   23.8%;  Pred. No. 0.0064;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy         11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
              | :| :|:  :|| :        || :  :          ::|: ::   :|: || : :
Db         14 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 67

Qy         65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
                 ::||| |    |  :       |  :: :  :: |||   |  |:  | :   || :
Db         68 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 127

Qy        121 AKV-----DRKDLELGVYKLEFSIEAI 142
              |::      ||:| ||:  |  |:||:
Db        128 AQITQGDQSRKELGLGIDLLSTSMEAV 154


RESULT 11
US-11-361-977A-35
; Sequence 35, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 275
;   TYPE: PRT
;   ORGANISM: Saponaria officinalis
US-11-361-977A-35

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 275;
  Best Local Similarity   23.8%;  Pred. No. 0.0071;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy         11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
              | :| :|:  :|| :        || :  :          ::|: ::   :|: || : :
Db         13 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 66
```

```
Qy          65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
               ::||| |   |  :      |  :: :  :: |||  |  |:  | :   || :
Db          67 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 126

Qy         121 AKV-----DRKDLELGVYKLEFSIEAI 142
               |::      ||:| ||:  |  |:||:
Db         127 AQITQGDQSRKELGLGIDLLSTSMEAV 153


RESULT 12
US-11-361-977A-79
; Sequence 79, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 327
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protei
;   OTHER INFORMATION: SDF-1-Beta-AM-SAPORIN
US-11-361-977A-79

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 327;
  Best Local Similarity   23.8%;  Pred. No. 0.0088;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy          11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
               | :| :|:  :|| :        || :  :          ::|: ::   :|: || : :
Db          87 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 140

Qy          65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
               ::||| |   |  :      |  :: :  :: |||  |  |:  | :   || :
Db         141 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 200

Qy         121 AKV-----DRKDLELGVYKLEFSIEAI 142
               |::      ||:| ||:  |  |:||:
Db         201 AQITQGDQSRKELGLGIDLLSTSMEAV 227


RESULT 13
US-11-361-977A-82
; Sequence 82, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protei
;   OTHER INFORMATION: EOTAXIN-AM-SAPORIN
US-11-361-977A-82

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 330;
  Best Local Similarity   23.8%;  Pred. No. 0.0089;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy          11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
               | :| :|:  :|| :        || :  :          ::|: ::   :|: || : :
Db          90 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 143

Qy          65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
               ::||| |   |  :      |  :: :  :: |||  |  |:  | :   || :
Db         144 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 203

Qy         121 AKV-----DRKDLELGVYKLEFSIEAI 142
               |::      ||:| ||:  |  |:||:
Db         204 AQITQGDQSRKELGLGIDLLSTSMEAV 230


RESULT 14
US-11-361-977A-73
; Sequence 73, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
;   LENGTH: 332
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protein
;   OTHER INFORMATION: MCP1-AM-SAPORIN
US-11-361-977A-73

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 332;
  Best Local Similarity   23.8%;  Pred. No. 0.009;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy          11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
               | :| :|:  :|| :        || :  :          ::|: ::   :|: || : :
Db          92 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 145

Qy          65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
               ::||| |   |  :      |  :: :  :: |||  |  |:  | :   || :
Db         146 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 205

Qy         121 AKV-----DRKDLELGVYKLEFSIEAI 142
               |::      ||:| ||:  |  |:||:
Db         206 AQITQGDQSRKELGLGIDLLSTSMEAV 232


RESULT 15
US-11-361-977A-76
; Sequence 76, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;   LENGTH: 332
;   TYPE: PRT
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Chemokine-toxin Fusion Prote
;   OTHER INFORMATION: MCP3-AM-SAPORIN
US-11-361-977A-76

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 332;
  Best Local Similarity   23.8%;  Pred. No. 0.009;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy         11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
              | :| :|:  :|| :         || :  :          ::|: ::   :|: || : :
Db         92 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 145

Qy         65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
                ::||| |   |  :    |  :: :  :: |||  |  |:  | :   || :
Db        146 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 205

Qy        121 AKV-----DRKDLELGVYKLEFSIEAI 142
              |::      ||:| ||:  |  |:||:
Db        206 AQITQGDQSRKELGLGIDLLSTSMEAV 232


RESULT 16
US-10-953-349-30545
; Sequence 30545, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30545
;   LENGTH: 277
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-10-953-349-30545

  Query Match             11.1%;  Score 85.5;  DB 6;  Length 277;
  Best Local Similarity   23.3%;  Pred. No. 0.57;
  Matches   38;  Conservative   29;  Mismatches   51;  Indels   45;  Gaps    8;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL------AKGTPVCQLPVTLQTIADDKRFVLVDITTT 55
              | :||:   : :| |||  :||:|      :   ||  ||     :   : | :|  |:
Db         11 TATFNVQASSTDYVTFITGIRNKLRNPGQSSHNRPV--LPPIEPNVPPSRWFHIVLKTSP 68

Qy         56 SKKTVKVAIDVTDVYVVGYQDK----WDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFD 111
              :   : :|    ::|  |::      |:               |  | || |    : |
Db         69 ANTGLTLATRADNLYWEGFKSSDGTWWE-------------LTPGLIPGAT---YVGFG 111

Qy        112 GSYQ-------KLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQ 147
              |:|:       || | |         ||  ::  :: |: |:|:
Db        112 GTYRDLLGDTDKLTNVA--------LGRQQMADAVTALHGRTK 146


RESULT 17
US-11-056-355B-61236
; Sequence 61236, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61236
;   LENGTH: 277
;   TYPE: prt
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(277)
;   OTHER INFORMATION: Ceres Seq. ID no. 13661990
US-11-056-355B-61236

  Query Match             11.1%;  Score 85.5;  DB 7;  Length 277;
  Best Local Similarity   23.3%;  Pred. No. 0.57;
  Matches   38;  Conservative   29;  Mismatches   51;  Indels   45;  Gaps    8;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL------AKGTPVCQLPVTLQTIADDKRFVLVDITTT 55
              | :||:   : :| |||  :||:|      :   ||  ||     :   : | :|  |:
Db         11 TATFNVQASSTDYVTFITGIRNKLRNPGQSSHNRPV--LPPIEPNVPPSRWFHIVLKTSP 68

Qy         56 SKKTVKVAIDVTDVYVVGYQDK----WDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFD 111
              :   : :|    ::|  |::      |:               |  | || |    : |
Db         69 ANTGLTLATRADNLYWEGFKSSDGTWWE-------------LTPGLIPGAT---YVGFG 111

Qy        112 GSYQ-------KLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQ 147
              |:|:       || | |         ||  ::  :: |: |:|:
Db        112 GTYRDLLGDTDKLTNVA--------LGRQQMADAVTALHGRTK 146


RESULT 18
US-10-953-349-30544
; Sequence 30544, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30544
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-10-953-349-30544

  Query Match             11.1%;  Score 85.5;  DB 6;  Length 281;
  Best Local Similarity   23.3%;  Pred. No. 0.58;
  Matches   38;  Conservative   29;  Mismatches   51;  Indels   45;  Gaps    8;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL------AKGTPVCQLPVTLQTIADDKRFVLVDITTT 55
              | :||:   : :| |||  :||:|      :   ||  ||     :   : | :|  |:
Db         15 TATFNVQASSTDYVTFITGIRNKLRNPGQSSHNRPV--LPPIEPNVPPSRWFHIVLKTSP 72

Qy         56 SKKTVKVAIDVTDVYVVGYQDK----WDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFD 111
              :   : :|    ::|  |::      |:               |  | || |    : |
Db         73 ANTGLTLATRADNLYWEGFKSSDGTWWE-------------LTPGLIPGAT---YVGFG 115

Qy        112 GSYQ-------KLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQ 147
              |:|:       || | |         ||  ::  :: |: |:|:
Db        116 GTYRDLLGDTDKLTNVA--------LGRQQMADAVTALHGRTK 150


RESULT 19
US-11-056-355B-61235
; Sequence 61235, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
```

```
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61235
;   LENGTH: 281
;   TYPE: prt
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(281)
;   OTHER INFORMATION: Ceres Seq. ID no. 13661989
US-11-056-355B-61235

  Query Match             11.1%;  Score 85.5;  DB 7;  Length 281;
  Best Local Similarity   23.3%;  Pred. No. 0.58;
  Matches   38;  Conservative   29;  Mismatches   51;  Indels   45;  Gaps    8;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL------AKGTPVCQLPVTLQTIADDKRFVLVDITTT 55
              | :||:   : :| |||  :||:|      :   ||  ||     :   : | :|  |:
Db         15 TATFNVQASSTDYVTFITGIRNKLRNPGQSSHNRPV--LPPIEPNVPPSRWFHIVLKTSP 72

Qy         56 SKKTVKVAIDVTDVYVVGYQDK----WDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFD 111
              :   : :|    ::|  |::      |:               |  | || |    : |
Db         73 ANTGLTLATRADNLYWEGFKSSDGTWWE-------------LTPGLIPGAT---YVGFG 115

Qy        112 GSYQ-------KLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQ 147
              |:|:       || | |        ||  ::  :: |: |:|:
Db        116 GTYRDLLGDTDKLTNVA--------LGRQQMADAVTALHGRTK 150


RESULT 20
US-10-953-349-30543
; Sequence.30543, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30543
;   LENGTH: 298
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-10-953-349-30543

  Query Match             11.1%;  Score 85.5;  DB 6;  Length 298;
  Best Local Similarity   23.3%;  Pred. No. 0.62;
  Matches   38;  Conservative   29;  Mismatches   51;  Indels   45;  Gaps    8;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL------AKGTPVCQLPVTLQTIADDKRFVLVDITTT 55
              | :||:   : :| |||  :||:|      :   ||  ||     :   : | :|  |:
Db         32 TATFNVQASSTDYVTFITGIRNKLRNPGQSSHNRPV--LPPIEPNVPPSRWFHIVLKTSP 89

Qy         56 SKKTVKVAIDVTDVYVVGYQDK----WDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFD 111
              :   : :|    ::|  |::      |:               |  | || |    : |
Db         90 ANTGLTLATRADNLYWEGFKSSDGTWWE-------------LTPGLIPGAT---YVGFG 132

Qy        112 GSYQ-------KLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQ 147
              |:|:       || | |        ||  ::  :: |: |:|:
Db        133 GTYRDLLGDTDKLTNVA--------LGRQQMADAVTALHGRTK 167


RESULT 21
US-11-056-355B-61234
; Sequence 61234, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 61234
;   LENGTH: 298
;   TYPE: prt
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(298)
;   OTHER INFORMATION: Ceres Seq. ID no. 13661988
US-11-056-355B-61234

  Query Match             11.1%;  Score 85.5;  DB 7;  Length 298;
  Best Local Similarity   23.3%;  Pred. No. 0.62;
  Matches   38;  Conservative   29;  Mismatches   51;  Indels   45;  Gaps    8;

Qy          3 TVSFNL-GEAYEYPTFIQDLRNEL------AKGTPVCQLPVTLQTIADDKRFVLVDITTT 55
              | :||:   : :| |||  :||:|      :   ||  ||     :   : | :|  |:
Db         32 TATFNVQASSTDYVTFITGIRNKLRNPGQSSHNRPV--LPPIEPNVPPSRWFHIVLKTSP 89

Qy         56 SKKTVKVAIDVTDVYVVGYQDK----WDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFD 111
              :   : :|    ::|  |::      |:               |  | || |    : |
Db         90 ANTGLTLATRADNLYWEGFKSSDGTWWE-------------LTPGLIPGAT---YVGFG 132

Qy        112 GSYQ-------KLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQ 147
              |:|:       || | |        ||  ::  :: |: |:|:
Db        133 GTYRDLLGDTDKLTNVA--------LGRQQMADAVTALHGRTK 167


RESULT 22
US-11-013-711-9
; Sequence 9, Application US/11013711
; Publication No. US20060159709A1
; GENERAL INFORMATION:
;  APPLICANT: Loosmore, Sheena M.
;  APPLICANT:  Sasaki, Ken
;  APPLICANT:  Yang, Yan Ping
;  APPLICANT:  Klein, Michel H.
;  TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
;  TITLE OF INVENTION:  PROTEIN OF MORAXELLA
;  FILE REFERENCE: 1038-921MIS:jb
;  CURRENT APPLICATION NUMBER: US/11/013,711
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: US/09/361,619
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 2053
;   TYPE: PRT
;   ORGANISM: Moraxella catarrhalis
US-11-013-711-9

  Query Match             10.5%;  Score 81;  DB 7;  Length 2053;
  Best Local Similarity   30.3%;  Pred. No. 19;
  Matches   30;  Conservative   12;  Mismatches   51;  Indels    6;  Gaps    2;

Qy         34 LPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV 93
              |  || :||      :    |  :|    |  : ||   |:  | :|||:    | | |
Db        805 LSPTLPSIASPSGRNIALGNTIEEKDKSNAASIDDVLNAGFNLKNNGKDK----DFVSTY 860

Qy         94 ATSKLFPGVTNRVTLTFDGSYQ--KLVNAAKVDRKDLEL 130
              |     |     |:|:| : |  |:     || | :||
Db        861 DTVDFIDGNATTATVTYDEANQTSKVAYDVNVDEKTIEL 899
```

```
RESULT 23
US-11-316-535A-133
; Sequence 133, Application US/11316535A
; Publication No. US20060148054A1
; GENERAL INFORMATION:
;  APPLICANT: Fukuyama, Shiro
;  APPLICANT:  Matsui, Tomoko
;  APPLICANT:  Soong, Chee Leong
;  APPLICANT:  Allain, Eric
;  APPLICANT:  Nielsen, Anders Vikso
;  APPLICANT:  Udagawa, Hiroaki
;  APPLICANT:  Liu, Ye
;  APPLICANT:  Duan, Junxin
;  APPLICANT:  Wu, Wenping
;  APPLICANT:  Andersen, Lene Nonboe
;  TITLE OF INVENTION: ENZYMES FOR STARCH PROCESSING
;  FILE REFERENCE: 10729.500-US
;  CURRENT APPLICATION NUMBER: US/11/316,535A
;  CURRENT FILING DATE:  2005-12-22
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 133
;   LENGTH: 435
;   TYPE: PRT
;   ORGANISM: Absidia crista
US-11-316-535A-133

  Query Match            10.5%;  Score 80.5;  DB 7;  Length 435;
  Best Local Similarity  26.7%;  Pred. No. 3.1;
  Matches   32;  Conservative   17;  Mismatches   30;  Indels   41;  Gaps    6;

Qy         41 IADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGY--------------QDKWDGKDRA-- 84
              :||    || || |     ||   |:   :|  |                || ||| : |
Db        150 VAD----VLPDINTEDDNVVKTLNDIVSNWVTTYGFDGIRIDTVKHVRQDFWDGYNEAAG 205

Qy         85 VFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEAIWG 144
              ||       || ::| | :: |     | ||| :::          |  | : :::  ::|
Db        206 VF-------ATGEVFDGDSSYV-----GGYQKHLDS---------LLNYPMYYALNDVFG 244


RESULT 24
US-11-316-535A-157
; Sequence 157, Application US/11316535A
; Publication No. US20060148054A1
; GENERAL INFORMATION:
;  APPLICANT: Fukuyama, Shiro
;  APPLICANT:  Matsui, Tomoko
;  APPLICANT:  Soong, Chee Leong
;  APPLICANT:  Allain, Eric
;  APPLICANT:  Nielsen, Anders Vikso
;  APPLICANT:  Udagawa, Hiroaki
;  APPLICANT:  Liu, Ye
;  APPLICANT:  Duan, Junxin
;  APPLICANT:  Wu, Wenping
;  APPLICANT:  Andersen, Lene Nonboe
;  TITLE OF INVENTION: ENZYMES FOR STARCH PROCESSING
;  FILE REFERENCE: 10729.500-US
;  CURRENT APPLICATION NUMBER: US/11/316,535A
;  CURRENT FILING DATE:  2005-12-22
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 157
;   LENGTH: 481
;   TYPE: PRT
;   ORGANISM: Absidia cristata
US-11-316-535A-157

  Query Match            10.5%;  Score 80.5;  DB 7;  Length 481;
  Best Local Similarity  26.7%;  Pred. No. 3.6;
  Matches   32;  Conservative   17;  Mismatches   30;  Indels   41;  Gaps    6;

Qy         41 IADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGY--------------QDKWDGKDRA-- 84
              :||    || || |     ||   |:   :|  |                || ||| : |
Db        196 VAD----VLPDINTEDDNVVKTLNDIVSNWVTTYGFDGIRIDTVKHVRQDFWDGYNEAAG 251

Qy         85 VFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEAIWG 144
              ||       || ::| | :: |     | ||| :::          |  | : :::  ::|
Db        252 VF-------ATGEVFDGDSSYV-----GGYQKHLDS---------LLNYPMYYALNDVFG 290


RESULT 25
US-11-192-046-44
; Sequence 44, Application US/11192046
; Publication No. US20060165716A1
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Barocchi, Michelle
;  APPLICANT:  Rappuoli, Rino
;  APPLICANT:  Grandi, Guido
;  APPLICANT:  Lauer, Peter
;  APPLICANT:  Mora, Marirosa
;  APPLICANT:  Y Ros, Immaculada
;  APPLICANT:  Maione, Domenico
;  APPLICANT:  Bensi, Guiliano
;  APPLICANT:  Rinaudo, Daniela
;  APPLICANT:  Masignani, Vega
;  TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR GRAM POSITIVE BACTERIA SUCH AS
;  TITLE OF INVENTION:  STREPTOCOCCUS AGALACTIAE
;  FILE REFERENCE: 002441.00168/PP22811.011
;  CURRENT APPLICATION NUMBER: US/11/192,046
;  CURRENT FILING DATE:  2005-07-29
;  PRIOR APPLICATION NUMBER: US 60/592,805
;  PRIOR FILING DATE: 2004-07-29
;  PRIOR APPLICATION NUMBER: US 60/609,833
;  PRIOR FILING DATE: 2004-09-13
;  PRIOR APPLICATION NUMBER: US 60/616,833
;  PRIOR FILING DATE: 2004-10-08
;  PRIOR APPLICATION NUMBER: US 60/633,418
;  PRIOR FILING DATE: 2004-12-07
;  PRIOR APPLICATION NUMBER: US 60/640,069
;  PRIOR FILING DATE: 2004-12-30
;  PRIOR APPLICATION NUMBER: US 60/660,321
;  PRIOR FILING DATE: 2005-03-11
;  PRIOR APPLICATION NUMBER: US 60/673,754
;  PRIOR FILING DATE: 2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/693,001
;  PRIOR FILING DATE: 2005-06-21
;  PRIOR APPLICATION NUMBER: US 60/695,453
;  PRIOR FILING DATE: 2005-07-01
;  PRIOR APPLICATION NUMBER: US 60/697,643
;  PRIOR FILING DATE: 2005-07-11
;  NUMBER OF SEQ ID NOS: 273
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
;   LENGTH: 1036
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-192-046-44

  Query Match            10.4%;  Score 80;  DB 7;  Length 1036;
  Best Local Similarity  23.6%;  Pred. No. 10;
  Matches   41;  Conservative   22;  Mismatches   51;  Indels   60;  Gaps    8;

Qy          2 NTVSFNLGEAYEYPTFIQDLRNELAKGTPV-----------------CQLPVTLQTIADD 44
              |   ::|| :       :|: :: |  :||                  :|  ||  | :|
Db        677 NLSIYSLGVS-------KDINSDTASSSPVVLKYLSGEEHYYGITDTAELEKTLNKIVED 729

Qy         45 KRFVLV-----------------DITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFL 87
                :   :                 |: | | |    | |::     | :  |||    :
Db        730 SKLSQLGISDSLSQYVDYYDKQPDVLVTRKSKVN---DETEILYQKDQVQEAGKD---II 783

Qy         88 DKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEA 141
              |||  | | |       :|||||   |       |||    :   | | |:::|
Db        784 DKV--VFTPKTTSQPKGKVTLTFKSDY-------KVD----DEYTYTLSFNVKA 824
```

```
RESULT 26
US-11-056-355B-86437
; Sequence 86437, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86437
;   LENGTH: 364
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(364)
;   OTHER INFORMATION: Ceres Seq. ID no. 12690539
US-11-056-355B-86437

  Query Match             9.7%;  Score 74.5;  DB 7;  Length 364;
  Best Local Similarity   25.5%;  Pred. No. 10;
  Matches   28;  Conservative   19;  Mismatches   40;  Indels   23;  Gaps    4;

Qy         41 IADDK--RFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKL 98
              ::| |  || |:     : | |:   : ::  ::   |               |:: |:|
Db          1 MSDTKTVRFGLLGCIRFASKFVRTVTESSNAVIIAISD-------------PSLETAKT 46

Qy         99 FPGVTN--RVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEAIWGKT 146
              |    |    |:|  |||::|:| | ||   | : | :       | | |
Db         47 FATGNNLSPETVTIYGSYEELLNDANVDAVYLTMPVTQ-----RARWAVT 91


RESULT 27
US-10-953-349-5406
; Sequence 5406, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5406
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5406

  Query Match             9.7%;  Score 74.5;  DB 6;  Length 487;
  Best Local Similarity   30.8%;  Pred. No. 14;
  Matches   32;  Conservative   10;  Mismatches   39;  Indels   23;  Gaps    3;

Qy         37 TLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATS 96
              | : ||:||          |   ||:|              ||  |:|  : | |:|    |
Db        291 TFELIAEDKE--------TQSLTVEVF-----------DKDVGQDERLGLVKLP---LS 327

Qy         97 KLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIE 140
              |  |||  : |    |   |    | ||  : | |:  ||: |
Db        328 SLEAGVTKELELNLLSSLDTLKVKDKKDRGSITLKVHYHEFNKE 371


RESULT 28
US-10-953-349-5405
; Sequence 5405, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5405
;   LENGTH: 493
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5405

  Query Match             9.7%;  Score 74.5;  DB 6;  Length 493;
  Best Local Similarity   30.8%;  Pred. No. 15;
  Matches   32;  Conservative   10;  Mismatches   39;  Indels   23;  Gaps    3;

Qy         37 TLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATS 96
              | : ||:||          |   ||:|              ||  |:|  : | |:|    |
Db        297 TFELIAEDKE--------TQSLTVEVF-----------DKDVGQDERLGLVKLP---LS 333

Qy         97 KLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIE 140
              |  |||  : |    |   |    | ||  : | |:  ||: |
Db        334 SLEAGVTKELELNLLSSLDTLKVKDKKDRGSITLKVHYHEFNKE 377


RESULT 29
US-10-953-349-5404
; Sequence 5404, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953;349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5404
;   LENGTH: 510
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5404

  Query Match             9.7%;  Score 74.5;  DB 6;  Length 510;
  Best Local Similarity   30.8%;  Pred. No. 15;
  Matches   32;  Conservative   10;  Mismatches   39;  Indels   23;  Gaps    3;

Qy         37 TLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATS 96
              | : ||:||          |   ||:|              ||  |:|  : | |:|    |
Db        314 TFELIAEDKE--------TQSLTVEVF-----------DKDVGQDERLGLVKLP---LS 350

Qy         97 KLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIE 140
              |  |||  : |    |   |    | ||  : | |:  ||: |
Db        351 SLEAGVTKELELNLLSSLDTLKVKDKKDRGSITLKVHYHEFNKE 394


RESULT 30
US-10-449-902-41289
; Sequence 41289, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
```

```
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41289
;   LENGTH: 1333
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-41289

  Query Match             9.7%;  Score 74.5;  DB 6;  Length 1333;
  Best Local Similarity   25.0%;  Pred. No. 50;
  Matches   32;  Conservative   16;  Mismatches   49;  Indels   31;  Gaps    4;

Qy         26 AKGTPVCQLPVTL-----QTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDG 80
              ||  |  :|    |     : :  |  | | : |  | :||   :  | :| | :   |
Db       1190 AKDAPEPRLREALKAVWRRAVVRDDWFALSETTNVSDQTVLADLQATALYAVLGEVLADD 1249

Qy         81 KDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQK-LVNAAKVDRKDLELGVYKLEFSI 139
               :|: :||    |                  ||   | || |   |: |:|         :
Db       1250 ANRSAYLDVHELVG----------------DGEDAKALVAARMADKGDVE---------V 1284

Qy        140 EAIWGKTQ 147
               :|:|   |
Db       1285 DAVWHDRQ 1292


RESULT 31
US-11-056-355B-97983
; Sequence 97983, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 97983
;   LENGTH: 689
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(689)
;   OTHER INFORMATION: Ceres Seq. ID no. 13578983
US-11-056-355B-97983

  Query Match             9.6%;  Score 74;  DB 7;  Length 689;
  Best Local Similarity   26.7%;  Pred. No. 25;
  Matches   32;  Conservative   22;  Mismatches   38;  Indels   28;  Gaps    7;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKW-----------DG 80
              | |  |:|:  |  ||: ::    :|  :|::|     |||  |:|           :|
Db        188 QRPFVLETVTVD-LFVIRNLGLFLRKFPQVSVD-----VVGLVDEWAARFFEELDYVNEG 241

Qy         81 KDRAVFLD----KVPTVATSKLFPGVTNRVTLT---FDGSYQKLVNAAKVDRKDL-ELGV 132
              ::   | :     :| |   | :   |:|  ||    ||  :||  : : |  :|  :||
Db        242 ENGTYFAEMMKKDLPQVVVPKTYQKYTSRKVLTTSWIDG--EKLSQSIESDVGELVNVGV 299


RESULT 32
US-11-056-355B-109222
; Sequence 109222, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 109222
;   LENGTH: 689
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(689)
;   OTHER INFORMATION: Ceres Seq. ID no. 13578983
US-11-056-355B-109222

  Query Match             9.6%;  Score 74;  DB 7;  Length 689;
  Best Local Similarity   26.7%;  Pred. No. 25;
  Matches   32;  Conservative   22;  Mismatches   38;  Indels   28;  Gaps    7;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKW-----------DG 80
              | |  |:|:  |  ||: ::    :|  :|::|     |||  |:|           :|
Db        188 QRPFVLETVTVD-LFVIRNLGLFLRKFPQVSVD-----VVGLVDEWAARFFEELDYVNEG 241

Qy         81 KDRAVFLD----KVPTVATSKLFPGVTNRVTLT---FDGSYQKLVNAAKVDRKDL-ELGV 132
              ::   | :     :| |   | :   |:|  ||    ||  :||  : : |  :|  :||
Db        242 ENGTYFAEMMKKDLPQVVVPKTYQKYTSRKVLTTSWIDG--EKLSQSIESDVGELVNVGV 299


RESULT 33
US-11-056-355B-97982
; Sequence 97982, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 97982
;   LENGTH: 699
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(699)
;   OTHER INFORMATION: Ceres Seq. ID no. 13578982
US-11-056-355B-97982

  Query Match             9.6%;  Score 74;  DB 7;  Length 699;
  Best Local Similarity   26.7%;  Pred. No. 25;
  Matches   32;  Conservative   22;  Mismatches   38;  Indels   28;  Gaps    7;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKW-----------DG 80
              | |  |:|:  |  ||: ::    :|  :|::|     |||  |:|           :|
Db        198 QRPFVLETVTVD-LFVIRNLGLFLRKFPQVSVD-----VVGLVDEWAARFFEELDYVNEG 251

Qy         81 KDRAVFLD----KVPTVATSKLFPGVTNRVTLT---FDGSYQKLVNAAKVDRKDL-ELGV 132
              ::   | :     :| |   | :   |:|  ||    ||  :||  : : |  :|  :||
Db        252 ENGTYFAEMMKKDLPQVVVPKTYQKYTSRKVLTTSWIDG--EKLSQSIESDVGELVNVGV 309
```

```
RESULT 34
US-11-056-355B-109221
; Sequence 109221, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 109221
;   LENGTH: 699
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(699)
;   OTHER INFORMATION: Ceres Seq. ID no. 13578982
US-11-056-355B-109221

  Query Match             9.6%;  Score 74;  DB 7;  Length 699;
  Best Local Similarity   26.7%;  Pred. No. 25;
  Matches   32;  Conservative   22;  Mismatches   38;  Indels   28;  Gaps    7;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKW-----------DG 80
              | |  |:|:  |  ||: ::    :|  :|::|     |||  |:|           :|
Db        198 QRPFVLETVTVD-LFVIRNLGLFLRKFPQVSVD-----VVGLVDEWAARFFEELDYVNEG 251

Qy         81 KDRAVFLD----KVPTVATSKLFPGVTNRVTLT---FDGSYQKLVNAAKVDRKDL-ELGV 132
              ::   | :     :| |   | :   |:|  ||    ||  :||  : : |  :|  :||
Db        252 ENGTYFAEMMKKDLPQVVVPKTYQKYTSRKVLTTSWIDG--EKLSQSIESDVGELVNVGV 309


RESULT 35
US-11-056-355B-97981
; Sequence 97981, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 97981
;   LENGTH: 793
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(793)
;   OTHER INFORMATION: Ceres Seq. ID no. 13578981
US-11-056-355B-97981

  Query Match             9.6%;  Score 74;  DB 7;  Length 793;
  Best Local Similarity   26.7%;  Pred. No. 30;
  Matches   32;  Conservative   22;  Mismatches   38;  Indels   28;  Gaps    7;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKW-----------DG 80
              | |  |:|:  |  ||: ::    :|  :|::|     |||  |:|           :|
Db        292 QRPFVLETVTVD-LFVIRNLGLFLRKFPQVSVD-----VVGLVDEWAARFFEELDYVNEG 345

Qy         81 KDRAVFLD----KVPTVATSKLFPGVTNRVTLT---FDGSYQKLVNAAKVDRKDL-ELGV 132
              ::   | :     :| |   | :   |:|  ||    ||  :||  : : |  :|  :||
Db        346 ENGTYFAEMMKKDLPQVVVPKTYQKYTSRKVLTTSWIDG--EKLSQSIESDVGELVNVGV 403


RESULT 36
US-11-056-355B-109220
; Sequence 109220, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 109220
;   LENGTH: 793
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(793)
;   OTHER INFORMATION: Ceres Seq. ID no. 13578981
US-11-056-355B-109220

  Query Match             9.6%;  Score 74;  DB 7;  Length 793;
  Best Local Similarity   26.7%;  Pred. No. 30;
  Matches   32;  Conservative   22;  Mismatches   38;  Indels   28;  Gaps    7;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKW-----------DG 80
              | |  |:|:  |  ||: ::    :|  :|::|     |||  |:|           :|
Db        292 QRPFVLETVTVD-LFVIRNLGLFLRKFPQVSVD-----VVGLVDEWAARFFEELDYVNEG 345

Qy         81 KDRAVFLD----KVPTVATSKLFPGVTNRVTLT---FDGSYQKLVNAAKVDRKDL-ELGV 132
              ::   | :     :| |   | :   |:|  ||    ||  :||  : : |  :|  :||
Db        346 ENGTYFAEMMKKDLPQVVVPKTYQKYTSRKVLTTSWIDG--EKLSQSIESDVGELVNVGV 403


RESULT 37
US-11-330-403-14433
; Sequence 14433, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 14433
;   LENGTH: 318
;   TYPE: PRT
;   ORGANISM: Mortierella sp. strain M10
US-11-330-403-14433

  Query Match             9.4%;  Score 72.5;  DB 7;  Length 318;
  Best Local Similarity   23.4%;  Pred. No. 13;
  Matches   36;  Conservative   25;  Mismatches   58;  Indels   35;  Gaps    7;

Qy          3 TVSFNLGEAYE--YPTFIQDLRNEL-----------AKGTPVCQLPVTLQTIADDK--- 45
              |    ||| |   :  | || || :           :   |   |   |:|  :::
Db        128 TAFMTLGEVYHNFHHQFPQDYRNAISLLPVRPHQSGSSPSAPFFGLASHLKTFPENEVRK 187

Qy         46 -RFVLVDITTTSKKT-VKVAIDVTDVYVVGYQD-----KWDGK----------DRAVFLD 88
               :  :::     ||| ::    : |: |: ::|     | |||          | | |::
Db        188 GQLQMIEKKVLEKKTKLQWGTPIADLPVLSFEDYQHACKNDGKKWILLEGVVYDVAEFMN 247

Qy         89 KVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAK 122
              : |      :  ||   :|  |:|      |||:
Db        248 EHPG-GEKYIKMGVGKDMTAAFNGGMYDHSNAAR 280
```

```
RESULT 38
US-10-505-928-471
; Sequence 471, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 471
;   LENGTH: 1403
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-505-928-471

  Query Match             9.4%;  Score 72.5;  DB 6;  Length 1403;
  Best Local Similarity   25.1%;  Pred. No. 85;
  Matches   44;  Conservative   16;  Mismatches   56;  Indels   59;  Gaps   10;

Qy          1 YNTVSFNLGEAYEYP-------------------------TFIQDLRNELAKGTP-VCQL 34
              |||   | ||  : |                         ||  ||  |  | |   |:
Db        344 YNT-RLNRGEYVDVPFPNQYQYIAAVDYNPRDNQLYVWNNNFI--LRYSLEFGPPDPAQV 400

Qy         35 PVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVA 94
              | |  ||          |:|||  : |  :  |   | | |:   |          | |:
Db        401 PTTAVTITSSAELFKTIISTTSTTSQKGPMSTT---VAGSQEGSKG------TKPPPAVS 451

Qy         95 TSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |:|: | :||   |      ::   |  :| | ::             | :|| |
Db        452 TTKI-PPITNIFPPLP-----ERFCEA--LDSKGIK------------WPQTQRG 485


RESULT 39
US-10-471-571A-706
; Sequence 706, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 706
;   LENGTH: 374
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(374)
;   OTHER INFORMATION: hypothetical protein
US-10-471-571A-706

  Query Match             9.4%;  Score 72;  DB 6;  Length 374;
  Best Local Similarity   23.4%;  Pred. No. 18;
  Matches   36;  Conservative   21;  Mismatches   51;  Indels   46;  Gaps    6;

Qy         23 NELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVA------IDVTDVYVVGYQD 76
              ::||||       ::  |: |||  :|  :   |  |: |      ||:   ||
Db         55 HDLAKGIKNAGQILSTMTVLDDKDRLLTTVKLKS-NTLNVTLPRQTLIDIIKSYV----- 108

Qy         77 KWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTF--------------DGSYQKLVNAAK 122
                 || |:| :   |   ::     |::||: |              || : |:  :
```

```
Db        109 ----KDDAIFTNHEVTHIDNE-----TDKVTIHFAEQESEAFDLCIGADGIHSKVRQSVN 159

Qy        123 VDRKDLELGVYKLEFSIEAI----------WGK 145
                | | |  |       |: |           ||:
Db        160 ADSKVLYQGYTCPRGLIDDIDLKHPDCAKEYWGR 193


RESULT 40
US-10-449-902-55385
; Sequence 55385, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55385
;   LENGTH: 593
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-55385

  Query Match             9.4%;  Score 72;  DB 6;  Length 593;
  Best Local Similarity   25.2%;  Pred. No. 33;
  Matches   28;  Conservative   11;  Mismatches   40;  Indels   32;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVV 72
              ::||   |       | || :  |   |    | |: :       |     ||    :||
Db        414 DFPTMPID-------GPPVMKTSVINSTY---KNFLEIVFQNNDTKVQTYHIDGYAFWVV 463

Qy         73 GYQ-----------DKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFD 111
              |           :|||  |           |:::|||    | |: |
Db        464 GMDYGEWTENSRGTYNKWDGVSR----------CTTQVFPGAWTAVMLSLD 504


RESULT 41
US-11-174-307B-3704
; Sequence 3704, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 3704
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: PFam Name: HSP70; PFam Description: Hsp70 protein
;   FEATURE:
```

```
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 19813; NR Description: luminal binding protein
;   OTHER INFORMATION: (BiP) [Nicotiana tabacum] >gi|100340|pir||S21880 dnaK-type
;   OTHER INFORMATION: molecular chaperone blp5 precursor - common tobacco
;   OTHER INFORMATION: >gi|729623|sp|Q03685|BIP5_TOBAC Luminal binding homolog 5) (GRP
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 19811; NR Description: luminal binding protein
;   OTHER INFORMATION: (BiP) [Nicotiana tabacum] >gi|100339|pir||S21879 dnaK-type
;   OTHER INFORMATION: molecular chaperone blp4 precursor - common tobacco
;   OTHER INFORMATION: >gi|729620|sp|Q03684|BIP4_TOBAC Luminal binding homolog 4) (GRP
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 1346172; NR Description: Luminal binding protein
;   OTHER INFORMATION: precursor (BiP) (78 kDa glucose-regulated protein homolog) (GRP 7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 13398537; NR Description: BiP-isoform D [Glycine max]
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 2642238; NR Description: endoplasmic reticulum
;   OTHER INFORMATION: HSC70-cognate binding protein precursor [Glycine max]
;   OTHER INFORMATION: >gi|11277127|pir||T46574 dnaK-type molecular chaperone BiP
US-11-174-307B-3704

  Query Match             9.2%;  Score 71;  DB 7;  Length 444;
  Best Local Similarity   23.9%;  Pred. No. 29;
  Matches   27;  Conservative   14;  Mismatches   36;  Indels   36;  Gaps    2;

Qy         55 TSKKTVKVAIDVTDVYVVGYQDKWDGKD------RAVF---------------------- 86
              |: : | |:   ||  :  :   || |       || |
Db        300 TACEQAKKALSSQDVAELSIKSLVDGVDFSGSLTRAEFEELNHDLFLKAMALVESAMRQA 359

Qy         87 --------LDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELG 131
                    ||::  |  | : ||:   ||  |||   | :||: :  : : ||
Db        360 GLDKNKELLDEIVLVGGSTMIPGIRRLVTDYFDGRELKNINASVMPDQTVTLG 412


RESULT 42
US-11-333-747A-44
; Sequence 44, Application US/11333747A
; Publication No. US20060160159A1
; GENERAL INFORMATION:
;  APPLICANT: Handfield, Martin
;  APPLICANT:  Hillman, Jeffrey
;  APPLICANT:  Progulske-Fox, Ann
;  TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans
;  TITLE OF INVENTION:  Antigens for Use in the Diagnosis, Treatment, and Monitoring
;  TITLE OF INVENTION:  of Periodontal Diseases
;  FILE REFERENCE: MBHB01-662C
;  CURRENT APPLICATION NUMBER: US/11/333,747A
;  CURRENT FILING DATE:  2006-01-17
;  PRIOR APPLICATION NUMBER: US 09/995493
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: PCT/US02/37235
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
;   LENGTH: 1531
;   TYPE: PRT
;   ORGANISM: Actinobacillus actinomycetemcomitans
US-11-333-747A-44

  Query Match             9.2%;  Score 71;  DB 7;  Length 1531;
  Best Local Similarity   23.9%;  Pred. No. 1.3e+02;
  Matches   37;  Conservative   16;  Mismatches   46;  Indels   56;  Gaps    8;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              : ||:  |:: :|                    ||     ||   | ||:  |:|  :
Db       1146 IKFNIKGGDSQKY--------------------VTTSGSGDD---VTVDLAQTTKNKID 1181

Qy         62 VAID-----VTD-------------------VYVVGYQDKWDGKDRAVFLDKVPTVATSK 97
                |  |     :||                    : |    |   |:        :||   :
Db       1182 NAADKDLANITDNGKKVITALGAVVKAADSTITVTDETDNTTGQKTYKIKANIPTPEKTA 1241

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRK-DLELG 131
              : ||  |  |:  |||      |  ||: | || ||
Db       1242 MAPG--NNTTIEGDGS---AANPFKVNLKDDLALG 1271


RESULT 43
US-10-953-349-3286
; Sequence 3286, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3286
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3286

  Query Match             9.2%;  Score 70.5;  DB 6;  Length 330;
  Best Local Similarity   21.5%;  Pred. No. 22;
  Matches   31;  Conservative   23;  Mismatches   57;  Indels   33;  Gaps    4;

Qy          5 SFNLG--------EAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTS 56
              ||||           |    : : ::  ::          | ::|   |::   |:|: |:
Db        132 SFNLDNSQQEKLINARSIASVLYEILRKIESSMGRASTPESIQLNRDEEIGELLDMDTSM 191

Qy         57 KKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQK 116
              ::| |:  | |                  |:|:   :   |       |:|  | | :|
Db        192 EETNKINSDET-----------------FVDQKAELVVEKSKVLEDERLTQMFQGDHQY 233

Qy        117 LVNAAKVDRKDLELGVYKLEFSIE 140
              |      | ||    :|| |  |:
Db        234 LTQ----DEKD---DIYKEEVQIK 250


RESULT 44
US-10-953-349-3285
; Sequence 3285, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3285
;   LENGTH: 347
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3285

  Query Match             9.2%;  Score 70.5;  DB 6;  Length 347;
  Best Local Similarity   21.5%;  Pred. No. 24;
  Matches   31;  Conservative   23;  Mismatches   57;  Indels   33;  Gaps    4;

Qy          5 SFNLG--------EAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTS 56
```

```
                ||||          |    : : ::  ::         | ::|   |::.  |:|: |:
Db        149 SFNLDNSQQEKLINARSIASVLYEILRKIESSMGRASTPESIQLNRDEEIGELLDMDTSM 208

Qy         57 KKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQK 116
               ::| |:  | |                  |:|:   :   |       |:|  | | :|
Db        209 EETNKINSDET-----------------FVDQKAELVVEKSKVLEDERLTQMFQGDHQY 250

Qy        117 LVNAAKVDRKDLELGVYKLEFSIE 140
                  |    | ||   :|| |  |:
Db        251 LTQ----DEKD---DIYKEEVQIK 267


RESULT 45
US-10-449-902-38378
; Sequence 38378, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38378
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-38378

  Query Match             9.2%;  Score 70.5;  DB 6;  Length 418;
  Best Local Similarity   24.8%;  Pred. No. 30;
  Matches   31;  Conservative   20;  Mismatches   39;  Indels   35;  Gaps    5;

Qy         17 FIQDLRNELAKG----TPVCQLPV-----TLQTIADDKRFVLV---------------- 50
              .  :|  | :: |:|     ||  :||      |  :|||:|  |:
Db        214 YIYQLESDGARGEPKLVPVAYVPVDAPSFRLTLVADDERERLMLMKEVFYVHAGEEVPPE 273

Qy         51 --DITTTSKKTVKVAIDVTDVYV----VGYQDKWDGKDRAVFLDK---VPTVATSKLFPG 101
                 |: |  :  |  |:|:    :    :| :  : | ||||:       | ||   :: |
Db        274 GPDMLTMPRVCVAYAVDMAARTIALSRLGARALFMGDDRAVWASPGAFSPGVAADTVYAG 333

Qy        102 VTNRV 106
                ||:
Db        334 RPNRL 338


RESULT 46
US-10-449-902-30832
; Sequence 30832, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30832
;   LENGTH: 366
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-30832

  Query Match             9.1%;  Score 70;  DB 6;  Length 366;
  Best Local Similarity   23.9%;  Pred. No. 28;
  Matches   28;  Conservative   23;  Mismatches   44;  Indels   22;  Gaps    4;

Qy         16 TFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQ 75
              |:| |:     :   : |: |  |  | :| :  :|  |  ::  :  : :||  :
Db        154 TYISDVSTVGTQDACISQVSVDPQ--ARNKAYQDIDDLTLFQQIEENLMSITDRQI---- 207

Qy         76 DKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGV 132
                    | |:||  | | :|  : |          |: ||  | | : :::| :||
Db        208 ------DEAIFLKAVRTSSTVDVVP---------VSGAIQK-PNEAPIPKEELTIGV 248


RESULT 47
US-10-449-902-50637
; Sequence 50637, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50637
;   LENGTH: 755
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-50637

  Query Match             9.1%;  Score 70;  DB 6;  Length 755;
  Best Local Similarity   38.5%;  Pred. No. 70;
  Matches   25;  Conservative   10;  Mismatches   16;  Indels   14;  Gaps    5;

Qy         43 DDKRFV--LVDITTTSKKTVKVAIDVTDVYVVGYQD-KWDGKDRAVFL----DKVPTVAT 95
              |||:|   :||   |: |  |:| |  || |:  :| ||:      |:    || | ||
Db        506 DDKKFYKGIVDSFDTASKRHKIAYDDGDVEVLLLRDEKWE------FVSEEQDKTPDVA- 558

Qy         96 SKLFP 100
              |:: |
Db        559 SEISP 563


RESULT 48
US-11-056-355B-46135
; Sequence 46135, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 46135
```

```
;   LENGTH: 768
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(768)
;   OTHER INFORMATION: Ceres Seq. ID no. 12574663
US-11-056-355B-46135

  Query Match             9.1%;  Score 70;  DB 7;  Length 768;
  Best Local Similarity   21.1%;  Pred. No. 72;
  Matches   30;  Conservative   30;  Mismatches   60;  Indels   22;  Gaps    6;

Qy         12 YEYPTFIQDLRNELAKGTPVCQLPVTLQTIA--DDKRFVLVDITTTSKKTVKVAIDVTDV 69
              : |  ::  ||       || :|   | | |  ::|  ::  :     | |     : |:
Db         26 FNYQNYVNTLR---TTQYPVDELEAALYTAAAGNNKTVIITMVNKAYVKEVGRGSTMLDL 82

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKD-L 128
              ::  :   |:|:     || :  ||  :            :|    | ::  |:: :| :
Db         83 FLESF---WEGEGTLPLLDHLMVVAVDQ----------TAYDRCRFKRLHCYKMETEDGV 129

Qy        129 ELGVYKLEFS---IEAIWGKTQ 147
              :|   |:  |   || :| :|:
Db        130 DLEGEKVFMSKDFIEMMWRRTR 151


RESULT 49
US-11-056-355B-86211
; Sequence 86211, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86211
;   LENGTH: 780
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(780)
;   OTHER INFORMATION: Ceres Seq. ID no. 12687656
US-11-056-355B-86211

  Query Match             9.1%;  Score 70;  DB 7;  Length 780;
  Best Local Similarity   21.1%;  Pred. No. 73;
  Matches   30;  Conservative   30;  Mismatches   60;  Indels   22;  Gaps    6;

Qy         12 YEYPTFIQDLRNELAKGTPVCQLPVTLQTIA--DDKRFVLVDITTTSKKTVKVAIDVTDV 69
              : |  ::  ||       || :|   | | |  ::|  ::  :     | |     : |:
Db         26 FNYQNYVNTLR---TTQYPVDELEAALYTAAAGNNKTVIITMVNKAYVKEVGRGSTMLDL 82

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKD-L 128
              ::  :   |:|:     || :  ||  :            :|    | ::  |:: :| :
Db         83 FLESF---WEGEGTLPLLDHLMVVAVDQ----------TAYDRCRFKRLHCYKMETEDGV 129

Qy        129 ELGVYKLEFS---IEAIWGKTQ 147
              :|   |:  |   || :| :|:
Db        130 DLEGEKVFMSKDFIEMMWRRTR 151


RESULT 50
US-11-056-355B-69910
; Sequence 69910, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 69910
;   LENGTH: 839
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(839)
;   OTHER INFORMATION: Ceres Seq. ID no. 2041498
US-11-056-355B-69910

  Query Match             9.1%;  Score 70;  DB 7;  Length 839;
  Best Local Similarity   21.1%;  Pred. No. 80;
  Matches   30;  Conservative   30;  Mismatches   60;  Indels   22;  Gaps    6;

Qy         12 YEYPTFIQDLRNELAKGTPVCQLPVTLQTIA--DDKRFVLVDITTTSKKTVKVAIDVTDV 69
              : |  ::  ||       || :|   | | |  ::|  ::  :     | |     : |:
Db         26 FNYQNYVNTLR---TTQYPVDELEAALYTAAAGNNKTVIITMVNKAYVKEVGRGSTMLDL 82

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKD-L 128
              ::  :   |:|:     || :  ||  :            :|    | ::  |:: :| :
Db         83 FLESF---WEGEGTLPLLDHLMVVAVDQ----------TAYDRCRFKRLHCYKMETEDGV 129

Qy        129 ELGVYKLEFS---IEAIWGKTQ 147
              :|   |:  |   || :| :|:
Db        130 DLEGEKVFMSKDFIEMMWRRTR 151


RESULT 51
US-10-548-463-223
; Sequence 223, Application US/10548463
; Publication No. US20060194751A1
; GENERAL INFORMATION:
;  APPLICANT: Intercell AG
;  TITLE OF INVENTION: S. pyogenes antigens
;  FILE REFERENCE: R 43092
;  CURRENT APPLICATION NUMBER: US/10/548,463
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: EP03450061.1
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 300
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
;   LENGTH: 1275
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-10-548-463-223

  Query Match             9.1%;  Score 70;  DB 6;  Length 1275;
  Best Local Similarity   30.0%;  Pred. No. 1.3e+02;
  Matches   30;  Conservative   12;  Mismatches   44;  Indels   14;  Gaps    4;

Qy         42 ADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRA----VFLDKVPTVATSK 97
              |:|::   :|:||  |    ||   |  :   :|   || |    |  |    :  ||
Db        289 AEDRQSTKLDVTTLEK-----AIKEADAIIAKESNKDAVKDLAEKLQVIKDSYKEIKDSK 343

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEF 137
              |    |:|:      |||    | :|   :|  | | | |
Db        344 LLAD-THRLLKDTIESYQ----AGEVSINNLTEGTYTLNF 378


RESULT 52
US-11-361-977A-38
; Sequence 38, Application US/11361977A
```

```
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-11-361-977A-38

  Query Match             9.0%;  Score 69.5;  DB 7;  Length 319;
  Best Local Similarity   21.6%;  Pred. No. 27;
  Matches   35;  Conservative   32;  Mismatches   50;  Indels   45;  Gaps    9;

Qy          3 TVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK- 61
              |: |:  ::  | : :  :| |::  ||       |: |:           |||   :
Db         26 TIDFSTQQS--YVSSLNSIRTEIS--TP-------LEHISQG---------TTSVSVINH 65

Qy         62 ------VAIDVTDVYVVGYQDKWDG-----KDRAVFLDKVPTVATSKLF----------P 100
                  |:|:  : |  || ::|      :   :::      ||:  :          |
Db         66 TPPGSYFAVDIRGLDV--YQARFDHLRLIIEQNNLYVAGFVNTATNTFYRFSDFTHISVP 123

Qy        101 GVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEAI 142
              |||  |::| | ||  |   | ::|  :::  : |  |  |:
Db        124 GVTT-VSMTTDSSYTTLQRVAALERSGMQISRHSLVSSYLAL 164


RESULT 53
US-11-330-403-459
; Sequence 459, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 459
;   LENGTH: 452
;   TYPE: PRT
;   ORGANISM: Magnaporthe grisea 70-15
US-11-330-403-459

  Query Match             9.0%;  Score 69.5;  DB 7;  Length 452;
  Best Local Similarity   23.7%;  Pred. No. 41;
  Matches   23;  Conservative   16;  Mismatches   29;  Indels   29;  Gaps    4;

Qy         41 IADDKRFVLVDITTTSKKTVK-VAI---DVTDVY-------VVGYQDKWDGKDRAVFLDK 89
              : |:|   | |:  ||   ||  |:   |   |:        : ||   :| :: :|:|
Db        196 VPDEKALYLSDVLPTSYNAVKDTAVYPGDTVAVFGAGPIGQMAGYWALLEGAEKVIFVDT 255

Qy         90 VPTVA-----------------TSKLFPGVTNRVTL 108
                | ::                ||  |:||: |:
Db        256 EPRLSYIQERFNAEQKAKTTCIDYKKLSSGITNKETV 292


RESULT 54
US-10-449-902-56587
; Sequence 56587, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56587
;   LENGTH: 282
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-56587

  Query Match             9.0%;  Score 69;  DB 6;  Length 282;
  Best Local Similarity   25.0%;  Pred. No. 26;
  Matches   39;  Conservative   29;  Mismatches   62;  Indels   26;  Gaps    8;

Qy          3 TVSFNL--GEAYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITT 54
              ||:||:    :  |  ||  :|  :|        ||  ||      :   : | :|  |
Db          8 TVTFNVSGSGSDNYGDFIAGIRKRVANPRHFSHNRPV--LPPVEPDVPPRRWFHVVLRTQ 65

Qy         55 TSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVT-LTFDGS 113
              ||: |:    |  ::|: |::  ||           | |  :|  |:    | | ||
Db         66 TSELTLATRAD--NLYLEGFRGS-DG----------TSAWWELTRGLIAGATYLGFGGS 111

Qy        114 YQKLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |::|:     :  : ||  ::  ::: : |   :|
Db        112 YRELLGHTD-NMVGVTLGPQQMTQAVDTLAGLAASG 146


RESULT 55
US-10-471-571A-2102
; Sequence 2102, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2102
;   LENGTH: 393
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(393)
;   OTHER INFORMATION: D-alanine-D-alanine ligase
US-10-471-571A-2102

  Query Match             9.0%;  Score 69;  DB 6;  Length 393;
  Best Local Similarity   18.4%;  Pred. No. 39;
  Matches   26;  Conservative   27;  Mismatches   66;  Indels   22;  Gaps    3;

Qy          8 LGEAYEYPTF---------IQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKK 58
              ||  |  |:          | :::  |    |:|  |           |: | :
Db        263 LGNDYPEATWPGEVVKDVAFYDYKSKYKDGKVQLQIPADLDE----------DVQLTLRN 312

Qy         59 TVKVAIDVTDVYVVGYQDKWDGKDRAVFLDK---VPTVATSKLFPGVTNRVTLTFDGSYQ 115
                  |   ||   :   | :  :|  :::::   :|       ::| :   : |::
Db        313 MALEAFKATDCSGLVRADFFVTEDNQIYINETNAMPGFTAFSMYPKLWENMGLSYPELIT 372

Qy        116 KLVNAAKVDRKDLELGVYKLE 136
              ||:  ||   :| :   ||::
Db        373 KLIELAKERHQDKQKNKYKID 393
```

```
RESULT 56
US-10-833-833-169
; Sequence 169, Application US/10833833
; Publication No. US20060194210A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  APPLICANT:  Lai, Albert
;  APPLICANT:  Tse, Christin
;  APPLICANT:  Fattaey, Ali
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-038001
;  CURRENT APPLICATION NUMBER: US/10/833,833
;  CURRENT FILING DATE:  2004-04-27
;  NUMBER OF SEQ ID NOS: 175
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 169
;   LENGTH: 1134
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-833-833-169

  Query Match             9.0%;  Score 69;  DB 6;  Length 1134;
  Best Local Similarity   21.1%;  Pred. No. 1.5e+02;
  Matches   31;  Conservative   31;  Mismatches   61;  Indels   24;  Gaps    6;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPV-CQLPVTLQTIADDKRFVLVDITTTSKKT 59
              :  | : : ::||     |||         |  |:: : :  : |:|  : ::: :  |:
Db        309 FKPVDYEITKSYEIDVQAQDLG---PNSIPAHCKIIIKVVDVNDNKPEISINLMSPGKEE 365

Qy         60 VKVAID----VTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
              |    :     | | :|  |||  | :  :           ||      ::  |:: :|
Db        366 VSYVFEGDPIDTFVAIVRVQDKDSGLNGEII---------CKLHGHGHFKLQKTYENNYL 416

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAI 142
              | ||  :||:       : |:|:  |
Db        417 ILTNAT-LDREK------RSEYSLTVI 436


RESULT 57
US-10-669-920-835
; Sequence 835, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-066001
;  CURRENT APPLICATION NUMBER: US/10/669,920
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/004,113
;  PRIOR FILING DATE: 2001-10-23
;  PRIOR APPLICATION NUMBER: US 10/052,482
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 09/997,722
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: US 10/034,650
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: US 10/085,117
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: US 10/087,192
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 10/322,281
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: US 10/322,696
;  PRIOR FILING DATE: 2002-12-17
;  NUMBER OF SEQ ID NOS: 1441
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 835
;   LENGTH: 1290
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-669-920-835

  Query Match             9.0%;  Score 69;  DB 6;  Length 1290;
  Best Local Similarity   33.3%;  Pred. No. 1.7e+02;
  Matches   33;  Conservative   12;  Mismatches   42;  Indels   12;  Gaps    6;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAID----VTD 68
              ||    :  :| || :| |:    :  :|  |    |: |  |  : |  |: |    | |
Db        413 EYKITVVPMRGEL-EGKPIL---LNGRTEIDSPTNVVTDRVT--EDTATVSWDPVQAVID 466

Qy         69 VYVVGYQD-KWDGKDRAVFLDKVPTVATSKLFPGVTNRV 106
              ||| |     | |: ||  |:  || |  | ||   :|
Db        467 KYVVRYTSADGDTKEMAVHKDESSTVLTG-LKPGEAYKV 504


RESULT 58
US-11-300-928-49
; Sequence 49, Application US/11300928
; Publication No. US20060166277A1
; GENERAL INFORMATION:
;  APPLICANT: Karumanchi, S. Ananth
;  APPLICANT:  Sukhatme, Vikas P.
;  TITLE OF INVENTION: Nucleic Acids and Polypeptides Useful For Diagnosing and Treating
;  TITLE OF INVENTION:  Complications of Pregnancy
;  FILE REFERENCE: 01948/108002
;  CURRENT APPLICATION NUMBER: US/11/300,928
;  CURRENT FILING DATE:  2005-12-15
;  PRIOR APPLICATION NUMBER: US 60/636,275
;  PRIOR FILING DATE: 2004-12-15
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
;   LENGTH: 1321
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-300-928-49

  Query Match             9.0%;  Score 69;  DB 7;  Length 1321;
  Best Local Similarity   24.6%;  Pred. No. 1.8e+02;
  Matches   31;  Conservative   24;  Mismatches   43;  Indels   28;  Gaps    6;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVD-----ITTTSKKTVK 61
              :| | ||  | :    ::|::|    |      : |  | : :|:|     : | |:|||:
Db       1203 SLPEKYE--TNVGSQGSQLSRGEK--QRIAIARAIVRDPKILLLDEATSALDTESEKTVQ 1258

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLF----PGV-----TNRVTLTFDG 112
              ||:|              :|:   |   :: |:  : :      ||     |:   :   |
Db       1259 VALDKAR----------EGRTCIVIAHRLSTIQNADIIAVMAQGVVIEKGTHEELMAQKG 1308

Qy        113 SYQKLV 118
              :| |||
Db       1309 AYYKLV 1314


RESULT 59
US-11-056-355B-17914
; Sequence 17914, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 17914
;   LENGTH: 271
;   TYPE: prt
;   ORGANISM: Zea mays subsp. mays
```

```
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(271)
;   OTHER INFORMATION: Ceres Seq. ID no. 12415234
US-11-056-355B-17914

  Query Match             8.9%;  Score 68;  DB 7;  Length 271;
  Best Local Similarity   25.4%;  Pred. No. 31;
  Matches   30;  Conservative   21;  Mismatches   53;  Indels   14;  Gaps    4;

Qy         28 GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQD-KWDGKDRAVF 86
              |||| :| :           || |    | ::     :|  | :|||| | :|:   |  :
Db        141 GTPVLRLGL--------HEFVEVVFQNTEEELQSWHLDGYDFWVVGYGDGQWNETQRQTY 192

Qy         87 -LDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDR----KDLELGVYKLEFSI 139
               |       | :::|   : : :: |      : :|  ||    : | | |:  | |:
Db        193 NLVDAQARHTVQVYPNGWSAILVSLDNQGMWNLRSAMWDRHYLGQQLYLRVWTPEQSL 250


RESULT 60
US-11-056-355B-17913
; Sequence 17913, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 17913
;   LENGTH: 339
;   TYPE: prt
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(339)
;   OTHER INFORMATION: Ceres Seq. ID no. 12415233
US-11-056-355B-17913

  Query Match             8.9%;  Score 68;  DB 7;  Length 339;
  Best Local Similarity   25.4%;  Pred. No. 41;
  Matches   30;  Conservative   21;  Mismatches   53;  Indels   14;  Gaps    4;

Qy         28 GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQD-KWDGKDRAVF 86
              |||| :| :           || |    | ::     :|  | :|||| | :|:   |  :
Db        209 GTPVLRLGL--------HEFVEVVFQNTEEELQSWHLDGYDFWVVGYGDGQWNETQRQTY 260

Qy         87 -LDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDR----KDLELGVYKLEFSI 139
               |       | :::|   : : :: |      : :|  ||    : | | |:  | |:
Db        261 NLVDAQARHTVQVYPNGWSAILVSLDNQGMWNLRSAMWDRHYLGQQLYLRVWTPEQSL 318


RESULT 61
US-11-361-977A-83
; Sequence 83, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Methionine-truncated Shiga-A1
;   OTHER INFORMATION: Subunit fusion protein
US-11-361-977A-83

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 247;
  Best Local Similarity   22.4%;  Pred. No. 31;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD-------------DKRF 47
              |: |:  : |       |  | :  | |||       ||||:             |  |
Db          5 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 51

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
                :    :|        ::: ::  ::|| |            |:::   |       :
Db         52 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG-----------FVNRTNNVFYRFADFSHV 99

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
              ||| |  |||: | ||  |   | : |  :::  : |  |
Db        100 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 139


RESULT 62
US-11-361-977A-84
; Sequence 84, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Methionine-truncated Shiga-A1
;   OTHER INFORMATION: Subunit HIS6 fusion protein
US-11-361-977A-84

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 249;
  Best Local Similarity   22.4%;  Pred. No. 31;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD-------------DKRF 47
              |: |:  : |       |  | :  | |||       ||||:             |  |
Db          5 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 51

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
                :    :|        ::: ::  ::|| |            |:::   |       :
Db         52 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG-----------FVNRTNNVFYRFADFSHV 99

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
              ||| |  |||: | ||  |   | : |  :::  : |  |
Db        100 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 139


RESULT 63
US-11-361-977A-37
; Sequence 37, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
```

```
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
;    LENGTH: 293
;    TYPE: PRT
;    ORGANISM: Shigella dysenteriae
US-11-361-977A-37

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 293;
  Best Local Similarity   22.4%;  Pred. No. 38;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD------------DKRF 47
              |: |:  : |       |  | :  | |||       ||||:             |  |
Db          4 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 50

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
               :    :|        ::: ::  ::|| |            |:::   |       :
Db         51 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG-----------FVNRTNNVFYRFADFSHV 98

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
              ||| |  |||: | ||  |   | : |  :::  : |  |
Db         99 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 138


RESULT 64
US-11-361-977A-77
; Sequence 77, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
;    LENGTH: 320
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protei
;    OTHER INFORMATION: SDF-1-Beta-AM-truncated Shiga-A1 Subunit
US-11-361-977A-77

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 320;
  Best Local Similarity   22.4%;  Pred. No. 43;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD------------DKRF 47
              |: |:  : |       |  | :  | |||       ||||:             |  |
Db         78 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 124

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
               :    :|        ::: ::  ::|| |            |:::   |       :
Db        125 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG-----------FVNRTNNVFYRFADFSHV 172

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
              ||| |  |||: | ||  |   | : |  :::  : |  |
Db        173 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 212


RESULT 65
US-11-361-977A-78
; Sequence 78, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
;    LENGTH: 322
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protei
;    OTHER INFORMATION: SDF-1-Beta-AM-truncated Shiga-A1 Subunit HIS6
US-11-361-977A-78

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 322;
  Best Local Similarity   22.4%;  Pred. No. 43;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD------------DKRF 47
              |: |:  : |       |  | :  | |||       ||||:             |  |
Db         78 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 124

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
               :    :|        ::: ::  ::|| |            |:::   |       :
Db        125 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG-----------FVNRTNNVFYRFADFSHV 172

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
              ||| |  |||: | ||  |   | : |  :::  : |  |
Db        173 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 212


RESULT 66
US-11-361-977A-80
; Sequence 80, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
;    LENGTH: 323
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protei
;    OTHER INFORMATION: EOTAXIN-AM-truncated Shiga-A1 Subunit
US-11-361-977A-80

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 323;
  Best Local Similarity   22.4%;  Pred. No. 43;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD------------DKRF 47
              |: |:  : |       |  | :  | |||       ||||:             |  |
Db         81 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 127

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
               :    :|        ::: ::  ::|| |            |:::   |       :
Db        128 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG-----------FVNRTNNVFYRFADFSHV 175

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
              ||| |  |||: | ||  |   | : |  :::  : |  |
Db        176 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 215
```

```
RESULT 67
US-11-361-977A-71
; Sequence 71, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
;   LENGTH: 325
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protei
;   OTHER INFORMATION: MCP1-AM-truncated Shiga-A1 Subunit
US-11-361-977A-71

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 325;
  Best Local Similarity   22.4%;  Pred. No. 44;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD-------------DKRF 47
              |: |:  : |       |  | :  | |||       ||||:             |  |
Db         83 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 129

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
               :    :|        ::: ::  ::|| |            |:::   |       :
Db        130 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG-----------FVNRTNNVFYRFADFSHV 177

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
               |||  |  |||: | ||  |    | : |  :::  : |  |
Db        178 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 217


RESULT 68
US-11-361-977A-74
; Sequence 74, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
;   LENGTH: 325
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Chemokine-toxin fusion prote
;   OTHER INFORMATION: MCP3-AM-truncated Shiga-A1 Subunit
US-11-361-977A-74

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 325;
  Best Local Similarity   22.4%;  Pred. No. 44;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD-------------DKRF 47
              |: |:  : |       |  | :  | |||       ||||:             |  |
Db         83 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 129

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
               :    :|        ::: ::  ::|| |            |:::   |       :
Db        130 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG-----------FVNRTNNVFYRFADFSHV 177

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
               |||  |  |||: | ||  |    | : |  :::  : |  |
Db        178 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 217


RESULT 69
US-11-361-977A-81
; Sequence 81, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
;   LENGTH: 325
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protein
;   OTHER INFORMATION: EOTAXIN-AM-truncated Shiga-A1 Subunit HIS6
US-11-361-977A-81

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 325;
  Best Local Similarity   22.4%;  Pred. No. 44;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD-------------DKRF 47
              |: |:  : |       |  | :  | |||       ||||:             |  |
Db         81 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 127

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
               :    :|        ::: ::  ::|| |            |:::   |       :
Db        128 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG-----------FVNRTNNVFYRFADFSHV 175

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
               |||  |  |||: | ||  |    | : |  :::  : |  |
Db        176 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 215


RESULT 70
US-11-361-977A-72
; Sequence 72, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
;   LENGTH: 327
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protein
;   OTHER INFORMATION: MCP1-AM-truncated Shiga-A1 Subunit HIS6
US-11-361-977A-72

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 327;
```

```
  Best Local Similarity   22.4%;  Pred. No. 44;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD-------------DKRF 47
              |: |:  : |        |  | :  | |||        ||||:               |  |
Db         83 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 129

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
               :    :|         ::: ::  ::|| |             |:::   |       :
Db        130 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG------------FVNRTNNVFYRFADFSHV 177

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
              ||| |  |||: | ||  |    | : |  :::  : |  |
Db        178 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 217


RESULT 71
US-11-361-977A-75
; Sequence 75, Application US/11361977A
; Publication No. US20060198820A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
;   LENGTH: 327
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Chemokine-toxin fusion prote
;   OTHER INFORMATION: MCP3-AM-truncated Shiga-A1 subunit HIS6
US-11-361-977A-75

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 327;
  Best Local Similarity   22.4%;  Pred. No. 44;
  Matches   36;  Conservative   24;  Mismatches   50;  Indels   51;  Gaps    8;

Qy          3 TVSFNLGEAYEYPTFIQDLRNEL--AKGTPVCQLPVTLQTIAD-------------DKRF 47
              |: |:  : |        |  | :  | |||        ||||:               |  |
Db         83 TLDFSTAKTY------VDSLNVIRSAIGTP-------LQTISSGGTSLLMIDSGTGDNLF 129

Qy         48 VL----VDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTV------ATSK 97
               :    :|         ::: ::  ::|| |             |:::   |       :
Db        130 AVDVRGIDPEEGRFNNLRLIVERNNLYVTG------------FVNRTNNVFYRFADFSHV 177

Qy         98 LFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFS 138
              ||| |  |||: | ||  |    | : |  :::  : |  |
Db        178 TFPG-TTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTS 217


RESULT 72
US-11-056-355B-86215
; Sequence 86215, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86215
;   LENGTH: 338
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(338)
;   OTHER INFORMATION: Ceres Seq. ID no. 12687660
US-11-056-355B-86215

  Query Match             8.8%;  Score 67.5;  DB 7;  Length 338;
  Best Local Similarity   22.6%;  Pred. No. 46;
  Matches   30;  Conservative   25;  Mismatches   47;  Indels   31;  Gaps    5;

Qy         29 TPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYV-----------VGYQDK 77
              | : | ||       |:   ||   :| : ||| :|: |   ||           :  :
Db         45 TRLIQYPV------DELETVLDKASTGNNKTVIIAM-VNKAYVEEDGGGRTMLDLFLESF 97

Qy         78 WDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLEL---GVYK 134
              |:|:      |: :  ||  :            :|    : ::  |:| : ::|    ||
Db         98 WEGEGTRPLLNHLMVVAADQ----------TAYDRCLFRRLHCYKMDTEGVDLEGEKVYM 147

Qy        135 LEFSIEAIWGKTQ 147
              :  || :| :|:
Db        148 SKDFIEMMWRRTR 160


RESULT 73
US-10-449-902-48581
; Sequence 48581, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48581
;   LENGTH: 478
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-48581

  Query Match             8.8%;  Score 67.5;  DB 6;  Length 478;
  Best Local Similarity   23.9%;  Pred. No. 70;
  Matches   28;  Conservative   17;  Mismatches   29;  Indels   43;  Gaps    6;

Qy         14 YPTFIQD-----LRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTD 68
              |  :::|     ::|| | |            ::|:                    || |
Db        347 YKAYVEDEEDEGVKNEFAAG----------YVSDE------------------DVLD 375

Qy         69 VYV---VGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAK 122
               ||     |   |||:|  |:| :  :  |: | |:   |: :  || :     |||
Db        376 -YVQDSTSKQSDMDGKERETFMDLLAALLVSEEFQGI---VSSSEPGSLRDSEQAAK 428


RESULT 74
US-10-449-902-55897
; Sequence 55897, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
```

```
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55897
;   LENGTH: 437
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-55897

  Query Match             8.7%;  Score 67;  DB 6;  Length 437;
  Best Local Similarity   26.4%;  Pred. No. 71;
  Matches   37;  Conservative   16;  Mismatches   63;  Indels   24;  Gaps    5;

Qy         14 YPTFIQDL------------RNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||  : ||             |  | :|     :|       ||:   :|    :     :
Db        209 YPGRVPDLDLMFDCADWPVVRTHLYRGKHAAFMPPLFSYCGDDRTLDIVFPDWSFWGWPE 268

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              : |   |       ||  || :|  :||:||  |  |  | |   ||          |:|||
Db        269 INIKPWDAL---RQDLKDGNNRVKWLDRVP-YAYWKGNPAVA--VT------RQELVNCN 316

Qy        122 KVDRKDLELGVYKLEFSIEA 141
                 ||    :|| ::  |:
Db        317 VSTTKDWNARIYKQDWFRES 336


RESULT 75
US-11-056-355B-22809
; Sequence 22809, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 22809
;   LENGTH: 354
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(354)
;   OTHER INFORMATION: Ceres Seq. ID no. 12338971
US-11-056-355B-22809

  Query Match             8.7%;  Score 66.5;  DB 7;  Length 354;
  Best Local Similarity   24.7%;  Pred. No. 61;
  Matches   23;  Conservative   16;  Mismatches   33;  Indels   21;  Gaps    3;

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTN--RVTLTFDGS 113
              : | |:   : ::  ::   |             |:: |:| |    |    |:|  ||
Db          8 ASKFVRTVTESSNAVIIAISD-------------PSLETAKTFATGNNLSPETVTIYGS 53

Qy        114 YQKLVNAAKVDRKDLELGVYKLEFSIEAIWGKT 146
              |::|:| | ||   | : | :      | |  |
Db         54 YEELLNDANVDAVYLTMPVTQ-----RAKWAVT 81


RESULT 76
US-10-449-902-45576
; Sequence 45576, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45576
;   LENGTH: 405
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-45576

  Query Match             8.7%;  Score 66.5;  DB 6;  Length 405;
  Best Local Similarity   22.3%;  Pred. No. 72;
  Matches   29;  Conservative   23;  Mismatches   37;  Indels   41;  Gaps    5;

Qy         27 KGTPVCQLPVTLQTIADDKRFVLVDITT----------TSKKTVKVAI--------DVT 67
              :|:|:      :  ||| |   ||:| :|          ||  || | :        | :
Db         71 RGSPISNPDTSQLTIATDGNMVLLDNSTTAIWSTNISNFTSNSTVGVILDSGNLVLADAS 130

Qy         68 DVYVVGYQ------DKW-----DGKDRAVFL----------DKVPTVATSKLFPGVTNR 105
              :  :: :|      | |      |:::   :          | || | : :| |  |::
Db        131 NTSIILWQSFDHFGDTWLPGGKLGRNKLTGVSTRLVAWKARNDPVPGVFSLELDPNGTSQ 190

Qy        106 VTLTFDGSYQ 115
                | :: : |
Db        191 YLLQWNSTLQ 200


RESULT 77
US-11-330-403-8002
; Sequence 8002, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 8002
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Emericella nidulans
US-11-330-403-8002

  Query Match             8.7%;  Score 66.5;  DB 7;  Length 455;
  Best Local Similarity   25.2%;  Pred. No. 83;
  Matches   40;  Conservative   19;  Mismatches   55;  Indels   45;  Gaps    8;

Qy          8 LGEAYEYPTF---------IQDLRNELAK-------GTPVCQLPVTLQTIADDKRFVLVD 51
              || ||:   |          :| |: :| :       |||: ||||      ||     |:
Db        288 LGLAYDLKKFRANEIEKGRVQQLQKKLDRKRATLDWGTPLDQLPVMEW---DD----YVE 340

Qy         52 ITTTSKKTVKVA---IDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTL 108
                  :  | :|    ||||      :|   ||          : :  |:   |
Db        341 QAKNGRGLVAIAGVVHDVTDF----IKDHPGGK-------------AMISSGIGKDATA 382

Qy        109 TFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQ 147
               |:|      |||      : :|| :    :| || : |
Db        383 MFNGGVYYHSNAAHNLLSTMRVGVIRGGCEVE-IWKRAQ 420
```

```
RESULT 78
US-11-330-403-15293
; Sequence 15293, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 15293
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-330-403-15293

  Query Match             8.7%;  Score 66.5;  DB 7;  Length 455;
  Best Local Similarity   25.2%;  Pred. No. 83;
  Matches   40;  Conservative   19;  Mismatches   55;  Indels   45;  Gaps    8;

Qy          8 LGEAYEYPTF---------IQDLRNELAK-------GTPVCQLPVTLQTIADDKRFVLVD 51
              || ||:  |          :| |: :| :       |||: ||||      ||     |:
Db        288 LGLAYDLKKFRANEIEKGRVQQLQKKLDRKRATLDWGTPLDQLPVMEW---DD----YVE 340

Qy         52 ITTTSKKTVKVA---IDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTL 108
                 : | :|    ||||      :|   ||               : :  |:    |
Db        341 QAKNGRGLVAIAGVVHDVTDF----IKDHPGGK-------------AMISSGIGKDATA 382

Qy        109 TFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQ 147
               |:|      |||      : :|| :    :| || : |
Db        383 MFNGGVYYHSNAAHNLLSTMRVGVIRGGCEVE-IWKRAQ 420


RESULT 79
US-11-056-355B-49172
; Sequence 49172, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 49172
;   LENGTH: 456
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(456)
;   OTHER INFORMATION: Ceres Seq. ID no. 12578034
US-11-056-355B-49172

  Query Match             8.7%;  Score 66.5;  DB 7;  Length 456;
  Best Local Similarity   24.6%;  Pred. No. 84;
  Matches   33;  Conservative   18;  Mismatches   52;  Indels   31;  Gaps    6;

Qy         36 VTLQTIADD-KRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVA 94
              ||:| | :: | |       |||        |       ::    :|  | |    |:|  |
Db        245 VTVQDIVEECKSFFFAGKQTTSNLLTWTTI------LLSMHPEWQAKAR----DEVLRVC 294

Qy         95 TSKLFPGVTNRV-----TLTFDGS---YQKLVNAAKVDRKDLELGVYKLEFSIE------ 140
               |:  |   : |     ::  : |   | :|  :  : |::|| ||:    |
Db        295 GSRDVPTKDHVVKLKTLSMILNESLRLYPPIVATIRRAKSDVKLGGYKIPCGTELLIPII 354

Qy        141 ------AIWGKTQN 148
                    ||||   |
Db        355 AVHHDQAIWGNDVN 368


RESULT 80
US-11-056-355B-49171
; Sequence 49171, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 49171
;   LENGTH: 493
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(493)
;   OTHER INFORMATION: Ceres Seq. ID no. 12578033
US-11-056-355B-49171

  Query Match             8.7%;  Score 66.5;  DB 7;  Length 493;
  Best Local Similarity   24.6%;  Pred. No. 92;
  Matches   33;  Conservative   18;  Mismatches   52;  Indels   31;  Gaps    6;

Qy         36 VTLQTIADD-KRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVA 94
              ||:| | :: | |       |||        |       ::    :|  | |    |:|  |
Db        282 VTVQDIVEECKSFFFAGKQTTSNLLTWTTI------LLSMHPEWQAKAR----DEVLRVC 331

Qy         95 TSKLFPGVTNRV-----TLTFDGS---YQKLVNAAKVDRKDLELGVYKLEFSIE------ 140
               |:  |   : |     ::  : |   | :|  :  : |::|| ||:    |
Db        332 GSRDVPTKDHVVKLKTLSMILNESLRLYPPIVATIRRAKSDVKLGGYKIPCGTELLIPII 391

Qy        141 ------AIWGKTQN 148
                    ||||   |
Db        392 AVHHDQAIWGNDVN 405


RESULT 81
US-11-056-355B-49170
; Sequence 49170, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 49170
;   LENGTH: 520
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(520)
;   OTHER INFORMATION: Ceres Seq. ID no. 12578032
US-11-056-355B-49170

  Query Match             8.7%;  Score 66.5;  DB 7;  Length 520;
  Best Local Similarity   24.6%;  Pred. No. 99;
  Matches   33;  Conservative   18;  Mismatches   52;  Indels   31;  Gaps    6;
```

```
Qy          36 VTLQTIADD-KRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVA 94
               ||:| | :: | |      |||      |      ::    :| | |    |:| |
Db         309 VTVQDIVEECKSFFFAGKQTTSNLLTWTTI------LLSMHPEWQAKAR----DEVLRVC 358

Qy          95 TSKLFPGVTNRV-----TLTFDGS---YQKLVNAAKVDRKDLELGVYKLEFSIE------ 140
                |:  |   : |     ::  : |  | :|  :  : |::|| ||:     |
Db         359 GSRDVPTKDHVVKLKTLSMILNESLRLYPPIVATIRRAKSDVKLGGYKIPCGTELLIPII 418

Qy         141 ------AIWGKTQN 148
                    ||||   |
Db         419 AVHHDQAIWGNDVN 432


RESULT 82
US-10-449-902-45335
; Sequence 45335, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45335
;   LENGTH: 645
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-45335

  Query Match             8.7%;  Score 66.5;  DB 6;  Length 645;
  Best Local Similarity   22.4%;  Pred. No. 1.3e+02;
  Matches   26;  Conservative   17;  Mismatches   46;  Indels   27;  Gaps    4;

Qy           8 LGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKR---FVLVDITTTSKKTVKVAI 64
               ||: ||: :|          |: :  : :   |||    | :|:   | | | :
Db         186 LGQFYEFFSFSH-------LSPPLHYIRRSTRPFVDDKTEDDFFQIDVRVCSGKPVTIVA 238

Qy          65 DVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
                 | |         ||:          |    |:  : :  |||:|: |: |
Db         239 SKAGFYPAG--------KRALI---------SHSLVGLLQQTSRAFDGAYKALMKA 277


RESULT 83
US-10-505-928-795
; Sequence 795, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 795
;   LENGTH: 967
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-505-928-795

  Query Match             8.7%;  Score 66.5;  DB 6;  Length 967;
  Best Local Similarity   17.6%;  Pred. No. 2.1e+02;
  Matches   38;  Conservative   36;  Mismatches   67;  Indels   75;  Gaps    9;

Qy           2 NTVSFNL---------GEAYEYPTFIQDLRNE--LAKGTPVCQLPVTLQTIADD------ 44
               ||:  ||          : : || ::|: |    |  | ||  :  :  |:: :
Db         511 NTIYLNLWDHLQEAVNNRSIQLPTTVRDIMNRWTLQMGFPVITVDTSTGTLSQEHFLLDP 570

Qy          45 --------------------------KRFVLVDI-------TTTSKKTVKVAIDVTDVY 70
                                          : : |:|:       :|:  : | : ::||  |
Db         571 DSNVTRPSEFNYVWIVPITSIRDGRQQQDYWLIDVRAQNDLFSTSGNEWVLLNLNVTGYY 630

Qy          71 VVGY-QDKW---------DGK-----DRAVFLDKVPTVATSKLFP---GVTNRVTLTFDG 112
               | | :: |         |       :||  ::    :|::    |    : | : |  :
Db         631 RVNYDEENWRKIQTQLQRDHSAIPVINRAQIINDAFNLASAHKVPVTLALNNTLFLIEER 690

Qy         113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQN 148
                 |      |         |  :|| |    ::|  :|
Db         691 QYMPWEAALS------SLSYFKLMFDRSEVYGPMKN 720


RESULT 84
US-10-700-439-143
; Sequence 143, Application US/10700439
; Publication No. US20060188889A1
; GENERAL INFORMATION:
;  APPLICANT: Mayo Foundation for Medical Education and Research
;  APPLICANT:  Bayer Healthcare LLC
;  APPLICANT:  Burgess, Christopher
;  APPLICANT:  Myerow, Susan
;  APPLICANT:  Thiagalingam, Arunthathi
;  APPLICANT:  Maimonis, Peter
;  APPLICANT:  Molino, Gary
;  APPLICANT:  Burgart, Lawrence
;  APPLICANT:  Boardman, Lisa A.
;  APPLICANT:  Thibodeau, Steven
;  APPLICANT:  Lewis, Marcia
;  TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
;  TITLE OF INVENTION:  Biomarkers for Cancer
;  FILE REFERENCE: 1657/2022
;  CURRENT APPLICATION NUMBER: US/10/700,439
;  CURRENT FILING DATE:  2003-11-04
;  NUMBER OF SEQ ID NOS: 186
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 143
;   LENGTH: 967
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-700-439-143

  Query Match             8.7%;  Score 66.5;  DB 6;  Length 967;
  Best Local Similarity   17.6%;  Pred. No. 2.1e+02;
  Matches   38;  Conservative   36;  Mismatches   67;  Indels   75;  Gaps    9;

Qy           2 NTVSFNL---------GEAYEYPTFIQDLRNE--LAKGTPVCQLPVTLQTIADD------ 44
               ||:  ||          : : || ::|: |    |  | ||  :  :  |:: :
Db         511 NTIYLNLWDHLQEAVNNRSIQLPTTVRDIMNRWTLQMGFPVITVDTSTGTLSQEHFLLDP 570

Qy          45 --------------------------KRFVLVDI-------TTTSKKTVKVAIDVTDVY 70
                                          : : |:|:       :|:  : | : ::||  |
Db         571 DSNVTRPSEFNYVWIVPITSIRDGRQQQDYWLIDVRAQNDLFSTSGNEWVLLNLNVTGYY 630

Qy          71 VVGY-QDKW---------DGK-----DRAVFLDKVPTVATSKLFP---GVTNRVTLTFDG 112
               | | :: |         |       :||  ::    :|::    |    : | : |  :
Db         631 RVNYDEENWRKIQTQLQRDHSAIPVINRAQIINDAFNLASAHKVPVTLALNNTLFLIEER 690

Qy         113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQN 148
                 |      |         |  :|| |    ::|  :|
Db         691 QYMPWEAALS------SLSYFKLMFDRSEVYGPMKN 720


RESULT 85
US-11-387-011-2
; Sequence 2, Application US/11387011
```

```
; Publication No. US20060166255A1
; GENERAL INFORMATION:
;  APPLICANT: Chun, Miyoung
;  TITLE OF INVENTION: METHODS OF USING 48149, A HUMAN
;  TITLE OF INVENTION:  AMINOPEPTIDASE FAMILY MEMBER
;  FILE REFERENCE: MPI01-174P1RM
;  CURRENT APPLICATION NUMBER: US/11/387,011
;  CURRENT FILING DATE:  2006-03-22
;  PRIOR APPLICATION NUMBER: US/10/281,904
;  PRIOR FILING DATE: 2002-10-28
;  PRIOR APPLICATION NUMBER: 60/335,084
;  PRIOR FILING DATE: 2001-10-31
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 967
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-11-387-011-2

  Query Match             8.7%;  Score 66.5;  DB 7;  Length 967;
  Best Local Similarity   17.6%;  Pred. No. 2.1e+02;
  Matches   38;  Conservative   36;  Mismatches   67;  Indels   75;  Gaps    9;

Qy          2 NTVSFNL---------GEAYEYPTFIQDLRNE--LAKGTPVCQLPVTLQTIADD------ 44
              ||:  ||           : : || ::|: |    |  | ||  :  :  |:: :
Db        511 NTIYLNLWDHLQEAVNNRSIQLPTTVRDIMNRWTLQMGFPVITVDTSTGTLSQEHFLLDP 570

Qy         45 --------------------------KRFVLVDI-------TTTSKKTVKVAIDVTDVY 70
                                        : : |:|:       :|:  : | : ::||  |
Db        571 DSNVTRPSEFNYVWIVPITSIRDGRQQQDYWLIDVRAQNDLFSTSGNEWVLLNLNVTGYY 630

Qy         71 VVGY-QDKW---------DGK-----DRAVFLDKVPTVATSKLFP---GVTNRVTLTFDG 112
               | | :: |          |        :||  ::    :|::    |    : | : |  :
Db        631 RVNYDEENWRKIQTQLQRDHSAIPVINRAQIINDAFNLASAHKVPVTLALNNTLFLIEER 690

Qy        113 SYQKLVNAAKVDRKDLELGVYKLEFSIEAIWGKTQN 148
                |     |          |  :|| |    ::|  :|
Db        691 QYMPWEAALS------SLSYFKLMFDRSEVYGPMKN 720


RESULT 86
US-11-070-573-11
; Sequence 11, Application US/11070573
; Publication No. US20060168683A1
; GENERAL INFORMATION:
;  APPLICANT: Hey, Timothy
;  APPLICANT:  Cai, Charles
;  APPLICANT:  Meade, Thomas
;  APPLICANT:  Moon, Haley
;  APPLICANT:  Burton, Stephanie
;  APPLICANT:  Sheets, Joel
;  APPLICANT:  Merlo, Donald
;  APPLICANT:  Woosley, Aaron
;  TITLE OF INVENTION: Insecticidal Toxin Complex Fusion Proteins
;  FILE REFERENCE: DAS-118XC1
;  CURRENT APPLICATION NUMBER: US/11/070,573
;  CURRENT FILING DATE:  2005-03-02
;  PRIOR APPLICATION NUMBER: 60/549,502
;  PRIOR FILING DATE: 2004-03-02
;  PRIOR APPLICATION NUMBER: 60/549,516
;  PRIOR FILING DATE: 2004-03-02
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
;   LENGTH: 1428
;   TYPE: PRT
;   ORGANISM: Serratia entomophila
US-11-070-573-11

  Query Match             8.7%;  Score 66.5;  DB 7;  Length 1428;
  Best Local Similarity   31.1%;  Pred. No. 3.5e+02;
  Matches   28;  Conservative   15;  Mismatches   26;  Indels   21;  Gaps    6;

Qy          2 NTVSFNLG--EAYEYPTFIQDLRNELAK-----GTPVCQLPVTLQTIADDKRFVLVDITT 54
              | :: |:|   |  | : :|   :| |:      :| | || || |:    | |: |  |
Db        707 NGMNNNMGARHALHYRSSVQFWLDEKAEALAAGSSPACYLPFTLHTL---WRSVVQDEIT 763

Qy         55 TSKKTVKVAIDVTDV-YVVGYQDKWDGKDR 83
                ::        |:|| |  |    |||::|
Db        764 GNRL-------VSDVLYRHGV---WDGQER 783


RESULT 87
US-11-330-403-5486
; Sequence 5486, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53629)B
;  CURRENT APPLICATION NUMBER: US/11/330,403
;  CURRENT FILING DATE:  2006-01-12
;  NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 5486
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Mesorhizobium loti MAFF303099
US-11-330-403-5486

  Query Match             8.6%;  Score 66;  DB 7;  Length 180;
  Best Local Similarity   31.4%;  Pred. No. 30;
  Matches   27;  Conservative    9;  Mismatches   26;  Indels   24;  Gaps    5;

Qy         16 TFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVA----IDVTDVYV 71
              || :||   |::|   | : | |     |||          ::|  ||     | | :|
Db        112 TFTRDLM--LSRGAKSCSIAVLL-----DKRM--------RRQTALVADYVGFDCPDYFV 156

Qy         72 VGYQDKWDGKDRAVFLDKVPTVATSK 97
              |||     | | |    ::| |   |
Db        157 VGY-----GMDVAHAFRELPFVGVVK 177


RESULT 88
US-10-534-238-2
; Sequence 2, Application US/10534238
; Publication No. US20060147440A1
; GENERAL INFORMATION:
;  APPLICANT: FESENKO, Evgeny Evgenyevich
;  APPLICANT:  NOVOSELOV, Vladimir Ivanovich
;  APPLICANT:  YANIN, Vadim Alekseevich
;  APPLICANT:  LIPKIN, Valery Mikhaylovich
;  APPLICANT:  SHUVAEVA, Tatyana Maratovna
;  TITLE OF INVENTION: ANTIOXIDANT PHARMACEUTICAL COMPOUND, METHOD FOR PRODUCING
;  TITLE OF INVENTION:  POLYPEPTIDE AND METHOD OF CURE
;  FILE REFERENCE: u015763-7
;  CURRENT APPLICATION NUMBER: US/10/534,238
;  CURRENT FILING DATE:  2005-05-06
;  PRIOR APPLICATION NUMBER: PCT/RU03/00473
;  PRIOR FILING DATE: 2003-11-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-534-238-2

  Query Match             8.6%;  Score 66;  DB 6;  Length 224;
  Best Local Similarity   22.7%;  Pred. No. 39;
  Matches   29;  Conservative   11;  Mismatches   44;  Indels   44;  Gaps    4;

Qy          5 SFNLGEAYEYPTF--IQDLRNELA------------KGTPVCQ---------------- 33
              ::|  |  |   |  | |   |||             || ||
Db         88 AYNCEEPTEKLPFPIIDDRNRELAILLGMLDPAEKDEKGMPVTARVVFVFGPDKKLKLSI 147
```

```
Qy          34 -LPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT 92
               | |     |:   |:: :  |::| |   :|             |   | : |  :|
Db         148 LYPATTGRNFDEILRVVISLQLTAEKRVATPVD-----------WKDGDSVMVLPTIPE 195

Qy          93 VATSKLFP 100
                ||||
Db         196 EEAKKLFP 203
```

RESULT 89
US-10-471-571A-3740
; Sequence 3740, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3740
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(273)
; OTHER INFORMATION: conserved hypothetical
US-10-471-571A-3740

Query Match 8.6%; Score 66; DB 6; Length 273;
Best Local Similarity 20.6%; Pred. No. 50;
Matches 32; Conservative 29; Mismatches 62; Indels 32; Gaps 6;

```
Qy           7 NLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVD-ITTTSKKTVKVAID 65
               |:      |:|  |    :||              :|:|  | : |    | |:  :||
Db         135 NINATVIKPSFFMDNFLRIAK-------------VEDERITLPEFINPNIKFTMISSID 180

Qy          66 VTDV--YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKV 123
               :  :  |:  :   :  :   :  |:|     : :|  || : |:  :| :   |      .
Db         181 IAKIASYIFAHPQSFTHQSIEIGSDEVTLSEAATIFSEVTGKSTV-IEGEFVSGV----A 235

Qy         124 DRKDLELGVYKLEFSIEA----------IWGKTQN 148
               ::: ||   |:::| : |           | | ||
Db         236 EKQWLEEKGYEVDFELMAEINPTRLSLSDWLKVQN 270
```

RESULT 90
US-10-953-349-31921
; Sequence 31921, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31921
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31921

Query Match 8.6%; Score 66; DB 6; Length 287;
Best Local Similarity 26.6%; Pred. No. 53;
Matches 29; Conservative 9; Mismatches 41; Indels 30; Gaps 4;

```
Qy          57 KKTVKVAIDVTDVYVVGYQ------------DKWDGK-DRAVF--------LDKVPTV- 93
               |: || | | | |  :| :                ||   || |          ||  |
Db          75 KRNVKAARDFTWVQALGIRFGGHRLYLGVKRTVTWDNAVDRLVITFDGVPVELDAAPAAS 134

Qy          94 -------ATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKL 135
                     | |    | | | :  || :: : ||  |  :|  :  | |
Db         135 WSPASAPALSVFRIGKANGVVVRLDGRFRIVANAVPVTEEDSRVHDYGL 183
```

RESULT 91
US-11-056-355B-64817
; Sequence 64817, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 64817
; LENGTH: 287
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(287)
; OTHER INFORMATION: Ceres Seq. ID no. 14302855
US-11-056-355B-64817

Query Match 8.6%; Score 66; DB 7; Length 287;
Best Local Similarity 26.6%; Pred. No. 53;
Matches 29; Conservative 9; Mismatches 41; Indels 30; Gaps 4;

```
Qy          57 KKTVKVAIDVTDVYVVGYQ------------DKWDGK-DRAVF--------LDKVPTV- 93
               |: || | | | |  :| :                ||   || |          ||  |
Db          75 KRNVKAARDFTWVQALGIRFGGHRLYLGVKRTVTWDNAVDRLVITFDGVPVELDAAPAAS 134

Qy          94 -------ATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKL 135
                     | |    | | | :  || :: : ||  |  :|  :  | |
Db         135 WSPASAPALSVFRIGKANGVVVRLDGRFRIVANAVPVTEEDSRVHDYGL 183
```

RESULT 92
US-10-953-349-31920
; Sequence 31920, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31920
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31920

Query Match 8.6%; Score 66; DB 6; Length 311;
Best Local Similarity 26.6%; Pred. No. 58;
Matches 29; Conservative 9; Mismatches 41; Indels 30; Gaps 4;

```
Qy          57 KKTVKVAIDVTDVYVVGYQ------------DKWDGK-DRAVF--------LDKVPTV- 93
               |: || | | | |  :| :                ||   || |          ||  |
Db          99 KRNVKAARDFTWVQALGIRFGGHRLYLGVKRTVTWDNAVDRLVITFDGVPVELDAAPAAS 158
```

```
Qy          94 -------ATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKL 135
                       | |    |  | | :  || :: : ||  |  :|  :  | |
Db         159 WSPASAPALSVFRIGKANGVVVRLDGRFRIVANAVPVTEEDSRVHDYGL 207
```

RESULT 93
US-11-056-355B-64816
; Sequence 64816, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 64816
; LENGTH: 311
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(311)
; OTHER INFORMATION: Ceres Seq. ID no. 14302854
US-11-056-355B-64816

Query Match 8.6%; Score 66; DB 7; Length 311;
Best Local Similarity 26.6%; Pred. No. 58;
Matches 29; Conservative 9; Mismatches 41; Indels 30; Gaps 4;

```
Qy          57 KKTVKVAIDVTDVYVVGYQ-------------DKWDGK-DRAVF--------LDKVPTV- 93
               |: || | | | |  :| :               ||   || |          ||  |
Db          99 KRNVKAARDFTWVQALGIRFGGHRLYLGVKRTVTWDNAVDRLVITFDGVPVELDAAPAAS 158

Qy          94 -------ATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKL 135
                       | |    |  | | :  || :: : ||  |  :|  :  | |
Db         159 WSPASAPALSVFRIGKANGVVVRLDGRFRIVANAVPVTEEDSRVHDYGL 207
```

RESULT 94
US-10-953-349-31919
; Sequence 31919, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31919
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31919

Query Match 8.6%; Score 66; DB 6; Length 353;
Best Local Similarity 26.6%; Pred. No. 68;
Matches 29; Conservative 9; Mismatches 41; Indels 30; Gaps 4;

```
Qy          57 KKTVKVAIDVTDVYVVGYQ-------------DKWDGK-DRAVF--------LDKVPTV- 93
               |: || | | | |  :| :               ||   || |          ||  |
Db         141 KRNVKAARDFTWVQALGIRFGGHRLYLGVKRTVTWDNAVDRLVITFDGVPVELDAAPAAS 200

Qy          94 -------ATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKL 135
                       | |    |  | | :  || :: : ||  |  :|  :  | |
Db         201 WSPASAPALSVFRIGKANGVVVRLDGRFRIVANAVPVTEEDSRVHDYGL 249
```

RESULT 95
US-11-056-355B-64815
; Sequence 64815, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 64815
; LENGTH: 353
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(353)
; OTHER INFORMATION: Ceres Seq. ID no. 14302853
US-11-056-355B-64815

Query Match 8.6%; Score 66; DB 7; Length 353;
Best Local Similarity 26.6%; Pred. No. 68;
Matches 29; Conservative 9; Mismatches 41; Indels 30; Gaps 4;

```
Qy          57 KKTVKVAIDVTDVYVVGYQ-------------DKWDGK-DRAVF--------LDKVPTV- 93
               |: || | | | |  :| :               ||   || |          ||  |
Db         141 KRNVKAARDFTWVQALGIRFGGHRLYLGVKRTVTWDNAVDRLVITFDGVPVELDAAPAAS 200

Qy          94 -------ATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKL 135
                       | |    |  | | :  || :: : ||  |  :|  :  | |
Db         201 WSPASAPALSVFRIGKANGVVVRLDGRFRIVANAVPVTEEDSRVHDYGL 249
```

RESULT 96
US-10-449-902-39182
; Sequence 39182, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39182
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-39182

Query Match 8.6%; Score 66; DB 6; Length 355;
Best Local Similarity 25.7%; Pred. No. 69;
Matches 28; Conservative 10; Mismatches 41; Indels 30; Gaps 4;

```
Qy          57 KKTVKVAIDVTDVYVVGYQ-------------DKWDGK-DRAVF--------LDKVPTV- 93
               |:    | | | |  :| :                 :||   || |          || ||
Db         143 KRNAAAARDFTWVQALGIRFGGHRLYLGVRRTVRWDAAVDRLVITFDGAPVELDAVPAAS 202
```

```
Qy          94 -------ATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKL 135
                   | |    |  | | :  || :: : ||  |  :|  :  | |
Db         203 WSPASVPALSVFRTGPANGVVVRLDGRFRIVANAVPVTEEDSRIHGYGL 251


RESULT 97
US-10-953-349-32766
; Sequence 32766, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32766
;   LENGTH: 406
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-10-953-349-32766

  Query Match             8.6%;  Score 66;  DB 6;  Length 406;
  Best Local Similarity   25.0%;  Pred. No. 81;
  Matches   30;  Conservative   22;  Mismatches   64;  Indels    4;  Gaps    3;

Qy          24 ELAKGTPVCQLPVTLQTIADDKRFVLVD-ITTTSKKTVKVAIDVTDVYVVGYQDKW-DGK 81
               |  : |      | | |: : :|  | ::      :  :::|||  |: ||   | : | |
Db          52 EPVRATATQAPPATPQSSSGEKTKVGINGFGRIGRLVLRIAIDRDDIEVVAVNDPFIDAK 111

Qy          82 DRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEA 141
                    |       |    |    | :  || :|  :|:   :| |  |:  | :  |: :|:
Db         112 YMAYMFKYDSTHGPFKGTITVLDESTLEING--KKVSVTSKRDPSDIPWGNFGAEYVVES 169


RESULT 98
US-11-056-355B-67038
; Sequence 67038, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 67038
;   LENGTH: 406
;   TYPE: prt
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(406)
;   OTHER INFORMATION: Ceres Seq. ID no. 14316051
US-11-056-355B-67038

  Query Match             8.6%;  Score 66;  DB 7;  Length 406;
  Best Local Similarity   25.0%;  Pred. No. 81;
  Matches   30;  Conservative   22;  Mismatches   64;  Indels    4;  Gaps    3;

Qy          24 ELAKGTPVCQLPVTLQTIADDKRFVLVD-ITTTSKKTVKVAIDVTDVYVVGYQDKW-DGK 81
               |  : |      | | |: : :|  | ::      :  :::|||  |: ||   | : | |
Db          52 EPVRATATQAPPATPQSSSGEKTKVGINGFGRIGRLVLRIAIDRDDIEVVAVNDPFIDAK 111

Qy          82 DRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEA 141
                    |       |    |    | :  || :|  :|:   :| |  |:  | :  |: :|:
Db         112 YMAYMFKYDSTHGPFKGTITVLDESTLEING--KKVSVTSKRDPSDIPWGNFGAEYVVES 169


RESULT 99
US-10-953-349-32765
; Sequence 32765, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32765
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-10-953-349-32765

  Query Match             8.6%;  Score 66;  DB 6;  Length 462;
  Best Local Similarity   25.0%;  Pred. No. 95;
  Matches   30;  Conservative   22;  Mismatches   64;  Indels    4;  Gaps    3;

Qy          24 ELAKGTPVCQLPVTLQTIADDKRFVLVD-ITTTSKKTVKVAIDVTDVYVVGYQDKW-DGK 81
               |  : |      | | |: : :|  | ::      :  :::|||  |: ||   | : | |
Db         108 EPVRATATQAPPATPQSSSGEKTKVGINGFGRIGRLVLRIAIDRDDIEVVAVNDPFIDAK 167

Qy          82 DRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEA 141
                    |       |    |    | :  || :|  :|:   :| |  |:  | :  |: :|:
Db         168 YMAYMFKYDSTHGPFKGTITVLDESTLEING--KKVSVTSKRDPSDIPWGNFGAEYVVES 225


RESULT 100
US-11-056-355B-67037
; Sequence 67037, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 67037
;   LENGTH: 462
;   TYPE: prt
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(462)
;   OTHER INFORMATION: Ceres Seq. ID no. 14316050
US-11-056-355B-67037

  Query Match             8.6%;  Score 66;  DB 7;  Length 462;
  Best Local Similarity   25.0%;  Pred. No. 95;
  Matches   30;  Conservative   22;  Mismatches   64;  Indels    4;  Gaps    3;

Qy          24 ELAKGTPVCQLPVTLQTIADDKRFVLVD-ITTTSKKTVKVAIDVTDVYVVGYQDKW-DGK 81
               |  : |      | | |: : :|  | ::      :  :::|||  |: ||   | : | |
Db         108 EPVRATATQAPPATPQSSSGEKTKVGINGFGRIGRLVLRIAIDRDDIEVVAVNDPFIDAK 167

Qy          82 DRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLEFSIEA 141
                    |       |    |    | :  || :|  :|:   :| |  |:  | :  |: :|:
Db         168 YMAYMFKYDSTHGPFKGTITVLDESTLEING--KKVSVTSKRDPSDIPWGNFGAEYVVES 225
```

Search completed: September 18, 2006, 19:36:21
Job time : 37.9609 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:14:52 ; Search time 721.693 Seconds
(without alignments)
315.254 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending_Patents_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/paa/PCTUS_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/paa/US066_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/paa/US073_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/paa/US074_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/paa/US075_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/paa/US076_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/paa/US077_COMB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/paa/US078_COMB.pep:*
9: /EMC_Celerra_SIDS3/ptodata/2/paa/US079_COMB.pep:*
10: /EMC_Celerra_SIDS3/ptodata/2/paa/US080_COMB.pep:*
11: /EMC_Celerra_SIDS3/ptodata/2/paa/US081_COMB.pep:*
12: /EMC_Celerra_SIDS3/ptodata/2/paa/US082_COMB.pep:*
13: /EMC_Celerra_SIDS3/ptodata/2/paa/US083_COMB.pep:*
14: /EMC_Celerra_SIDS3/ptodata/2/paa/US084_COMB.pep:*
15: /EMC_Celerra_SIDS3/ptodata/2/paa/US085_COMB.pep:*
16: /EMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*
17: /EMC_Celerra_SIDS3/ptodata/2/paa/US087_COMB.pep:*
18: /EMC_Celerra_SIDS3/ptodata/2/paa/US088_COMB.pep:*
19: /EMC_Celerra_SIDS3/ptodata/2/paa/US089_COMB.pep:*
20: /EMC_Celerra_SIDS3/ptodata/2/paa/US090_COMB.pep:*
21: /EMC_Celerra_SIDS3/ptodata/2/paa/US091_COMB.pep:*
22: /EMC_Celerra_SIDS3/ptodata/2/paa/US092_COMB.pep:*
23: /EMC_Celerra_SIDS3/ptodata/2/paa/US093_COMB.pep:*
24: /EMC_Celerra_SIDS3/ptodata/2/paa/US094_COMB.pep:*
25: /EMC_Celerra_SIDS3/ptodata/2/paa/US095_COMB.pep:*
26: /EMC_Celerra_SIDS3/ptodata/2/paa/US096_COMB.pep:*
27: /EMC_Celerra_SIDS3/ptodata/2/paa/US097_COMB.pep:*
28: /EMC_Celerra_SIDS3/ptodata/2/paa/US098_COMB.pep:*
29: /EMC_Celerra_SIDS3/ptodata/2/paa/US099_COMB.pep:*
30: /EMC_Celerra_SIDS3/ptodata/2/paa/US100_COMB.pep:*
31: /EMC_Celerra_SIDS3/ptodata/2/paa/US101_COMB.pep:*
32: /EMC_Celerra_SIDS3/ptodata/2/paa/US102_COMB.pep:*
33: /EMC_Celerra_SIDS3/ptodata/2/paa/US103_COMB.pep:*
34: /EMC_Celerra_SIDS3/ptodata/2/paa/US104_COMB.pep:*
35: /EMC_Celerra_SIDS3/ptodata/2/paa/US105_COMB.pep:*
36: /EMC_Celerra_SIDS3/ptodata/2/paa/US106_COMB.pep:*
37: /EMC_Celerra_SIDS3/ptodata/2/paa/US107_COMB.pep:*
38: /EMC_Celerra_SIDS3/ptodata/2/paa/US108_COMB.pep:*
39: /EMC_Celerra_SIDS3/ptodata/2/paa/US109_COMB.pep:*
40: /EMC_Celerra_SIDS3/ptodata/2/paa/US110_COMB.pep:*
41: /EMC_Celerra_SIDS3/ptodata/2/paa/US111_COMB.pep:*
42: /EMC_Celerra_SIDS3/ptodata/2/paa/US112_COMB.pep:*
43: /EMC_Celerra_SIDS3/ptodata/2/paa/US113_COMB.pep:*
44: /EMC_Celerra_SIDS3/ptodata/2/paa/US114_COMB.pep:*
45: /EMC_Celerra_SIDS3/ptodata/2/paa/US600_COMB.pep:*
46: /EMC_Celerra_SIDS3/ptodata/2/paa/US601_COMB.pep:*
47: /EMC_Celerra_SIDS3/ptodata/2/paa/US602_COMB.pep:*
48: /EMC_Celerra_SIDS3/ptodata/2/paa/US603_COMB.pep:*
49: /EMC_Celerra_SIDS3/ptodata/2/paa/US604_COMB.pep:*
50: /EMC_Celerra_SIDS3/ptodata/2/paa/US605_COMB.pep:*
51: /EMC_Celerra_SIDS3/ptodata/2/paa/US606_COMB.pep:*
52: /EMC_Celerra_SIDS3/ptodata/2/paa/US607_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	768	100.0	149	24	US-09-446-351B-1	Sequence 1, Appli
2	768	100.0	149	24	US-09-446-351D-1	Sequence 1, Appli
3	768	100.0	149	37	US-10-758-902-9	Sequence 9, Appli
4	747	97.3	250	40	US-11-084-080-1	Sequence 1, Appli
5	738	96.1	250	40	US-11-084-080-129	Sequence 129, App
6	727	94.7	250	40	US-11-084-080-14	Sequence 14, Appl
7	726	94.5	250	40	US-11-084-080-13	Sequence 13, Appl
8	726	94.5	750	40	US-11-084-080-16	Sequence 16, Appl
9	726	94.5	750	40	US-11-084-080-20	Sequence 20, Appl
10	726	94.5	750	40	US-11-084-080-22	Sequence 22, Appl
11	726	94.5	750	40	US-11-084-080-24	Sequence 24, Appl
12	726	94.5	759	40	US-11-084-080-28	Sequence 28, Appl
13	721	93.9	250	40	US-11-084-080-11	Sequence 11, Appl
14	721	93.9	250	40	US-11-084-080-12	Sequence 12, Appl
15	221.5	28.8	250	7	US-07-787-567A-8	Sequence 8, Appli
16	221.5	28.8	250	21	US-09-120-523-36	Sequence 36, Appl
17	221.5	28.8	250	23	US-09-360-242-36	Sequence 36, Appl
18	221.5	28.8	250	24	US-09-453-851A-36	Sequence 36, Appl
19	221.5	28.8	250	27	US-09-792-793A-36	Sequence 36, Appl
20	221.5	28.8	250	31	US-10-127-890-8	Sequence 8, Appli
21	221.5	28.8	250	33	US-10-375-209A-36	Sequence 36, Appl
22	221.5	28.8	250	36	US-10-613-755-8	Sequence 8, Appli
23	221.5	28.8	250	37	US-10-717-243-8	Sequence 8, Appli
24	221.5	28.8	251	27	US-09-791-537-113633	Sequence 113633,
25	221.5	28.8	278	27	US-09-791-537-3997	Sequence 3997, Ap
26	220.5	28.7	263	7	US-07-787-567A-4	Sequence 4, Appli
27	220.5	28.7	263	31	US-10-127-890-4	Sequence 4, Appli
28	220.5	28.7	263	36	US-10-613-755-4	Sequence 4, Appli
29	220.5	28.7	263	37	US-10-717-243-4	Sequence 4, Appli
30	220.5	28.7	286	11	US-08-141-891-13	Sequence 13, Appl
31	220.5	28.7	286	27	US-09-791-537-3969	Sequence 3969, Ap
32	217.5	28.3	278	27	US-09-791-537-51973	Sequence 51973, A
33	215.5	28.1	249	27	US-09-791-537-102332	Sequence 102332,
34	215.5	28.1	263	27	US-09-791-537-57371	Sequence 57371, A
35	215.5	28.1	286	27	US-09-791-537-56331	Sequence 56331, A
36	212.5	27.7	251	27	US-09-791-537-116435	Sequence 116435,
37	194.5	25.3	545	27	US-09-791-537-5912	Sequence 5912, Ap
38	191	24.9	563	27	US-09-791-537-79846	Sequence 79846, A
39	183.5	23.9	247	5	US-07-504-775-10	Sequence 10, Appl
40	183.5	23.9	247	12	US-08-263-261-10	Sequence 10, Appl
41	183.5	23.9	247	21	US-09-120-523-39	Sequence 39, Appl
42	183.5	23.9	247	23	US-09-360-242-39	Sequence 39, Appl
43	183.5	23.9	247	24	US-09-453-851A-39	Sequence 39, Appl
44	183.5	23.9	247	27	US-09-791-537-57417	Sequence 57417, A
45	183.5	23.9	247	27	US-09-791-537-89783	Sequence 89783, A
46	183.5	23.9	247	27	US-09-791-537-92216	Sequence 92216, A
47	183.5	23.9	247	27	US-09-791-537-126580	Sequence 126580,
48	183.5	23.9	247	27	US-09-792-793A-39	Sequence 39, Appl
49	183.5	23.9	247	29	US-09-905-247A-8	Sequence 8, Appli
50	183.5	23.9	247	31	US-10-127-890-6	Sequence 6, Appli
51	183.5	23.9	247	33	US-10-375-209A-39	Sequence 39, Appl
52	183.5	23.9	247	36	US-10-613-755-6	Sequence 6, Appli
53	183.5	23.9	247	37	US-10-717-243-6	Sequence 6, Appli
54	183.5	23.9	249	27	US-09-791-537-92230	Sequence 92230, A

55	183.5	23.9	289	5	US-07-504-775-9	Sequence 9, Appli
56	183.5	23.9	289	7	US-07-739-143-4	Sequence 4, Appli
57	183.5	23.9	289	12	US-08-263-261-9	Sequence 9, Appli
58	183.5	23.9	289	14	US-08-480-432-4	Sequence 4, Appli
59	183.5	23.9	289	27	US-09-791-537-3999	Sequence 3999, Ap
60	183.5	23.9	289	27	US-09-791-537-26832	Sequence 26832, A
61	183.5	23.9	289	27	US-09-791-537-55667	Sequence 55667, A
62	183.5	23.9	289	27	US-09-791-537-132717	Sequence 132717,
63	183.5	23.9	289	29	US-09-905-247A-1	Sequence 1, Appli
64	183.5	23.9	289	32	US-10-280-679B-4	Sequence 4, Appli
65	183.5	23.9	289	32	US-10-280-725B-4	Sequence 4, Appli
66	183	23.8	528	27	US-09-791-537-75941	Sequence 75941, A
67	183	23.8	528	27	US-09-791-537-78018	Sequence 78018, A
68	183	23.8	562	27	US-09-791-537-110085	Sequence 110085,
69	182.5	23.8	248	5	US-07-504-775-4	Sequence 4, Appli
70	182.5	23.8	248	12	US-08-263-261-4	Sequence 4, Appli
71	182.5	23.8	272	5	US-07-504-775-3	Sequence 3, Appli
72	182.5	23.8	272	12	US-08-263-261-3	Sequence 3, Appli
73	181.5	23.6	247	27	US-09-791-537-24434	Sequence 24434, A
74	180.5	23.5	289	29	US-09-905-247-1	Sequence 1, Appli
75	179.5	23.4	247	21	US-09-120-523-34	Sequence 34, Appl
76	179.5	23.4	247	23	US-09-360-242-34	Sequence 34, Appl
77	179.5	23.4	247	24	US-09-453-851A-34	Sequence 34, Appl
78	179.5	23.4	247	27	US-09-791-537-112051	Sequence 112051,
79	179.5	23.4	247	27	US-09-792-793A-34	Sequence 34, Appl
80	179.5	23.4	247	33	US-10-375-209A-34	Sequence 34, Appl
81	179.5	23.4	248	26	US-09-663-826-7	Sequence 7, Appli
82	179.5	23.4	248	27	US-09-791-537-79197	Sequence 79197, A
83	179.5	23.4	254	27	US-09-791-537-111149	Sequence 111149,
84	179.5	23.4	254	40	US-11-042-707-37	Sequence 37, Appl
85	179.5	23.4	256	40	US-11-042-707-5	Sequence 5, Appli
86	179.5	23.4	256	40	US-11-042-707-38	Sequence 38, Appl
87	179.5	23.4	267	26	US-09-633-516B-11	Sequence 11, Appl
88	179.5	23.4	267	35	US-10-517-707A-1	Sequence 1, Appli
89	179.5	23.4	496	26	US-09-663-826-15	Sequence 15, Appl
90	179	23.3	253	40	US-11-042-707-39	Sequence 39, Appl
91	176.5	23.0	252	23	US-09-347-064-2	Sequence 2, Appli
92	176.5	23.0	252	23	US-09-347-064-8	Sequence 8, Appli
93	176.5	23.0	252	23	US-09-347-064-2	Sequence 2, Appli
94	176.5	23.0	252	23	US-09-347-064-8	Sequence 8, Appli
95	176.5	23.0	252	23	US-09-347-064F-2	Sequence 2, Appli
96	176.5	23.0	252	23	US-09-347-064F-8	Sequence 8, Appli
97	176.5	23.0	252	23	US-09-347-064G-2	Sequence 2, Appli
98	176.5	23.0	252	23	US-09-347-064G-8	Sequence 8, Appli
99	176.5	23.0	252	23	US-09-347-064H-2	Sequence 2, Appli
100	176.5	23.0	252	23	US-09-347-064H-8	Sequence 8, Appli

ALIGNMENTS

```
RESULT 1
US-09-446-351B-1
; Sequence 1, Application US/09446351B
; GENERAL INFORMATION:
;  APPLICANT: De Boer, Mark
;  APPLICANT:  Den Hartog, Marcel Theodorus
;  TITLE OF INVENTION: Anti-CD40L Immunotoxins for the Treatment of Diseases
;  FILE REFERENCE: DE BOER
;  CURRENT APPLICATION NUMBER: US/09/446,351B
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: PCT/NL98/00357
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EP 97201895
;  PRIOR FILING DATE: 1997-06-20
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn ver. 1.0
; SEQ ID NO 1
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Bougainvillea spectrabilis
;   LOCATION: 143
;   OTHER INFORMATION: Trp uncertain
US-09-446-351B-1

  Query Match             100.0%;  Score 768;  DB 24;  Length 149;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-78;
  Matches  149;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |||||||||||||||||||||||||||||
Db        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149


RESULT 2
US-09-446-351D-1
; Sequence 1, Application US/09446351D
; GENERAL INFORMATION:
;  APPLICANT: TANOX PHARMA, INC.
;  APPLICANT:  De Boer, Mark
;  APPLICANT:  MARCEL, Theodorus
;  TITLE OF INVENTION: ANTI-CD40L IMMUNOTOXINS FOR THE TREATMENT OF DISEASES
;  FILE REFERENCE: TNXPHARMA00357
;  CURRENT APPLICATION NUMBER: US/09/446,351D
;  CURRENT FILING DATE:  2000-02-07
;  PRIOR APPLICATION NUMBER: EP97201895.6
;  PRIOR FILING DATE: 1997-06-20
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-09-446-351D-1

  Query Match             100.0%;  Score 768;  DB 24;  Length 149;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-78;
  Matches  149;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |||||||||||||||||||||||||||||
Db        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149


RESULT 3
US-10-758-902-9
; Sequence 9, Application US/10758902
; GENERAL INFORMATION:
;  APPLICANT: Stirpe, Fiorenzo
;  APPLICANT:  Bolognesi, Andrea
;  TITLE OF INVENTION: Type-1 Ribosome-Inactivating Protein
;  FILE REFERENCE: PNJ-005CN
;  CURRENT APPLICATION NUMBER: US/10/758,902
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: US 09/445160
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: EP 97201725.5
;  PRIOR FILING DATE: 1997-06-06
```

```
;  PRIOR APPLICATION NUMBER: PCT/NL98/0336
;  PRIOR FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Bougainvillaea Spectabilis
US-10-758-902-9

  Query Match           100.0%;  Score 768;  DB 37;  Length 149;
  Best Local Similarity  100.0%;  Pred. No. 4.8e-78;
  Matches  149;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |||||||||||||||||||||||||||||
Db        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149


RESULT 4
US-11-084-080-1
; Sequence 1, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis Wild
US-11-084-080-1

  Query Match           97.3%;  Score 747;  DB 40;  Length 250;
  Best Local Similarity  98.7%;  Pred. No. 2.3e-75;
  Matches  147;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |||||||||||||||||||| ||| ||
Db        121 AKVDRKDLELGVYKLEFSIEAIHGKTING 149


RESULT 5
US-11-084-080-129
; Sequence 129, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-129

  Query Match           96.1%;  Score 738;  DB 40;  Length 250;
  Best Local Similarity  98.0%;  Pred. No. 2.4e-74;
  Matches  146;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVAVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              |||||||||||||||||||| ||| ||
Db        121 AKVDRKDLELGVYKLEFSIEAIHGKTING 149


RESULT 6
US-11-084-080-14
; Sequence 14, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
;   LENGTH: 250.
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
```

```
US-11-084-080-14

  Query Match             94.7%;  Score 727;  DB 40;  Length 250;
  Best Local Similarity   96.6%;  Pred. No. 4.3e-73;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        121 AKADRKALELGVQKLEFSIEAIHGKTING 149


RESULT 7
US-11-084-080-13
; Sequence 13, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
US-11-084-080-13

  Query Match             94.5%;  Score 726;  DB 40;  Length 250;
  Best Local Similarity   96.6%;  Pred. No. 5.5e-73;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        121 AKADRKALELGVNKLEFSIEAIHGKTING 149


RESULT 8
US-11-084-080-16
; Sequence 16, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845
US-11-084-080-16

  Query Match             94.5%;  Score 726;  DB 40;  Length 750;
  Best Local Similarity   96.6%;  Pred. No. 2.3e-72;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 313

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 373

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        374 AKADRKALELGVNKLEFSIEAIHGKTING 402


RESULT 9
US-11-084-080-20
; Sequence 20, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-20

  Query Match             94.5%;  Score 726;  DB 40;  Length 750;
  Best Local Similarity   96.6%;  Pred. No. 2.3e-72;
```

```
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 560

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 620

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        621 AKADRKALELGVNKLEFSIEAIHGKTING 649


RESULT 10
US-11-084-080-22
; Sequence 22, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-22

  Query Match             94.5%;  Score 726;  DB 40;  Length 750;
  Best Local Similarity   96.6%;  Pred. No. 2.3e-72;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 82

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 142

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        143 AKADRKALELGVNKLEFSIEAIHGKTING 171


RESULT 11
US-11-084-080-24
; Sequence 24, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
;   LENGTH: 750
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-24

  Query Match             94.5%;  Score 726;  DB 40;  Length 750;
  Best Local Similarity   96.6%;  Pred. No. 2.3e-72;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 329

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 389

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        390 AKADRKALELGVNKLEFSIEAIHGKTING 418


RESULT 12
US-11-084-080-28
; Sequence 28, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
;   LENGTH: 759
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VB6-011
US-11-084-080-28

  Query Match             94.5%;  Score 726;  DB 40;  Length 759;
  Best Local Similarity   96.6%;  Pred. No. 2.3e-72;
  Matches  144;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
```

```
Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 322

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 382

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| ||||| ||||||||| ||| ||
Db        383 AKADRKALELGVNKLEFSIEAIHGKTING 411


RESULT 13
US-11-084-080-11
; Sequence 11, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (123)..(123)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (127)..(127)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (129)..(129)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (133)..(133)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (152)..(152)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-084-080-11

  Query Match           93.9%;  Score 721;  DB 40;  Length 250;
  Best Local Similarity   96.0%;  Pred. No. 2e-72;
  Matches  143;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| | ||| ||||||||| ||| ||
Db        121 AKXDRKXLXLGVXKLEFSIEAIHGKTING 149


RESULT 14
US-11-084-080-12
; Sequence 12, Application US/11084080
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  APPLICANT:  HELLENDOORN, Koen
;  APPLICANT:  CIZEAU, Jeannick
;  APPLICANT:  MACDONALD, Glen Christopher
;  APPLICANT:  ENTWISTLE, Joycelyn
;  APPLICANT:  BOSC, Denis Georges
;  APPLICANT:  GLOVER, Nicholas Ronald
;  TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 10241-44
;  CURRENT APPLICATION NUMBER: US/11/084,080
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/554,580
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: US 60/630,571
;  PRIOR FILING DATE: 2004-11-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Bougainvillea spectabilis
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (123)..(123)
;   OTHER INFORMATION: Xaa can be T or A or Q
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (127)..(127)
;   OTHER INFORMATION: Xaa can be G or A
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (129)..(129)
;   OTHER INFORMATION: Xaa can be Q or G
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (133)..(133)
;   OTHER INFORMATION: Xaa can be N or D or T or A or R or Q or E or G or H or K or S
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (152)..(152)
;   OTHER INFORMATION: Xaa can be Q or A
US-11-084-080-12

  Query Match           93.9%;  Score 721;  DB 40;  Length 250;
  Best Local Similarity   96.0%;  Pred. No. 2e-72;
  Matches  143;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YNTVSFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTV 60

Qy         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNA 120

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGKTQNG 149
              || ||| | ||| ||||||||| ||| ||
Db        121 AKXDRKXLXLGVXKLEFSIEAIHGKTING 149


RESULT 15
```

```
US-07-787-567A-8
; Sequence 8, Application US/07787567A
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/787,567A
;      FILING DATE:  19911104
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gruber, Lewis S.
;      REGISTRATION NUMBER:  30,060
;      REFERENCE/DOCKET NUMBER:  27129/30545
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-787-567A-8

  Query Match             28.8%;  Score 221.5;  DB 7;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 9.7e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 16
US-09-120-523-36
; Sequence 36, Application US/09120523
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT: Coggins, Philip J.
;  TITLE OF INVENTION: Methods and Compositions for Treating
;  TITLE OF INVENTION: Secondary Tissue Damage
;  FILE REFERENCE: OSPRE1100
;  CURRENT APPLICATION NUMBER: US/09/120,523
;  CURRENT FILING DATE: 1998-07-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-09-120-523-36

  Query Match             28.8%;  Score 221.5;  DB 21;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 9.7e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 17
US-09-360-242-36
; Sequence 36, Application US/09360242A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT: Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601B
;  CURRENT APPLICATION NUMBER: US/09/360,242A
;  CURRENT FILING DATE: 1999-07-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-09-360-242-36

  Query Match             28.8%;  Score 221.5;  DB 23;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 9.7e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 18
US-09-453-851A-36
; Sequence 36, Application US/09453851A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601C
;  CURRENT APPLICATION NUMBER: US/09/453,851A
;  CURRENT FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
```

```
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-09-453-851A-36

  Query Match             28.8%;  Score 221.5;  DB 24;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 9.7e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 19
US-09-792-793A-36
; Sequence 36, Application US/09792793A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601D
;  CURRENT APPLICATION NUMBER: US/09/792,793A
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-09-792-793A-36

  Query Match             28.8%;  Score 221.5;  DB 27;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 9.7e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 20
US-10-127-890-8
; Sequence 8, Application US/10127890
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 250 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-127-890-8

  Query Match             28.8%;  Score 221.5;  DB 31;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 9.7e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 21
US-10-375-209A-36
; Sequence 36, Application US/10375209A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601E
;  CURRENT APPLICATION NUMBER: US/10/375,209A
;  CURRENT FILING DATE:  2003-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 250
```

```
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-10-375-209A-36

  Query Match             28.8%;  Score 221.5;  DB 33;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 9.7e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :|  : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 22
US-10-613-755-8
; Sequence 8, Application US/10613755
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/613,755
;             FILING DATE: 02-Jul-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 250 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-613-755-8

  Query Match             28.8%;  Score 221.5;  DB 36;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 9.7e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :|  : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 23
US-10-717-243-8
; Sequence 8, Application US/10717243
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 250 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
```

```
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-717-243-8

  Query Match             28.8%;  Score 221.5;  DB 37;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 9.7e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |     |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 24
US-09-791-537-113633
; Sequence 113633, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 113633
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: synthetic construct
US-09-791-537-113633

  Query Match             28.8%;  Score 221.5;  DB 27;  Length 251;
  Best Local Similarity   37.2%;  Pred. No. 9.8e-16;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |     |:| |:    :|:  :|:  :| : : :
Db         10 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 65

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         66 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 125

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        126 GGL-RKDNPLGIFRLENSIVNIYGK 149


RESULT 25
US-09-791-537-3997
; Sequence 3997, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3997
;   LENGTH: 278
;   TYPE: PRT
;   ORGANISM: Mirabilis jalapa
US-09-791-537-3997

  Query Match             28.8%;  Score 221.5;  DB 27;  Length 278;
  Best Local Similarity   37.2%;  Pred. No. 1.1e-15;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |     |:| |:    :|:  :|:  :| : : :
Db         37 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 92

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         93 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 152

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        153 GGL-RKDNPLGIFRLENSIVNIYGK 176


RESULT 26
US-07-787-567A-4
; Sequence 4, Application US/07787567A
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Steve F.
;    APPLICANT:  Lane, Julie A.
;    TITLE OF INVENTION:  Materials Comprising and Methods of
;    TITLE OF INVENTION:  Preparation and Use for Ribosome-Inactivating Proteins
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/787,567A
;      FILING DATE:  19911104
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gruber, Lewis S.
;      REGISTRATION NUMBER:  30,060
;      REFERENCE/DOCKET NUMBER:  27129/30545
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-787-567A-4

  Query Match             28.7%;  Score 220.5;  DB 7;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 1.3e-15;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |     | .:|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61
```

```
Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :| ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 27
US-10-127-890-4
; Sequence 4, Application US/10127890
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 263 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-127-890-4

  Query Match           28.7%;  Score 220.5;  DB 31;  Length 263;
  Best Local Similarity  36.6%;  Pred. No. 1.3e-15;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      | :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61
```

```
Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138


RESULT 28
US-10-613-755-4
; Sequence 4, Application US/10613755
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/613,755
;             FILING DATE: 02-Jul-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 263 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-613-755-4

  Query Match           28.7%;  Score 220.5;  DB 36;  Length 263;
  Best Local Similarity  36.6%;  Pred. No. 1.3e-15;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      | :|:   ||:| :||:|:|:|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61
```

```
Qy          62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
               ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db          62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy         122 KVDRKDLELGVYKLEFSIEAIW 143
                  |::::||:  |  :|  ::
Db         117 HKIRENIDLGLPALSSAITTLF 138


RESULT 29
US-10-717-243-4
; Sequence 4, Application US/10717243
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 169
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/717,243
;             FILING DATE: 18-Nov-2003
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/839,765
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 08/425,336
;             FILING DATE: 18-APR-1995
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 263 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-717-243-4

  Query Match             28.7%;  Score 220.5;  DB 37;  Length 263;
  Best Local Similarity   36.6%;  Pred. No. 1.3e-15;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy           4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
               |:|:|    |  |  ||:| |  |     |  :|:   ||:| :|||:|:|:|: : :|:
Db           2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61

Qy          62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
               ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db          62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy         122 KVDRKDLELGVYKLEFSIEAIW 143
                  |::::||:  |  :|  ::
Db         117 HKIRENIDLGLPALSSAITTLF 138


RESULT 30
US-08-141-891-13
; Sequence 13, Application US/08141891
;  GENERAL INFORMATION:
;    APPLICANT:  Siegall, Clay B.
;    APPLICANT:  Gawlak, Susan L.
;    APPLICANT:  Marquardt, Hans
;    TITLE OF INVENTION:  A NEW RIBOSOME-INACTIVATING PROTEIN
;    TITLE OF INVENTION:  ISOLATED FROM THE PLANT BRYONIA DIOICA
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/141,891
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-728-4800
;      TELEFAX:  206-727-3601
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  286 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Momordica charantia
US-08-141-891-13

  Query Match             28.7%;  Score 220.5;  DB 11;  Length 286;
  Best Local Similarity   36.6%;  Pred. No. 1.5e-15;
  Matches   52;  Conservative   33;  Mismatches   50;  Indels    7;  Gaps    3;

Qy           4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
               |:|:|    |  |  ||:| |  |     |  :|:   ||:| :|||:|:|:|: : :|:
Db          25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 84

Qy          62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
               ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db          85 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 139

Qy         122 KVDRKDLELGVYKLEFSIEAIW 143
                  |::::||:  |  :|  ::
Db         140 HKIRENIDLGLPALSSAITTLF 161
```

RESULT 31
US-09-791-537-3969
; Sequence 3969, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3969
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Momordica balsamina
US-09-791-537-3969

Query Match 28.7%; Score 220.5; DB 27; Length 286;
Best Local Similarity 36.6%; Pred. No. 1.5e-15;
Matches 52; Conservative 33; Mismatches 50; Indels 7; Gaps 3;

```
Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:|:|: : :|:
Db         25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         85 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 139

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                 |::::||:  |  :|  ::
Db        140 HKIRENIDLGLPALSSAITTLF 161
```

RESULT 32
US-09-791-537-51973
; Sequence 51973, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51973
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Mirabilis jalapa
US-09-791-537-51973

Query Match 28.3%; Score 217.5; DB 27; Length 278;
Best Local Similarity 36.6%; Pred. No. 3.2e-15;
Matches 53; Conservative 27; Mismatches 56; Indels 9; Gaps 4;

```
Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::   |  |    |:| |:   :|:  :|:  :| : : :
Db         37 SLDLNNPTTYLSFITNIRTKVVDKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 92

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    :  |||  |||: ||| |||  |
Db         93 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 152

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        153 GGL-RKDNPLGIFRLENSIVNIYGK 176
```

RESULT 33
US-09-791-537-102332
; Sequence 102332, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102332
; LENGTH: 249
; TYPE: PRT
; ORGANISM: pdb 1CF5A
US-09-791-537-102332

Query Match 28.1%; Score 215.5; DB 27; Length 249;
Best Local Similarity 35.9%; Pred. No. 4.6e-15;
Matches 51; Conservative 34; Mismatches 50; Indels 7; Gaps 3;

```
Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:::|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                 |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138
```

RESULT 34
US-09-791-537-57371
; Sequence 57371, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57371
; LENGTH: 263
; TYPE: PRT
; ORGANISM: pdb 1D8VA
US-09-791-537-57371

Query Match 28.1%; Score 215.5; DB 27; Length 263;
Best Local Similarity 35.9%; Pred. No. 5e-15;
Matches 51; Conservative 34; Mismatches 50; Indels 7; Gaps 3;

```
Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|    |  |  ||:| |  |      |  :|:   ||:| :||:|:::|: : :|:
Db          2 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         62 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 116

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                 |::::||:  |  :|  ::
Db        117 HKIRENIDLGLPALSSAITTLF 138
```

```
RESULT 35
US-09-791-537-56331
; Sequence 56331, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56331
;   LENGTH: 286
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-09-791-537-56331

  Query Match             28.1%;  Score 215.5;  DB 27;  Length 286;
  Best Local Similarity   35.9%;  Pred. No. 5.5e-15;
  Matches   51;  Conservative   34;  Mismatches   50;  Indels    7;  Gaps    3;

Qy          4 VSFNL--GEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |:|:|     |  |  ||:| |  |      |  :|:° ||:| :||:|:::|: : :|:
Db         25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||| |:     :| : |  : |  | : || | | ::|| : |:|: |  ||
Db         85 VAIDVTNVYVVAYRT----RDVSYFFKESPPEAYNILFKG-TRKITLPYTGNYENLQTAA 139

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                 |::::||:  |  :|  ::
Db        140 HKIRENIDLGLPALSSAITTLF 161


RESULT 36
US-09-791-537-116435
; Sequence 116435, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116435
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Mirabilis jalapa
US-09-791-537-116435

  Query Match             27.7%;  Score 212.5;  DB 27;  Length 251;
  Best Local Similarity   37.7%;  Pred. No. 1e-14;
  Matches   55;  Conservative   24;  Mismatches   56;  Indels   11;  Gaps    5;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|     | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITK 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKL-VN 119
              |||: | ||:|| |  : | || |    :  |||   |||: ||| |||  |  |
Db         65 AIDMADKYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        120 AAKVDRKDLELGVYKLEFSIEAIWGK 145
                 |  |||   |:::|| ||  |:||


Db        125 GGK--RKDNPKGIFRLENSIVNIYGK 148


RESULT 37
US-09-791-537-5912
; Sequence 5912, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5912
;   LENGTH: 545
;   TYPE: PRT
;   ORGANISM: Cinnamomum camphora
US-09-791-537-5912

  Query Match             25.3%;  Score 194.5;  DB 27;  Length 545;
  Best Local Similarity   35.8%;  Pred. No. 3.1e-12;
  Matches   53;  Conservative   24;  Mismatches   62;  Indels    9;  Gaps    5;

Qy          1 YNTVSFNLGEAYE--YPTFIQDLRNELAKGTPVCQLPVTLQ--TIADDKRFVLVDITT-T 55
              | ||:|   :| :  |  ||: || :|| |     :||  :  |: | |||:||:::
Db          1 YQTVTFTTKKATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWA 60

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
                :  | :|:|||: ||| |:    |       :  |  |   |  | | | | ||||
Db         61 ADSPVTLAVDVTNAYVVAYR---TGSQSFFLREDNPDPAIENLLPD-TKRYTFPFSGSYT 116

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW 143
                |   |   |::: ||:  || :| |:|
Db        117 DLEGVAGERREEILLGMDPLENAISALW 144


RESULT 38
US-09-791-537-79846
; Sequence 79846, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79846
;   LENGTH: 563
;   TYPE: PRT
;   ORGANISM: Sambucus nigra
US-09-791-537-79846

  Query Match             24.9%;  Score 191;  DB 27;  Length 563;
  Best Local Similarity   36.5%;  Pred. No. 8.1e-12;
  Matches   54;  Conservative   26;  Mismatches   58;  Indels   10;  Gaps    5;

Qy          1 YNTVSFNL--GEAYEYPTFIQDLRNELAKGT-PVCQLPVTLQ--TIADDKRFVLVDITTT 55
              | :|||||   ::  |  |: :||  :| ||  |  |||  :   :    |||||  :|
Db         28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY 87

Qy         56 SKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQ 115
                :  || :|:|||::||| :      |   : |       |  | || | | : ||:| |:|
Db         88 NGNTVTLAVDVTNLYVVAF----SGNANSYFFKDATEVQKSNLFVG-TKQNTLSFTGNYD 142

Qy        116 KLVNAAKVDRKDLELGVYKLEFSIEAIW 143
```

```
                |  ||   |: :|||   |: :| :::
Db        143 NLETAANTRRESIELGPSPLDGAITSLY 170


RESULT 39
US-07-504-775-10
; Sequence 10, Application US/07504775
;  GENERAL INFORMATION:
;    APPLICANT:  Piatak Jr., Michael
;    APPLICANT:  Chow, Theresa P.
;    APPLICANT:  Fry, Kirk
;    TITLE OF INVENTION:  RECOMBINANT TRICHOSANTHIN AND CODING
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Peter Dehlinger
;      STREET:  350 Cambridge Avenue, Suite 300
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/504,775
;      FILING DATE:  19900404
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/333,184
;      FILING DATE:  04-APR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0066.23
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  TRICHOSANTHES KIRILOWII
;    IMMEDIATE SOURCE:
;      LIBRARY:  from pQ21D
US-07-504-775-10

  Query Match             23.9%;  Score 183.5;  DB 5;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     : :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 40
US-08-263-261-10
; Sequence 10, Application US/08263261
;  GENERAL INFORMATION:
;    APPLICANT:  Piatak Jr., Michael
;    APPLICANT:  Chow, Theresa P.
;    APPLICANT:  Fry, Kirk
;    TITLE OF INVENTION:  RECOMBINANT TRICHOSANTHIN AND CODING
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Peter Dehlinger
;      STREET:  350 Cambridge Avenue, Suite 300
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/263,261
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,671
;      FILING DATE:  21-APR-1990
;      APPLICATION NUMBER:  US 07/333,184
;      FILING DATE:  04-APR-1989
;      APPLICATION NUMBER:  US 07/504,775
;      FILING DATE:  4-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0066.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  TRICHOSANTHES KIRILOWII
;    IMMEDIATE SOURCE:
;      LIBRARY:  from pQ21D
US-08-263-261-10

  Query Match             23.9%;  Score 183.5;  DB 12;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     : :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 41
US-09-120-523-39
; Sequence 39, Application US/09120523
; GENERAL INFORMATION:
```

```
;  APPLICANT: McDonald, John R.
;  APPLICANT: Coggins, Philip J.
;  TITLE OF INVENTION: Methods and Compositions for Treating
;  TITLE OF INVENTION: Secondary Tissue Damage
;  FILE REFERENCE: OSPRE1100
;  CURRENT APPLICATION NUMBER: US/09/120,523
;  CURRENT FILING DATE: 1998-07-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthews kirilowii
US-09-120-523-39

  Query Match             23.9%;  Score 183.5;  DB 21;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :||  |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 42
US-09-360-242-39
; Sequence 39, Application US/09360242A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT: Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601B
;  CURRENT APPLICATION NUMBER: US/09/360,242A
;  CURRENT FILING DATE: 1999-07-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthews kirilowii
US-09-360-242-39

  Query Match             23.9%;  Score 183.5;  DB 23;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :||  |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 43
US-09-453-851A-39
; Sequence 39, Application US/09453851A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601C
;  CURRENT APPLICATION NUMBER: US/09/453,851A
;  CURRENT FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthews kirilowii
US-09-453-851A-39

  Query Match             23.9%;  Score 183.5;  DB 24;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :||  |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 44
US-09-791-537-57417
; Sequence 57417, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57417
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthes kirilowii
US-09-791-537-57417

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 247;
  Best Local Similarity   32.4%;  Pred. No. 2e-11;
  Matches   46;  Conservative   30;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :||  |      :  :|:   |:   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||:||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYVMGYR---AGDTSYFFNEASATEAAKYVFKDAKRKVTLPYSGNYERLQIAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 45
US-09-791-537-89783
; Sequence 89783, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
```

```
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89783
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: pdb 1MRJ
US-09-791-537-89783

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||::||:    |      | :  | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 46
US-09-791-537-92216
; Sequence 92216, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92216
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthes kirilowii var
US-09-791-537-92216

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 247;
  Best Local Similarity   32.4%;  Pred. No. 2e-11;
  Matches   46;  Conservative   30;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||.:|| |     :  :|:   |:   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||:||:    |      | :  | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYVMGYR---AGDTSYFFNEASATEAAKYVFKDAKRKVTLPYSGNYERLQIAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 47
US-09-791-537-126580
; Sequence 126580, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 126580
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthes sp
US-09-791-537-126580

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 247;
  Best Local Similarity   32.4%;  Pred. No. 2e-11;
  Matches   46;  Conservative   30;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   |:   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||:||:    |      | :  | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYVMGYR---AGDTSYFFNEASATEAAKYVFKDAKRKVTLPYSGNYERLQIAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 48
US-09-792-793A-39
; Sequence 39, Application US/09792793A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601D
;  CURRENT APPLICATION NUMBER: US/09/792,793A
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthews kirilowii
US-09-792-793A-39

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :|| |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||::||:    |      | :  | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 49
US-09-905-247A-8
; Sequence 8, Application US/09905247A
; GENERAL INFORMATION:
```

```
;  APPLICANT: Ke, Yi-Bao
;  APPLICANT:  Nie, Hui-Ling
;  TITLE OF INVENTION: MUTANT TRICHOSANTHIN
;  FILE REFERENCE: 04399/000J615-US0
;  CURRENT APPLICATION NUMBER: US/09/905,247A
;  CURRENT FILING DATE:  2001-07-13
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthes Kirilowii M.
US-09-905-247A-8

  Query Match             23.9%;  Score 183.5;  DB 29;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 50
US-10-127-890-6
; Sequence 6, Application US/10127890
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
;                   Studnika, Gary M.
;        TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                            Proteins
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;             STREET: 500 West Madison Street, 34th floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60661
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/127,890
;             FILING DATE: 23-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,360
;             FILING DATE: 13-MAY-1996
;             APPLICATION NUMBER: PCT/US94/05348
;             FILING DATE: 12-MAY-1994
;             APPLICATION NUMBER: US 08/064,691
;             FILING DATE: 12-MAY-1993
;             APPLICATION NUMBER: US 07/988,430
;             FILING DATE: 09-DEC-1992
;             APPLICATION NUMBER: US 07/901,707
;             FILING DATE: 19-JUN-1992
;             APPLICATION NUMBER: US 07/787,567
;             FILING DATE: 04-NOV-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McNicholas, Janet M.
;             REGISTRATION NUMBER: 32,918
;             REFERENCE/DOCKET NUMBER: 200-70.P4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/707-8889
;             TELEFAX: 312/707-9155
;             TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 247 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-890-6

  Query Match             23.9%;  Score 183.5;  DB 31;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 51
US-10-375-209A-39
; Sequence 39, Application US/10375209A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601E
;  CURRENT APPLICATION NUMBER: US/10/375,209A
;  CURRENT FILING DATE:  2003-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthews kirilowii
US-10-375-209A-39

  Query Match             23.9%;  Score 183.5;  DB 33;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 52
US-10-613-755-6
; Sequence 6, Application US/10613755
;   GENERAL INFORMATION:
;        APPLICANT: Better, Marc D.
;                   Carroll, Stephen F.
```

```
;                 Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 173
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/613,755
;            FILING DATE: 02-Jul-2003
;            CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,360
;            FILING DATE: 13-MAY-1996
;            APPLICATION NUMBER: PCT/US94/05348
;            FILING DATE: 12-MAY-1994
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 247 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-613-755-6

  Query Match             23.9%;  Score 183.5;  DB 36;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :||  |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|      :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 53
US-10-717-243-6
; Sequence 6, Application US/10717243
;   GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
```

```
;                 Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 169
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/717,243
;            FILING DATE: 18-Nov-2003
;            CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/839,765
;            FILING DATE: 15-APR-1997
;            APPLICATION NUMBER: US 08/425,336
;            FILING DATE: 18-APR-1995
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 247 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-717-243-6

  Query Match             23.9%;  Score 183.5;  DB 37;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :||  |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   | |   :|      :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 54
US-09-791-537-92230
; Sequence 92230, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
```

```
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92230
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Trichosanthes kirilowii var
US-09-791-537-92230

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 249;
  Best Local Similarity   32.4%;  Pred. No. 2e-11;
  Matches   46;  Conservative   30;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |||| |  |    |  || :|| |      :  :|:   |:   :|: |: :|  : :|:
Db          4 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS 63

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||:||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         64 VAIDVTNVYVMGYR---AGDTSYFFNEASATEAAKYVFKDAKRKVTLPYSGNYERLQIAA 120

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        121 GKIRENIPLGLPALDSAITTLF 142


RESULT 55
US-07-504-775-9
; Sequence 9, Application US/07504775
;  GENERAL INFORMATION:
;    APPLICANT:  Piatak Jr., Michael
;    APPLICANT:  Chow, Theresa P.
;    APPLICANT:  Fry, Kirk
;    TITLE OF INVENTION:  RECOMBINANT TRICHOSANTHIN AND CODING
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Peter Dehlinger
;      STREET:  350 Cambridge Avenue, Suite 300
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/504,775
;      FILING DATE:  19900404
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/333,184
;      FILING DATE:  04-APR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0066.23
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  289 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  TRICHOSANTHES KIRILOWII
;    IMMEDIATE SOURCE:
;      CLONE:  from pQ21D
US-07-504-775-9

  Query Match             23.9%;  Score 183.5;  DB 5;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 56
US-07-739-143-4
; Sequence 4, Application US/07739143
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Venable, Baetjer, Howard & Civiletti
;      STREET:  1201 New York Avenue N.W., Suite 1000
;      CITY:  Washington
;      STATE:  DC
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/739,143
;      FILING DATE:  19910801
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
```

```
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ihnen, Jeffrey L.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  18604-090574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-962-4810
;      TELEFAX:  202-962-8300
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  289 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-739-143-4

  Query Match             23.9%;  Score 183.5;  DB 7;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :||  |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 57
US-08-263-261-9
; Sequence 9, Application US/08263261
;  GENERAL INFORMATION:
;    APPLICANT:  Piatak Jr., Michael
;    APPLICANT:  Chow, Theresa P.
;    APPLICANT:  Fry, Kirk
;    TITLE OF INVENTION:  RECOMBINANT TRICHOSANTHIN AND CODING
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Peter Dehlinger
;      STREET:  350 Cambridge Avenue, Suite 300
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/263,261
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,671
;      FILING DATE:  21-APR-1990
;      APPLICATION NUMBER:  US 07/333,184
;      FILING DATE:  04-APR-1989
;      APPLICATION NUMBER:  US 07/504,775
;      FILING DATE:  4-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0066.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  289 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  TRICHOSANTHES KIRILOWII
;    IMMEDIATE SOURCE:
;      CLONE:  from pQ21D
US-08-263-261-9

  Query Match             23.9%;  Score 183.5;  DB 12;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :||  |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |      | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 58
US-08-480-432-4
; Sequence 4, Application US/08480432
;  GENERAL INFORMATION:
;    APPLICANT:  Donson, Jon
;    APPLICANT:  Dawson, William O.
;    APPLICANT:  Grantham, George L.
;    APPLICANT:  Turpen, Thomas H.
;    APPLICANT:  Turpen, Ann Myers
;    APPLICANT:  Garger, Stephen J.
;    APPLICANT:  Grill, Laurence K.
;    TITLE OF INVENTION:  RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent in Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,432
;      FILING DATE:  07-JUNE-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 184,237
;      FILING DATE:  19-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,244
;      FILING DATE:  22-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 641,617
;      FILING DATE:  16-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 310,881
;      FILING DATE:  17-FEB-1989
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,766
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 160,771
;      FILING DATE:  26-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 347,637
;      FILING DATE:  05-MAY-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 363,138
;      FILING DATE:  08-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 219,279
;      FILING DATE:  15-JUL-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  28,957
;      REFERENCE/DOCKET NUMBER:  8129-111
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  289 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-480-432-4

  Query Match             23.9%;  Score 183.5;  DB 14;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 59
US-09-791-537-3999
; Sequence 3999, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3999
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Trichosanthes kirilowii
US-09-791-537-3999

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 60
US-09-791-537-26832
; Sequence 26832, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26832
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Trichosanthes kirilowii
US-09-791-537-26832

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 289;
  Best Local Similarity   31.7%;  Pred. No. 2.4e-11;
  Matches   45;  Conservative   30;  Mismatches   62;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   ::   :|: || :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALVHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTSVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 61
US-09-791-537-55667
; Sequence 55667, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55667
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Trichosanthes kirilowii
US-09-791-537-55667

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
```

```
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 62
US-09-791-537-132717
; Sequence 132717, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 132717
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Trichosanthes kirilowii
US-09-791-537-132717

  Query Match             23.9%;  Score 183.5;  DB 27;  Length 289;
  Best Local Similarity   32.4%;  Pred. No. 2.4e-11;
  Matches   46;  Conservative   30;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   |:   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:|||:||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYVMGYR---AGDTSYFFNEASATEAAKYVFKDAKRKVTLPYSGNYERLQIAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 63
US-09-905-247A-1
; Sequence 1, Application US/09905247A
; GENERAL INFORMATION:
;  APPLICANT: Ke, Yi-Bao
;  APPLICANT:  Nie, Hui-Ling
;  TITLE OF INVENTION: MUTANT TRICHOSANTHIN
;  FILE REFERENCE: 04399/000J615-US0
;  CURRENT APPLICATION NUMBER: US/09/905,247A
;  CURRENT FILING DATE:  2001-07-13
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Trichosanthes Kirilowii M.
US-09-905-247A-1

  Query Match             23.9%;  Score 183.5;  DB 29;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   ::   :|: |: :|  : :|:

Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 64
US-10-280-679B-4
; Sequence 4, Application US/10280679B
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
;  FILE REFERENCE: LSBC-0109-US03
;  CURRENT APPLICATION NUMBER: US/10/280,679B
;  CURRENT FILING DATE:  2000-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Chinese cucumber protein alpha-trichosanthin
US-10-280-679B-4

  Query Match             23.9%;  Score 183.5;  DB 32;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
               |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 65
US-10-280-725B-4
; Sequence 4, Application US/10280725B
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Recombinant Viral Nucleic Acids
;  FILE REFERENCE: LSBC-0109-US02
```

```
;  CURRENT APPLICATION NUMBER: US/10/280,725B
;  CURRENT FILING DATE:  2002-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Chinese cucumber
US-10-280-725B-4

  Query Match             23.9%;  Score 183.5;  DB 32;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-11;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :   | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 66
US-09-791-537-75941
; Sequence 75941, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75941
;   LENGTH: 528
;   TYPE: PRT
;   ORGANISM: Abrus precatorius
US-09-791-537-75941

  Query Match             23.8%;  Score 183;  DB 27;  Length 528;
  Best Local Similarity   33.1%;  Pred. No. 6e-11;
  Matches   46;  Conservative   28;  Mismatches   53;  Indels   12;  Gaps    4;

Qy         14 YPTFIQDLRNELAKG----TPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDV 69
                |  ||: ||  |  |      ||   | |::   :  |:: |::: : :::::| ||||:
Db         17 YKQFIEALRQRLTGGLIHDIPVLPDPTTVE---ERNRYITVELSNSERESIEVGIDVTNA 73

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| |:       :: ||   |  |:: |||| | | :| |||||  |   |   |:::
Db         74 YVVAYR----AGSQSYFLRDAPASASTYLFPG-TQRYSLRFDGSYGDLERWAHQTREEIS 128

Qy        130 LGVYKLEFSIEAIWGKTQN 148
              ||:  |  :|  :     |
Db        129 LGLQALTHAISFLRSGASN 147


RESULT 67
US-09-791-537-78018
; Sequence 78018, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 78018
;   LENGTH: 528
;   TYPE: PRT
;   ORGANISM: Abrus precatorius
US-09-791-537-78018

  Query Match             23.8%;  Score 183;  DB 27;  Length 528;
  Best Local Similarity   33.1%;  Pred. No. 6e-11;
  Matches   46;  Conservative   28;  Mismatches   53;  Indels   12;  Gaps    4;

Qy         14 YPTFIQDLRNELAKG----TPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDV 69
                |  ||: ||  |  |      ||   | |::   :  |:: |::: : :::::| ||||:
Db         17 YKQFIEALRQRLTGGLIHDIPVLPDPTTVE---ERNRYITVELSNSERESIEVGIDVTNA 73

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| |:       :: ||   |  |:: |||| | | :| |||||  |   |   |:::
Db         74 YVVAYR----AGSQSYFLRDAPASASTYLFPG-TQRYSLRFDGSYGDLERWAHQTREEIS 128

Qy        130 LGVYKLEFSIEAIWGKTQN 148
              ||:  |  :|  :     |
Db        129 LGLQALTHAISFLRSGASN 147


RESULT 68
US-09-791-537-110085
; Sequence 110085, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 110085
;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Abrus precatorius
US-09-791-537-110085

  Query Match             23.8%;  Score 183;  DB 27;  Length 562;
  Best Local Similarity   33.1%;  Pred. No. 6.5e-11;
  Matches   46;  Conservative   28;  Mismatches   53;  Indels   12;  Gaps    4;
```

```
Qy         14 YPTFIQDLRNELAKG----TPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              |  ||: ||  |  |      ||   | |::   :  |:: |::: : :::::| ||||:
Db         51 YKQFIEALRQRLTGGLIHDIPVLPDPTTVE---ERNRYITVELSNSERESIEVGIDVTNA 107

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| |:       :: ||   |  |:: |||| | | :| |||||  |   |   |:::
Db        108 YVVAYR----AGSQSYFLRDAPASASTYLFPG-TQRYSLRFDGSYGDLERWAHQTREEIS 162

Qy        130 LGVYKLEFSIEAIWGKTQN 148
              ||:  |  :|  :     |
Db        163 LGLQALTHAISFLRSGASN 181


RESULT 69
US-07-504-775-4
; Sequence 4, Application US/07504775
;  GENERAL INFORMATION:
;    APPLICANT:  Piatak Jr., Michael
;    APPLICANT:  Chow, Theresa P.
;    APPLICANT:  Fry, Kirk
;    TITLE OF INVENTION:  RECOMBINANT TRICHOSANTHIN AND CODING
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Peter Dehlinger
;      STREET:  350 Cambridge Avenue, Suite 300
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/504,775
;      FILING DATE:  19900404
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/333,184
;      FILING DATE:  04-APR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0066.23
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  248 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  TRICHOSANTHES KIRILOWII
;    IMMEDIATE SOURCE:
;      CLONE:  from pQ3
US-07-504-775-4

  Query Match           23.8%;  Score 182.5;  DB 5;  Length 248;
  Best Local Similarity   31.0%;  Pred. No. 2.6e-11;
  Matches   45;  Conservative   32;  Mismatches   61;  Indels    7;  Gaps    3;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKT 59
              | : |::  |     |  ||  ||: | |   | ::|: | : :  :|: |: ::   :||
Db          1 NDIIFSMASADSRSYRKFITSLRSVLPKDGEVFKIPLLLASSSGSRRYKLMQLSNYEEKT 60

Qy         60 VKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLV 118
              : ||||||:||::||         : | ::    ' || :|      ||| : |:|:||
Db         61 ITVAIDVTNVYIMGYL----VNTTSYFFNEPDAATASKFVFTNAQKSVTLPYSGNYEKLQ 116

Qy        119 NAAKVDRKDLELGVYKLEFSIEAIW 143
                 ||   |: : ||:  |  :|  ::
Db        117 TAADKKREKIPLGLPALSSAISTLY 141


RESULT 70
US-08-263-261-4
; Sequence 4, Application US/08263261
;  GENERAL INFORMATION:
;    APPLICANT:  Piatak Jr., Michael
;    APPLICANT:  Chow, Theresa P.
;    APPLICANT:  Fry, Kirk
;    TITLE OF INVENTION:  RECOMBINANT TRICHOSANTHIN AND CODING
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Peter Dehlinger
;      STREET:  350 Cambridge Avenue, Suite 300
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/263,261
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,671
;      FILING DATE:  21-APR-1990
;      APPLICATION NUMBER:  US 07/333,184
;      FILING DATE:  04-APR-1989
;      APPLICATION NUMBER:  US 07/504,775
;      FILING DATE:  4-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0066.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  248 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  TRICHOSANTHES KIRILOWII
;    IMMEDIATE SOURCE:
;      CLONE:  from pQ3
US-08-263-261-4

  Query Match           23.8%;  Score 182.5;  DB 12;  Length 248;
  Best Local Similarity   31.0%;  Pred. No. 2.6e-11;
  Matches   45;  Conservative   32;  Mismatches   61;  Indels    7;  Gaps    3;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKT 59
              | : |::  |     |  ||  ||: | |   | ::|: | : :  :|: |: ::   :||
Db          1 NDIIFSMASADSRSYRKFITSLRSVLPKDGEVFKIPLLLASSSGSRRYKLMQLSNYEEKT 60

Qy         60 VKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLV 118
              : ||||||:||::||         : | ::      || :|      ||| : |:|:||
Db         61 ITVAIDVTNVYIMGYL----VNTTSYFFNEPDAATASKFVFTNAQKSVTLPYSGNYEKLQ 116
```

```
Qy        119 NAAKVDRKDLELGVYKLEFSIEAIW 143
              ||   |: : ||:  |  :|  ::
Db        117 TAADKKREKIPLGLPALSSAISTLY 141


RESULT 71
US-07-504-775-3
; Sequence 3, Application US/07504775
;  GENERAL INFORMATION:
;    APPLICANT:  Piatak Jr., Michael
;    APPLICANT:  Chow, Theresa P.
;    APPLICANT:  Fry, Kirk
;    TITLE OF INVENTION:  RECOMBINANT TRICHOSANTHIN AND CODING
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Peter Dehlinger
;      STREET:  350 Cambridge Avenue, Suite 300
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/504,775
;      FILING DATE:  19900404
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/333,184
;      FILING DATE:  04-APR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0066.23
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  272 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  TRICHOSANTHES KIRILOWII
;    IMMEDIATE SOURCE:
;      CLONE:  from pQ3
US-07-504-775-3

  Query Match             23.8%;  Score 182.5;  DB 5;  Length 272;
  Best Local Similarity   31.0%;  Pred. No. 2.9e-11;
  Matches   45;  Conservative   32;  Mismatches   61;  Indels    7;  Gaps    3;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKT 59
              | : |::  |     |  ||  ||: | |    | ::|: | : :  :|: |: ::   :||
Db         24 NDIIFSMASADSRSYRKFITSLRSVLPKDGEVFKIPLLLASSSGSRRYKLMQLSNYEEKT 83

Qy         60 VKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLV 118
              : ||||||:||::||          : | ::       || :|      ||| : |:|:||
Db         84 ITVAIDVTNVYIMGYL----VNTTSYFFNEPDAATASKFVFTNAQKSVTLPYSGNYEKLQ 139

Qy        119 NAAKVDRKDLELGVYKLEFSIEAIW 143
              ||   |: : ||:  |  :|  ::
Db        140 TAADKKREKIPLGLPALSSAISTLY 164


RESULT 72
```

```
US-08-263-261-3
; Sequence 3, Application US/08263261
;  GENERAL INFORMATION:
;    APPLICANT:  Piatak Jr., Michael
;    APPLICANT:  Chow, Theresa P.
;    APPLICANT:  Fry, Kirk
;    TITLE OF INVENTION:  RECOMBINANT TRICHOSANTHIN AND CODING
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Peter Dehlinger
;      STREET:  350 Cambridge Avenue, Suite 300
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/263,261
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,671
;      FILING DATE:  21-APR-1990
;      APPLICATION NUMBER:  US 07/333,184
;      FILING DATE:  04-APR-1989
;      APPLICATION NUMBER:  US 07/504,775
;      FILING DATE:  4-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0066.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  272 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  TRICHOSANTHES KIRILOWII
;    IMMEDIATE SOURCE:
;      CLONE:  from pQ3
US-08-263-261-3

  Query Match             23.8%;  Score 182.5;  DB 12;  Length 272;
  Best Local Similarity   31.0%;  Pred. No. 2.9e-11;
  Matches   45;  Conservative   32;  Mismatches   61;  Indels    7;  Gaps    3;

Qy          2 NTVSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKT 59
              | : |::  |     |  ||  ||: | |    | ::|: | : :  :|: |: ::   :||
Db         24 NDIIFSMASADSRSYRKFITSLRSVLPKDGEVFKIPLLLASSSGSRRYKLMQLSNYEEKT 83

Qy         60 VKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLV 118
              : ||||||:||::||          : | ::       || :|      ||| : |:|:||
Db         84 ITVAIDVTNVYIMGYL----VNTTSYFFNEPDAATASKFVFTNAQKSVTLPYSGNYEKLQ 139

Qy        119 NAAKVDRKDLELGVYKLEFSIEAIW 143
              ||   |: : ||:  |  :|  ::
Db        140 TAADKKREKIPLGLPALSSAISTLY 164


RESULT 73
US-09-791-537-24434
; Sequence 24434, Application US/09791537
```

```
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24434
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthes kirilowii
US-09-791-537-24434

  Query Match            23.6%;  Score 181.5;  DB 27;  Length 247;
  Best Local Similarity  30.3%;  Pred. No. 3.3e-11;
  Matches   43;  Conservative   33;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || ::|  |     :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNIRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     | :  | |   :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 74
US-09-905-247-1
; Sequence 1, Application US/09905247
; GENERAL INFORMATION:
;  APPLICANT: KE, YI-BAO
;  APPLICANT:  NIE, HUI-LING
;  TITLE OF INVENTION: Mutant Trichosanthin
;  FILE REFERENCE: 04399/000J615-US0
;  CURRENT APPLICATION NUMBER: US/09/905,247
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: CN 00119553.0
;  PRIOR FILING DATE: 2000-08-02
;  PRIOR APPLICATION NUMBER: CN 01103102.6
;  PRIOR FILING DATE: 2001-01-18
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Trichosanthes Kirilowii M.
US-09-905-247-1

  Query Match            23.5%;  Score 180.5;  DB 29;  Length 289;
  Best Local Similarity  31.0%;  Pred. No. 5.3e-11;
  Matches   44;  Conservative   31;  Mismatches   62;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  || :||  |     :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:    |     |     | |   :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNGASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 75
US-09-120-523-34
; Sequence 34, Application US/09120523
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT: Coggins, Philip J.
;  TITLE OF INVENTION: Methods and Compositions for Treating
;  TITLE OF INVENTION: Secondary Tissue Damage
;  FILE REFERENCE: OSPRE1100
;  CURRENT APPLICATION NUMBER: US/09/120,523
;  CURRENT FILING DATE: 1998-07-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Bryonia dioica
US-09-120-523-34

  Query Match            23.4%;  Score 179.5;  DB 21;  Length 247;
  Best Local Similarity  30.8%;  Pred. No. 5.6e-11;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||::||  |     |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140


RESULT 76
US-09-360-242-34
; Sequence 34, Application US/09360242A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT: Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601B
;  CURRENT APPLICATION NUMBER: US/09/360,242A
;  CURRENT FILING DATE: 1999-07-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Bryonia dioica
US-09-360-242-34

  Query Match            23.4%;  Score 179.5;  DB 23;  Length 247;
  Best Local Similarity  30.8%;  Pred. No. 5.6e-11;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||::||  |     |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140


RESULT 77
```

US-09-453-851A-34
; Sequence 34, Application US/09453851A
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601C
; CURRENT APPLICATION NUMBER: US/09/453,851A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Bryonia dioica
US-09-453-851A-34

Query Match 23.4%; Score 179.5; DB 24; Length 247;
Best Local Similarity 30.8%; Pred. No. 5.6e-11;
Matches 44; Conservative 34; Mismatches 58; Indels 7; Gaps 3;

```
Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140
```

RESULT 78
US-09-791-537-112051
; Sequence 112051, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 112051
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Bryonia dioica
US-09-791-537-112051

Query Match 23.4%; Score 179.5; DB 27; Length 247;
Best Local Similarity 30.8%; Pred. No. 5.6e-11;
Matches 44; Conservative 34; Mismatches 58; Indels 7; Gaps 3;

```
Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140
```

RESULT 79

US-09-792-793A-34
; Sequence 34, Application US/09792793A
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Bryonia dioica
US-09-792-793A-34

Query Match 23.4%; Score 179.5; DB 27; Length 247;
Best Local Similarity 30.8%; Pred. No. 5.6e-11;
Matches 44; Conservative 34; Mismatches 58; Indels 7; Gaps 3;

```
Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140
```

RESULT 80
US-10-375-209A-34
; Sequence 34, Application US/10375209A
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Bryonia dioica
US-10-375-209A-34

Query Match 23.4%; Score 179.5; DB 33; Length 247;
Best Local Similarity 30.8%; Pred. No. 5.6e-11;
Matches 44; Conservative 34; Mismatches 58; Indels 7; Gaps 3;

```
Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140
```

RESULT 81
US-09-663-826-7

```
; Sequence 7, Application US/09663826
;  GENERAL INFORMATION:
;       APPLICANT: Russel, David R.
;                  Fuller, James T.
;       TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
;                          PROTEIN TOXINS IN PLANT CELLS
;       NUMBER OF SEQUENCES: 15
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Quarles & Brady
;            STREET: 1 South Pinckney Street
;            CITY: Madison
;            STATE: WI
;            COUNTRY: US
;            ZIP: 53701-2113
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/663,826
;            FILING DATE: 15-Sep-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/902,486
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Seay, Nicholas J.
;            REGISTRATION NUMBER: 27386
;            REFERENCE/DOCKET NUMBER: 670513.90261
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 608-251-5000
;            TELEFAX: 608-251-9166
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 248 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-663-826-7

  Query Match             23.4%;  Score 179.5;  DB 26;  Length 248;
  Best Local Similarity   30.8%;  Pred. No. 5.6e-11;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db          3 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 62

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         63 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 118

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        119 AGKIRENIPLGLPALDSAITTLY 141


RESULT 82
US-09-791-537-79197
; Sequence 79197, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79197
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: pdb 1BRYY
US-09-791-537-79197

  Query Match             23.4%;  Score 179.5;  DB 27;  Length 248;
  Best Local Similarity   30.8%;  Pred. No. 5.6e-11;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db          3 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 62

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||       | : | ::      :| :|     :||| : |:|::|  |
Db         63 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 118

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
              |   |::: ||:  |: :|  ::
Db        119 AGKIRENIPLGLPALDSAITTLY 141


RESULT 83
US-09-791-537-111149
; Sequence 111149, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 111149
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-791-537-111149

  Query Match             23.4%;  Score 179.5;  DB 27;  Length 254;
  Best Local Similarity   37.6%;  Pred. No. 5.8e-11;
  Matches   50;  Conservative   26;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSVTAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   | | : || | | | :| |:|||   |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        130 LGIDQLIQSVTAL 142


RESULT 84
US-11-042-707-37
; Sequence 37, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
```

```
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 37
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1
US-11-042-707-37

  Query Match             23.4%;  Score 179.5;  DB 40;  Length 254;
  Best Local Similarity   37.6%;  Pred. No. 5.8e-11;
  Matches   50;  Conservative   26;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSVTAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:||| |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        130 LGIDQLIQSVTAL 142


RESULT 85
US-11-042-707-5
; Sequence 5, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 5
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Lectin A2
US-11-042-707-5

  Query Match             23.4%;  Score 179.5;  DB 40;  Length 256;
  Best Local Similarity   36.6%;  Pred. No. 5.8e-11;
  Matches   49;  Conservative   27;  Mismatches   49;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : ::  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSITAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||      |:: ||   |  | : || | | :| :| | ||| |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFTGSYTDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 PLGIEQLIQSVSAL 144


RESULT 86
US-11-042-707-38
; Sequence 38, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 38
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A2
US-11-042-707-38

  Query Match             23.4%;  Score 179.5;  DB 40;  Length 256;
  Best Local Similarity   36.6%;  Pred. No. 5.8e-11;
  Matches   49;  Conservative   27;  Mismatches   49;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : ::  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSITAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVT-NRVTLTFDGSYQKLVNAAKVDRKDL 128
              ||| ||      |:: ||   |  | : || | | :| :| | ||| |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTGTTRDRSSLPFTGSYTDLERYAG-HRDQI 130

Qy        129 ELGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 PLGIEQLIQSVSAL 144


RESULT 87
US-09-633-516B-11
; Sequence 11, Application US/09633516B
; GENERAL INFORMATION:
;  APPLICANT: Francis Joseph CARR
;  APPLICANT:  Fiona Suzanne ADAIR
;  APPLICANT:  Anita Anne HAMILTON
;  APPLICANT:  Graham CARTER
;  TITLE OF INVENTION: Modifying Protein Immunogenicity
;  FILE REFERENCE: 112408-120
;  CURRENT APPLICATION NUMBER: US/09/633,516B
;    2000-08-04
;  CURRENT FILING DATE:  2000-08-04
;  PRIOR APPLICATION NUMBER: PCT/GB99/04119
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: GB9826925.1
;  PRIOR FILING DATE: 1998-12-08
;  PRIOR APPLICATION NUMBER: GB9902139.6
;  PRIOR FILING DATE: 1999-02-02
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Bryonia dionia
US-09-633-516B-11

  Query Match             23.4%;  Score 179.5;  DB 26;  Length 267;
  Best Local Similarity   30.8%;  Pred. No. 6.2e-11;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||::||  |     |  :|:   :|:   |: |: :|  : :|:
```

```
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||        | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
                 |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140


RESULT 88
US-10-517-707A-1
; Sequence 1, Application US/10517707A
; GENERAL INFORMATION:
;  APPLICANT: BAKER, Matthew
;  APPLICANT:  CARR, Francis J.
;  TITLE OF INVENTION: MODIFIED BRYODIN 1 WITH REDUCED
;  TITLE OF INVENTION:  IMMUNOGENICITY
;  FILE REFERENCE: MER-134
;  CURRENT APPLICATION NUMBER: US/10/517,707A
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: PCT/EP03/06055
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: EP 02012911.0
;  PRIOR FILING DATE: 2002-06-11
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-707A-1

  Query Match             23.4%;  Score 179.5;  DB 35;  Length 267;
  Best Local Similarity   30.8%;  Pred. No. 6.2e-11;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||::||  |     |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||        | : | ::      :| :|     :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
                 |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140


RESULT 89
US-09-663-826-15
; Sequence 15, Application US/09663826
;   GENERAL INFORMATION:
;        APPLICANT: Russel, David R.
;                   Fuller, James T.
;        TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
;                            PROTEIN TOXINS IN PLANT CELLS
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Quarles & Brady
;             STREET: 1 South Pinckney Street
;             CITY: Madison
;             STATE: WI
;             COUNTRY: US
;             ZIP: 53701-2113
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,826
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/902,486
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Seay, Nicholas J.
;             REGISTRATION NUMBER: 27386
;             REFERENCE/DOCKET NUMBER: 670513.90261
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 608-251-5000
;             TELEFAX: 608-251-9166
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 496 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-663-826-15

  Query Match             23.4%;  Score 179.5;  DB 26;  Length 496;
  Best Local Similarity   30.8%;  Pred. No. 1.4e-10;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |    |  ||::||  |     |  :|:   :|:   |: |: :|  : :|:
Db          3 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 62

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||        | : | ::      :| :|     :||| : |:|::|  |
Db         63 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 118

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
                 |   |::: ||:  |: :|  ::
Db        119 AGKIRENIPLGLPALDSAITTLY 141


RESULT 90
US-11-042-707-39
; Sequence 39, Application US/11042707
; GENERAL INFORMATION:
;  APPLICANT: Morris, Peter
;  APPLICANT:  Stiefel, Thomas
;  APPLICANT:  Voelter, Wolfgang
;  APPLICANT:  Welters, Peter
;  TITLE OF INVENTION: Recombinant Mistletoe Lectins
;  FILE REFERENCE: 29841/36636
;  CURRENT APPLICATION NUMBER: US/11/042,707
;  CURRENT FILING DATE:  2005-01-25
;  PRIOR APPLICATION NUMBER: PCT/EP99/00696
;  PRIOR FILING DATE: 1999-02-03
;  PRIOR APPLICATION NUMBER: D 198 04 210.8
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 39
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mistletoe lectin A1 (matched)
US-11-042-707-39

  Query Match             23.3%;  Score 179;  DB 40;  Length 253;
  Best Local Similarity   36.8%;  Pred. No. 6.5e-11;
  Matches   49;  Conservative   27;  Mismatches   47;  Indels   10;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|   : :|  |||||:
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGQDSVTAAIDVTNA 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
```

```
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |    : :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYA--GHRQIP 128

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        129 LGIDQLIQSVTAL 141


RESULT 91
US-09-347-064-2
; Sequence 2, Application US/09347064
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064-2

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         17 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 76

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   | :
Db         77 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 130

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 LGIDQLIQSVTAL 143


RESULT 92
US-09-347-064-8
; Sequence 8, Application US/09347064
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
.
US-09-347-064-8

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   | :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        130 LGIDQLIQSVTAL 142


RESULT 93
US-09-347-064-2
; Sequence 2, Application US/09347064A
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064-2

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         17 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 76

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   | :
Db         77 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 130

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 LGIDQLIQSVTAL 143


RESULT 94
US-09-347-064-8
; Sequence 8, Application US/09347064A
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT: Schmidt, Arno
;  APPLICANT: Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION: album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064A
```

```
;  CURRENT FILING DATE: 1999-07-02
;  EARLIER APPLICATION NUMBER: PCT/EP98/00009
;  EARLIER FILING DATE: 1998-01-02
;  EARLIER APPLICATION NUMBER: EP 97 10 0012.0
;  EARLIER FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064-8

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        130 LGIDQLIQSVTAL 142


RESULT 95
US-09-347-064F-2
; Sequence 2, Application US/09347064F
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION:  Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION:  album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064F
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064F-2

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         17 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 76

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   |  :
Db         77 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 130

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        131 LGIDQLIQSVTAL 143


RESULT 96
US-09-347-064F-8
; Sequence 8, Application US/09347064F
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION:  Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION:  album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064F
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064F-8

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 75

Qy         70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
              ||| ||      |:: ||   |  | : || | | | :| |:|||  |   |   |  :
Db         76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy        130 LGVYKLEFSIEAI 142
              ||: :|  |: |:
Db        130 LGIDQLIQSVTAL 142


RESULT 97
US-09-347-064G-2
; Sequence 2, Application US/09347064G
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION:  Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION:  album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064G
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064G-2

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy         13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
              ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db         17 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 76
```

```
Qy          70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
               ||| ||       |:: ||    |  | : || | | | :| |:|||  |    |   | :
Db          77 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 130

Qy         130 LGVYKLEFSIEAI 142
               ||: :|  |: |:
Db         131 LGIDQLIQSVTAL 143


RESULT 98
US-09-347-064G-8
; Sequence 8, Application US/09347064G
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on
;  TITLE OF INVENTION:  Ribosome-Inactivating Proteins of the mistletoe Viscum
;  TITLE OF INVENTION:  album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064G
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064G-8

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy          13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
               ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db          16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 75

Qy          70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
               ||| ||       |:: ||    |  | : || | | | :| |:|||  |    |   | :
Db          76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy         130 LGVYKLEFSIEAI 142
               ||: :|  |: |:
Db         130 LGIDQLIQSVTAL 142


RESULT 99
US-09-347-064H-2
; Sequence 2, Application US/09347064H
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on Ribosome-
;  TITLE OF INVENTION:  Inactivating Proteins of
;  TITLE OF INVENTION:  the Mistletoe Viscum album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064H
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064H-2

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy          13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
               ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db          17 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 76

Qy          70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
               ||| ||       |:: ||    |  | : || | | | :| |:|||  |    |   | :
Db          77 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 130

Qy         130 LGVYKLEFSIEAI 142
               ||: :|  |: |:
Db         131 LGIDQLIQSVTAL 143


RESULT 100
US-09-347-064H-8
; Sequence 8, Application US/09347064H
; GENERAL INFORMATION:
;  APPLICANT: Eck, Jurgen
;  APPLICANT:  Schmidt, Arno
;  APPLICANT:  Zinke, Holger
;  TITLE OF INVENTION: Recombinant Fusion Proteins Based on Ribosome-
;  TITLE OF INVENTION:  Inactivating Proteins of
;  TITLE OF INVENTION:  the Mistletoe Viscum album
;  FILE REFERENCE: 09282-5
;  CURRENT APPLICATION NUMBER: US/09/347,064H
;  CURRENT FILING DATE:  1999-07-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/00009
;  PRIOR FILING DATE: 1998-01-02
;  PRIOR APPLICATION NUMBER: EP 97 10 0012.0
;  PRIOR FILING DATE: 1997-01-02
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Viscum album
US-09-347-064H-8

  Query Match             23.0%;  Score 176.5;  DB 23;  Length 252;
  Best Local Similarity   36.8%;  Pred. No. 1.3e-10;
  Matches   49;  Conservative   27;  Mismatches   48;  Indels    9;  Gaps    4;

Qy          13 EYPTFIQDLRNELAKGTPVCQLPVTLQT---IADDKRFVLVDITTTSKKTVKVAIDVTDV 69
               ||  ||  ||: :: |:   ::|:  |:   ::| :|||||::|     ::  |||||::
Db          16 EYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNL 75

Qy          70 YVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLE 129
               ||| ||       |:: ||    |  | : || | | | :| |:|||  |    |   | :
Db          76 YVVAYQ----AGDQSYFLRDAPRGAETHLFTG-TTRSSLPFNGSYPDLERYAG-HRDQIP 129

Qy         130 LGVYKLEFSIEAI 142
               ||: :|  |: |:
Db         130 LGIDQLIQSVTAL 142


Search completed: September 18, 2006, 19:30:09
Job time : 725.693 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 18, 2006, 19:15:47 ; Search time 51.6089 Seconds
(without alignments)
303.155 Million cell updates/sec

Title: US-10-758-902-9
Perfect score: 768
Sequence: 1 YNTVSFNLGEAYEYPTFIQD.....LGVYKLEFSIEAIWGKTQNG 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 428092 seqs, 105003536 residues

Total number of hits satisfying chosen parameters: 428092

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending_Patents_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	221.5	28.8	250	7	US-11-361-977A-36	Sequence 36, Appl
2	183.5	23.9	247	7	US-11-361-977A-39	Sequence 39, Appl
3	183.5	23.9	289	6	US-10-280-725D-4	Sequence 4, Appli
4	179.5	23.4	247	7	US-11-361-977A-34	Sequence 34, Appl
5	104.5	13.6	254	7	US-11-361-977A-85	Sequence 85, Appl
6	104.5	13.6	275	7	US-11-361-977A-35	Sequence 35, Appl
7	104.5	13.6	327	7	US-11-361-977A-79	Sequence 79, Appl
8	104.5	13.6	330	7	US-11-361-977A-82	Sequence 82, Appl
9	104.5	13.6	332	7	US-11-361-977A-73	Sequence 73, Appl
10	104.5	13.6	332	7	US-11-361-977A-76	Sequence 76, Appl
11	82.5	10.7	179	7	US-11-434-137-7206	Sequence 7206, Ap
12	82.5	10.7	179	7	US-11-434-184-7206	Sequence 7206, Ap
13	82.5	10.7	179	7	US-11-434-203-7206	Sequence 7206, Ap
14	82.5	10.7	179	7	US-11-434-127-7206	Sequence 7206, Ap
15	82.5	10.7	179	7	US-11-434-199-7206	Sequence 7206, Ap
16	82	10.7	1167	7	US-11-434-137-5140	Sequence 5140, Ap
17	82	10.7	1167	7	US-11-434-184-5140	Sequence 5140, Ap
18	82	10.7	1167	7	US-11-434-203-5140	Sequence 5140, Ap
19	82	10.7	1167	7	US-11-434-127-5140	Sequence 5140, Ap
20	82	10.7	1167	7	US-11-434-199-5140	Sequence 5140, Ap
21	81.5	10.6	241	1	PCT-US06-18535-5915	Sequence 5915, Ap
22	81.5	10.6	241	7	US-11-431-855-5915	Sequence 5915, Ap
23	79.5	10.4	1184	8	US-60-838-415-16584	Sequence 16584, A
24	78.5	10.2	166	7	US-11-434-137-7210	Sequence 7210, Ap
25	78.5	10.2	166	7	US-11-434-184-7210	Sequence 7210, Ap
26	78.5	10.2	166	7	US-11-434-203-7210	Sequence 7210, Ap
27	78.5	10.2	166	7	US-11-434-127-7210	Sequence 7210, Ap
28	78.5	10.2	166	7	US-11-434-199-7210	Sequence 7210, Ap
29	78.5	10.2	177	7	US-11-434-137-7126	Sequence 7126, Ap
30	78.5	10.2	177	7	US-11-434-184-7126	Sequence 7126, Ap
31	78.5	10.2	177	7	US-11-434-203-7126	Sequence 7126, Ap
32	78.5	10.2	177	7	US-11-434-127-7126	Sequence 7126, Ap
33	78.5	10.2	177	7	US-11-434-199-7126	Sequence 7126, Ap
34	78.5	10.2	197	7	US-11-434-137-7204	Sequence 7204, Ap
35	78.5	10.2	197	7	US-11-434-184-7204	Sequence 7204, Ap
36	78.5	10.2	197	7	US-11-434-203-7204	Sequence 7204, Ap
37	78.5	10.2	197	7	US-11-434-127-7204	Sequence 7204, Ap
38	78.5	10.2	197	7	US-11-434-199-7204	Sequence 7204, Ap
39	78.5	10.2	219	7	US-11-434-137-7220	Sequence 7220, Ap
40	78.5	10.2	219	7	US-11-434-184-7220	Sequence 7220, Ap
41	78.5	10.2	219	7	US-11-434-203-7220	Sequence 7220, Ap
42	78.5	10.2	219	7	US-11-434-127-7220	Sequence 7220, Ap
43	78.5	10.2	219	7	US-11-434-199-7220	Sequence 7220, Ap
44	78.5	10.2	234	7	US-11-434-137-6972	Sequence 6972, Ap
45	78.5	10.2	234	7	US-11-434-137-10774	Sequence 10774, A
46	78.5	10.2	234	7	US-11-434-184-6972	Sequence 6972, Ap
47	78.5	10.2	234	7	US-11-434-184-10774	Sequence 10774, A
48	78.5	10.2	234	7	US-11-434-203-6972	Sequence 6972, Ap
49	78.5	10.2	234	7	US-11-434-203-10774	Sequence 10774, A
50	78.5	10.2	234	7	US-11-434-127-6972	Sequence 6972, Ap
51	78.5	10.2	234	7	US-11-434-127-10774	Sequence 10774, A
52	78.5	10.2	234	7	US-11-434-199-6972	Sequence 6972, Ap
53	78.5	10.2	234	7	US-11-434-199-10774	Sequence 10774, A
54	78.5	10.2	258	7	US-11-434-137-6970	Sequence 6970, Ap
55	78.5	10.2	258	7	US-11-434-184-6970	Sequence 6970, Ap
56	78.5	10.2	258	7	US-11-434-203-6970	Sequence 6970, Ap
57	78.5	10.2	258	7	US-11-434-127-6970	Sequence 6970, Ap
58	78.5	10.2	258	7	US-11-434-199-6970	Sequence 6970, Ap
59	78.5	10.2	392	7	US-11-434-137-758	Sequence 758, App
60	78.5	10.2	392	7	US-11-434-184-758	Sequence 758, App
61	78.5	10.2	392	7	US-11-434-203-758	Sequence 758, App
62	78.5	10.2	392	7	US-11-434-127-758	Sequence 758, App
63	78.5	10.2	392	7	US-11-434-199-758	Sequence 758, App
64	78.5	10.2	454	7	US-11-434-137-9592	Sequence 9592, Ap
65	78.5	10.2	454	7	US-11-434-184-9592	Sequence 9592, Ap
66	78.5	10.2	454	7	US-11-434-203-9592	Sequence 9592, Ap
67	78.5	10.2	454	7	US-11-434-127-9592	Sequence 9592, Ap
68	78.5	10.2	454	7	US-11-434-199-9592	Sequence 9592, Ap
69	78.5	10.2	467	7	US-11-434-137-764	Sequence 764, App
70	78.5	10.2	467	7	US-11-434-184-764	Sequence 764, App
71	78.5	10.2	467	7	US-11-434-203-764	Sequence 764, App
72	78.5	10.2	467	7	US-11-434-127-764	Sequence 764, App
73	78.5	10.2	467	7	US-11-434-199-764	Sequence 764, App
74	78.5	10.2	1389	7	US-11-434-137-9594	Sequence 9594, Ap
75	78.5	10.2	1389	7	US-11-434-184-9594	Sequence 9594, Ap
76	78.5	10.2	1389	7	US-11-434-203-9594	Sequence 9594, Ap
77	78.5	10.2	1389	7	US-11-434-127-9594	Sequence 9594, Ap
78	78.5	10.2	1389	7	US-11-434-199-9594	Sequence 9594, Ap
79	76.5	10.0	242	7	US-11-434-137-7202	Sequence 7202, Ap
80	76.5	10.0	242	7	US-11-434-184-7202	Sequence 7202, Ap
81	76.5	10.0	242	7	US-11-434-203-7202	Sequence 7202, Ap
82	76.5	10.0	242	7	US-11-434-127-7202	Sequence 7202, Ap
83	76.5	10.0	242	7	US-11-434-199-7202	Sequence 7202, Ap
84	75.5	9.8	1274	8	US-60-836-986-5988	Sequence 5988, Ap
85	75.5	9.8	1314	8	US-60-836-986-5989	Sequence 5989, Ap
86	75.5	9.8	1353	8	US-60-836-986-5987	Sequence 5987, Ap
87	73.5	9.6	341	7	US-11-434-137-8456	Sequence 8456, Ap
88	73.5	9.6	341	7	US-11-434-184-8456	Sequence 8456, Ap
89	73.5	9.6	341	7	US-11-434-203-8456	Sequence 8456, Ap
90	73.5	9.6	341	7	US-11-434-127-8456	Sequence 8456, Ap
91	73.5	9.6	341	7	US-11-434-199-8456	Sequence 8456, Ap
92	73	9.5	372	6	US-10-805-394A-6425	Sequence 6425, Ap
93	73	9.5	372	7	US-11-508-066-42	Sequence 42, Appl
94	73	9.5	2172	7	US-11-027-891A-5266	Sequence 5266, Ap
95	73	9.5	2172	7	US-11-027-879A-5266	Sequence 5266, Ap
96	73	9.5	2172	7	US-11-027-892A-5266	Sequence 5266, Ap
97	72.5	9.4	288	1	PCT-US06-18535-4363	Sequence 4363, Ap
98	72.5	9.4	288	7	US-11-431-855-4363	Sequence 4363, Ap

99	72.5	9.4	369	1	PCT-US06-18535-10164	Sequence 10164, A
100	72.5	9.4	369	7	US-11-431-855-10164	Sequence 10164, A

ALIGNMENTS

```
RESULT 1
US-11-361-977A-36
; Sequence 36, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Momordica charantia
US-11-361-977A-36

  Query Match             28.8%;  Score 221.5;  DB 7;  Length 250;
  Best Local Similarity   37.2%;  Pred. No. 4.7e-14;
  Matches   54;  Conservative   27;  Mismatches   55;  Indels    9;  Gaps    4;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIAD--DKRFVLVDITTTSKKTVKV 62
              | :|      | :|| ::| ::|  |  |    |:| |:    :|:  :|:  :| : : :
Db          9 SLDLNNPTTYLSFITNIRTKVADKTEQC----TIQKISKTFTQRYSYIDLIVSSTQKITL 64

Qy         63 AIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGV--TNRVTLTFDGSYQKLVNA 120
              |||: |:||:|| |  : | || |    |      :  |||   |||: ||| |||  |
Db         65 AIDMADLYVLGYSDIANNKGRAFFFKDVTEAVANNFFPGATGTNRIKLTFTGSYGDLEKN 124

Qy        121 AKVDRKDLELGVYKLEFSIEAIWGK 145
                : |||  ||:::|| ||  |:||
Db        125 GGL-RKDNPLGIFRLENSIVNIYGK 148


RESULT 2
US-11-361-977A-39
; Sequence 39, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Trichosanthews kirilowii
US-11-361-977A-39

  Query Match             23.9%;  Score 183.5;  DB 7;  Length 247;
  Best Local Similarity   31.0%;  Pred. No. 2.4e-10;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db          2 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   :|    :|     :||| : |:|::|  ||
Db         62 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 118

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        119 GKIRENIPLGLPALDSAITTLF 140


RESULT 3
US-10-280-725D-4
; Sequence 4, Application US/10280725D
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology Corporation
;  TITLE OF INVENTION: Recombinant Viral Nucleic Acids
;  FILE REFERENCE: LSBC-0109-US02
;  CURRENT APPLICATION NUMBER: US/10/280,725D
;  CURRENT FILING DATE:  2002-10-24
;  PRIOR APPLICATION NUMBER: 09/557,941
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 08/484,341
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 07/923,692
;  PRIOR FILING DATE: 1992-07-31
;  PRIOR APPLICATION NUMBER: 07/600,244
;  PRIOR FILING DATE: 1990-10-22
;  PRIOR APPLICATION NUMBER: 07/641,617
;  PRIOR FILING DATE: 1991-01-16
;  PRIOR APPLICATION NUMBER: 07/737,899
;  PRIOR FILING DATE: 1991-07-26
;  PRIOR APPLICATION NUMBER: 07/739,143
;  PRIOR FILING DATE: 1991-08-01
;  PRIOR APPLICATION NUMBER: 07/310,881
;  PRIOR FILING DATE: 1989-02-17
;  PRIOR APPLICATION NUMBER: 07/160,766
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 07/160,771
;  PRIOR FILING DATE: 1988-02-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Trichosanthes kirilowii
US-10-280-725D-4

  Query Match             23.9%;  Score 183.5;  DB 6;  Length 289;
  Best Local Similarity   31.0%;  Pred. No. 2.9e-10;
  Matches   44;  Conservative   32;  Mismatches   61;  Indels    5;  Gaps    2;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              ||| |  |     |  || :|| |      :  :|:   ::   :|: |: :|  : :|:
Db         25 VSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETIS 84

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
              ||||||:||::||:     |      | :   :|    :|     :||| : |:|::|  ||
Db         85 VAIDVTNVYIMGYR---AGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAA 141

Qy        122 KVDRKDLELGVYKLEFSIEAIW 143
                |::: ||:  |: :|  ::
Db        142 GKIRENIPLGLPALDSAITTLF 163


RESULT 4
US-11-361-977A-34
; Sequence 34, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
```

```
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Bryonia dioica
US-11-361-977A-34

  Query Match             23.4%;  Score 179.5;  DB 7;  Length 247;
  Best Local Similarity   30.8%;  Pred. No. 6e-10;
  Matches   44;  Conservative   34;  Mismatches   58;  Indels    7;  Gaps    3;

Qy          4 VSFNLGEA--YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVK 61
              |||  |   |    |  ||::||  |      |  :|:   :|:   |: |: :|  : :|:
Db          2 VSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETIS 61

Qy         62 VAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSK-LFPGVTNRVTLTFDGSYQKLVNA 120
              ||:|||:||::||      | : | ::      :| :|    :||| : |:|::|  |
Db         62 VAVDVTNVYIMGYL----AGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTA 117

Qy        121 AKVDRKDLELGVYKLEFSIEAIW 143
                 |   |::: ||:  |: :|  ::
Db        118 AGKIRENIPLGLPALDSAITTLY 140


RESULT 5
US-11-361-977A-85
; Sequence 85, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Methionine-Saporin fusion pro
US-11-361-977A-85

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 254;
  Best Local Similarity   23.8%;  Pred. No. 0.014;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy         11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
                | :| :|:  :|| :         || :  :           ::|: ::   :|: || : :
Db         14 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 67

Qy         65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
                ::||| |   |  :      |  :: :  :: |||  |  |:  | :   || :
Db         68 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 127

Qy        121 AKV-----DRKDLELGVYKLEFSIEAI 142
                |::      ||:| ||:  |  |:||:
Db        128 AQITQGDQSRKELGLGIDLLSTSMEAV 154


RESULT 6
US-11-361-977A-35
; Sequence 35, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 275
;   TYPE: PRT
;   ORGANISM: Saponaria officinalis
US-11-361-977A-35

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 275;
  Best Local Similarity   23.8%;  Pred. No. 0.015;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy         11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
                | :| :|:  :|| :         || :  :           ::|: ::   :|: || : :
Db         13 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 66

Qy         65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
                ::||| |   |  :      |  :: :  :: |||  |  |:  | :   || :
Db         67 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 126

Qy        121 AKV-----DRKDLELGVYKLEFSIEAI 142
                |::      ||:| ||:  |  |:||:
Db        127 AQITQGDQSRKELGLGIDLLSTSMEAV 153


RESULT 7
US-11-361-977A-79
; Sequence 79, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 327
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protei
;   OTHER INFORMATION: SDF-1-Beta-AM-SAPORIN
US-11-361-977A-79

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 327;
  Best Local Similarity   23.8%;  Pred. No. 0.018;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy         11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
                | :| :|:  :|| :         || :  :           ::|: ::   :|: || : :
Db         87 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 140

Qy         65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
                ::||| |   |  :      |  :: :  :: |||  |  |:  | :   || :
Db        141 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 200

Qy        121 AKV-----DRKDLELGVYKLEFSIEAI 142
                |::      ||:| ||:  |  |:||:
Db        201 AQITQGDQSRKELGLGIDLLSTSMEAV 227


RESULT 8
US-11-361-977A-82
; Sequence 82, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
```

```
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protei
;   OTHER INFORMATION: EOTAXIN-AM-SAPORIN
US-11-361-977A-82

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 330;
  Best Local Similarity   23.8%;  Pred. No. 0.018;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy         11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
                | :| :|:  :|| :         || :  :           ::|: ::   :|: || : :
Db         90 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 143

Qy         65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
                ::||| |    |  :       |  :: :  :: |||  |  |:  | :   || :
Db        144 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 203

Qy        121 AKV-----DRKDLELGVYKLEFSIEAI 142
                |::      ||:| ||:  |  |:||:
Db        204 AQITQGDQSRKELGLGIDLLSTSMEAV 230


RESULT 9
US-11-361-977A-73
; Sequence 73, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
;   LENGTH: 332
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protei
;   OTHER INFORMATION: MCP1-AM-SAPORIN
US-11-361-977A-73

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 332;
  Best Local Similarity   23.8%;  Pred. No. 0.018;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy         11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
                | :| :|:  :|| :         || :  :           ::|: ::   :|: || : :
Db         92 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 145

Qy         65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
                ::||| |    |  :       |  :: :  :: |||  |  |:  | :   || :
Db        146 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 205

Qy        121 AKV-----DRKDLELGVYKLEFSIEAI 142
                |::      ||:| ||:  |  |:||:
Db        206 AQITQGDQSRKELGLGIDLLSTSMEAV 232


RESULT 10
US-11-361-977A-76
; Sequence 76, Application US/11361977A
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 17080-002005/601F
;  CURRENT APPLICATION NUMBER: US/11/361,977A
;  CURRENT FILING DATE:  2006-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;   LENGTH: 332
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Chemokine-toxin Fusion Protei
;   OTHER INFORMATION: MCP3-AM-SAPORIN
US-11-361-977A-76

  Query Match             13.6%;  Score 104.5;  DB 7;  Length 332;
  Best Local Similarity   23.8%;  Pred. No. 0.018;
  Matches   35;  Conservative   33;  Mismatches   58;  Indels   21;  Gaps    6;

Qy         11 AYEYPTFIQDLRNELAK------GTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAI 64
                | :| :|:  :|| :         || :  :           ::|: ::   :|: || : :
Db         92 AGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGP-----PSKEKFLRINF-QSSRGTVSLGL 145

Qy         65 DVTDVYVVGY--QDKWDGKDRAVFLDKVPTVATSKLFPGVT--NRVTLTFDGSYQKLVNA 120
                ::||| |    |  :       |  :: :  :: |||  |  |:  | :   || :
Db        146 KRDNLYVVAYLAMDNTNVNRAYYFRSEITSAESTALFPEATTANQKALEYTEDYQSIEKN 205

Qy        121 AKV-----DRKDLELGVYKLEFSIEAI 142
                |::      ||:| ||:  |  |:||:
Db        206 AQITQGDQSRKELGLGIDLLSTSMEAV 232


RESULT 11
US-11-434-137-7206
; Sequence 7206, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7206
;   LENGTH: 179
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(179)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-137-7206

  Query Match             10.7%;  Score 82.5;  DB 7;  Length 179;
  Best Local Similarity   30.8%;  Pred. No. 1.3;
  Matches   33;  Conservative   14;  Mismatches   57;  Indels    3;  Gaps    3;
```

```
Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : | |     |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGKTPKAEDSIGNLPDLPKGTTVAFE 142
```

RESULT 12
US-11-434-184-7206
; Sequence 7206, Application US/11434184
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,184
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7206
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(179)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-184-7206

Query Match 10.7%; Score 82.5; DB 7; Length 179;
Best Local Similarity 30.8%; Pred. No. 1.3;
Matches 33; Conservative 14; Mismatches 57; Indels 3; Gaps 3;

```
Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : | |     |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGKTPKAEDSIGNLPDLPKGTTVAFE 142
```

RESULT 13
US-11-434-203-7206
; Sequence 7206, Application US/11434203
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,203
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7206
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(179)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-203-7206

Query Match 10.7%; Score 82.5; DB 7; Length 179;
Best Local Similarity 30.8%; Pred. No. 1.3;
Matches 33; Conservative 14; Mismatches 57; Indels 3; Gaps 3;

```
Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : | |     |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGKTPKAEDSIGNLPDLPKGTTVAFE 142
```

RESULT 14
US-11-434-127-7206
; Sequence 7206, Application US/11434127
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Masignani, Vega
; APPLICANT: Ros, Immaculada Margarit Y
; APPLICANT: Fraser, Claire
; APPLICANT: Tettelin, Herve
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/434,127
; CURRENT FILING DATE: 2006-05-16
; PRIOR APPLICATION NUMBER: US 10/415,182
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/GB01/04789
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12025
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7206
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(179)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-127-7206

Query Match 10.7%; Score 82.5; DB 7; Length 179;
Best Local Similarity 30.8%; Pred. No. 1.3;
Matches 33; Conservative 14; Mismatches 57; Indels 3; Gaps 3;

```
Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
```

```
                |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : | |     |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGKTPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 15
US-11-434-199-7206
; Sequence 7206, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7206
;   LENGTH: 179
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(179)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-199-7206

  Query Match             10.7%;  Score 82.5;  DB 7;  Length 179;
  Best Local Similarity   30.8%;  Pred. No. 1.3;
  Matches   33;  Conservative   14;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : | |     |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGKTPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 16
US-11-434-137-5140
; Sequence 5140, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5140
;   LENGTH: 1167
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-137-5140

  Query Match             10.7%;  Score 82;  DB 7;  Length 1167;
  Best Local Similarity   30.6%;  Pred. No. 12;
  Matches   30;  Conservative   11;  Mismatches   35;  Indels   22;  Gaps    4;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT 92
              ||   |||  |||:  | |:   ||   |   |:     : |: :|        || :|
Db        241 QLEKALQTAQDDKKSYLEDVLAVSKNGFKHK-DIRKFQSLFYEKEWS------LLDYIP- 292

Qy         93 VATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLEL 130
                        : |  |   :||||:  |  | |||:
Db        293 -----------KGTPIFFDDFQKLVD--KNARFDLEI 316


RESULT 17
US-11-434-184-5140
; Sequence 5140, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5140
;   LENGTH: 1167
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-184-5140

  Query Match             10.7%;  Score 82;  DB 7;  Length 1167;
  Best Local Similarity   30.6%;  Pred. No. 12;
  Matches   30;  Conservative   11;  Mismatches   35;  Indels   22;  Gaps    4;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT 92
              ||   |||  |||:  | |:   ||   |   |:     : |: :|        || :|
Db        241 QLEKALQTAQDDKKSYLEDVLAVSKNGFKHK-DIRKFQSLFYEKEWS------LLDYIP- 292

Qy         93 VATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLEL 130
                        : |  |   :||||:  |  | |||:
Db        293 -----------KGTPIFFDDFQKLVD--KNARFDLEI 316


RESULT 18
US-11-434-203-5140
```

```
; Sequence 5140, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5140
;   LENGTH: 1167
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-203-5140

  Query Match             10.7%;  Score 82;  DB 7;  Length 1167;
  Best Local Similarity   30.6%;  Pred. No. 12;
  Matches   30;  Conservative   11;  Mismatches   35;  Indels   22;  Gaps    4;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT 92
              ||   |||  |||:  | |:   ||   |   |:     : |: :|        || :|
Db        241 QLEKALQTAQDDKKSYLEDVLAVSKNGFKHK-DIRKFQSLFYEKEWS------LLDYIP- 292

Qy         93 VATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLEL 130
                       : |  |   :||||:  |  | |||:
Db        293 -----------KGTPIFFDDFQKLVD--KNARFDLEI 316


RESULT 19
US-11-434-127-5140
; Sequence 5140, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5140
;   LENGTH: 1167
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-127-5140

  Query Match             10.7%;  Score 82;  DB 7;  Length 1167;
  Best Local Similarity   30.6%;  Pred. No. 12;
  Matches   30;  Conservative   11;  Mismatches   35;  Indels   22;  Gaps    4;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT 92
              ||   |||  |||:  | |:   ||   |   |:     : |: :|        || :|
Db        241 QLEKALQTAQDDKKSYLEDVLAVSKNGFKHK-DIRKFQSLFYEKEWS------LLDYIP- 292

Qy         93 VATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLEL 130
                       : |  |   :||||:  |  | |||:
Db        293 -----------KGTPIFFDDFQKLVD--KNARFDLEI 316


RESULT 20
US-11-434-199-5140
; Sequence 5140, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5140
;   LENGTH: 1167
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-199-5140

  Query Match             10.7%;  Score 82;  DB 7;  Length 1167;
  Best Local Similarity   30.6%;  Pred. No. 12;
  Matches   30;  Conservative   11;  Mismatches   35;  Indels   22;  Gaps    4;

Qy         33 QLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPT 92
              ||   |||  |||:  | |:   ||   |   |:     : |: :|        || :|
Db        241 QLEKALQTAQDDKKSYLEDVLAVSKNGFKHK-DIRKFQSLFYEKEWS------LLDYIP- 292

Qy         93 VATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDRKDLEL 130
                       : |  |   :||||:  |  | |||:
Db        293 -----------KGTPIFFDDFQKLVD--KNARFDLEI 316


RESULT 21
PCT-US06-18535-5915
; Sequence 5915, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5915
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
PCT-US06-18535-5915
```

```
  Query Match             10.6%;  Score 81.5;  DB 1;  Length 241;
  Best Local Similarity   24.3%;  Pred. No. 2.3;
  Matches   35;  Conservative   25;  Mismatches   61;  Indels   23;  Gaps    7;

Qy          8 LGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADD--KRFVL--VDITTTSKKTVKVA 63
              ||:| |    :| |: |:  |    ||      |  ::  ||     :|         ||
Db         48 LGKATEKD--LQQLKAEIMDGLQSVQLNAEHSTSVEEEVKRIKAEHIDRNAIIHGRVKGK 105

Qy         64 IDVTDVYVVGY--QDKWD-----------GKDRAVFLDKVPTVATSKLFPGVTNRVTLT 109
              :::|  :  ||  : ||:           |||   ::: :|::   :: |     : |:
Db        106 LNITRAFGAGYLKEPKWNSMLLACFKIDYIGKD--PYINCIPSLHHHRIGPN-DKFLVLS 162

Qy        110 FDGSYQKLVNAAKVDRKDLELGVY 133
              || ||   |   ||  ::    |
Db        163 SDGLYQYFTNKEVVDEVEMFTAAY 186


RESULT 22
US-11-431-855-5915
; Sequence 5915, Application US/11431855
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5915
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-11-431-855-5915

  Query Match             10.6%;  Score 81.5;  DB 7;  Length 241;
  Best Local Similarity   24.3%;  Pred. No. 2.3;
  Matches   35;  Conservative   25;  Mismatches   61;  Indels   23;  Gaps    7;

Qy          8 LGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADD--KRFVL--VDITTTSKKTVKVA 63
              ||:| |    :| |: |:  |    ||      |  ::  ||     :|         ||
Db         48 LGKATEKD--LQQLKAEIMDGLQSVQLNAEHSTSVEEEVKRIKAEHIDRNAIIHGRVKGK 105

Qy         64 IDVTDVYVVGY--QDKWD-----------GKDRAVFLDKVPTVATSKLFPGVTNRVTLT 109
              :::|  :  ||  : ||:           |||   ::: :|::   :: |     : |:
Db        106 LNITRAFGAGYLKEPKWNSMLLACFKIDYIGKD--PYINCIPSLHHHRIGPN-DKFLVLS 162

Qy        110 FDGSYQKLVNAAKVDRKDLELGVY 133
              || ||   |   ||  ::    |
Db        163 SDGLYQYFTNKEVVDEVEMFTAAY 186


RESULT 23
US-60-838-415-16584
; Sequence 16584, Application US/60838415
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et al.
;  TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
;  FILE REFERENCE: 38-21(54146)A
;  CURRENT APPLICATION NUMBER: US/60/838,415
;  CURRENT FILING DATE:  2006-08-17
;  NUMBER OF SEQ ID NOS: 30376
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16584
;   LENGTH: 1184
;   TYPE: PRT
;   ORGANISM: Anabaena variabilis ATCC 29413
US-60-838-415-16584

  Query Match             10.4%;  Score 79.5;  DB 8;  Length 1184;
  Best Local Similarity   27.3%;  Pred. No. 21;
  Matches   33;  Conservative   21;  Mismatches   46;  Indels   21;  Gaps    7;

Qy          4 VSFNLGEAYEYP----TFIQDLRNE-----LAKGTPVCQLPVTLQTIADDKRFVLVD--- 51
              :| | | | : |      | ||: |      :      ||:   |::| |   ||  |
Db         66 ISVNAGNAEQQPILATVFNQDINNHQQLQLVTSPETECQVTTILESITD--AFVAFDENW 123

Qy         52 -ITTTSKKTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTF 110
               |  ::  ||: :  | | ::| :  ||      || : |  ||  :|   |  :| :::
Db        124 HYTYVNQAAVKI-LHKTPVELIG-KHVWD----EVFPELVGGVAYQELHRAVAEQVAVSW 177

Qy        111 D 111
              :
Db        178 E 178


RESULT 24
US-11-434-137-7210
; Sequence 7210, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7210
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(166)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-137-7210

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 166;
  Best Local Similarity   29.9%;  Pred. No. 3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |   | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 25
US-11-434-184-7210
; Sequence 7210, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
```

```
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7210
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(166)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-184-7210

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 166;
  Best Local Similarity   29.9%;  Pred. No. 3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
                | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 26
US-11-434-203-7210
; Sequence 7210, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7210
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(166)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-203-7210

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 166;
  Best Local Similarity   29.9%;  Pred. No. 3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
                | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 27
US-11-434-127-7210
; Sequence 7210, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7210
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(166)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-127-7210

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 166;
  Best Local Similarity   29.9%;  Pred. No. 3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
                | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 28
US-11-434-199-7210
; Sequence 7210, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
```

```
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7210
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(166)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-199-7210

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 166;
  Best Local Similarity   29.9%;  Pred. No. 3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 29
US-11-434-137-7126
; Sequence 7126, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7126
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(177)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-137-7126

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 177;
  Best Local Similarity   29.9%;  Pred. No. 3.2;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 30
US-11-434-184-7126
; Sequence 7126, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7126
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(177)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-184-7126

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 177;
  Best Local Similarity   29.9%;  Pred. No. 3.2;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 31
US-11-434-203-7126
; Sequence 7126, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
```

```
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7126
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(177)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-203-7126

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 177;
  Best Local Similarity   29.9%;  Pred. No. 3.2;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 32
US-11-434-127-7126
; Sequence 7126, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7126
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(177)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-127-7126

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 177;
  Best Local Similarity   29.9%;  Pred. No. 3.2;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 33
US-11-434-199-7126
; Sequence 7126, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7126
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(177)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-199-7126

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 177;
  Best Local Similarity   29.9%;  Pred. No. 3.2;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 34
US-11-434-137-7204
; Sequence 7204, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
```

```
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7204
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(197)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-137-7204

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 197;
  Best Local Similarity   29.9%;  Pred. No. 3.6;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 35
US-11-434-184-7204
; Sequence 7204, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7204
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(197)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-184-7204

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 197;
  Best Local Similarity   29.9%;  Pred. No. 3.6;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 36
US-11-434-203-7204
; Sequence 7204, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7204
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(197)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-203-7204

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 197;
  Best Local Similarity   29.9%;  Pred. No. 3.6;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 37
US-11-434-127-7204
; Sequence 7204, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
```

```
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7204
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(197)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-127-7204

  Query Match            10.2%;  Score 78.5;  DB 7;  Length 197;
  Best Local Similarity   29.9%;  Pred. No. 3.6;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 38
US-11-434-199-7204
; Sequence 7204, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7204
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(197)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-199-7204

  Query Match            10.2%;  Score 78.5;  DB 7;  Length 197;
  Best Local Similarity   29.9%;  Pred. No. 3.6;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::.  |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 39
US-11-434-137-7220
; Sequence 7220, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7220
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(219)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-137-7220

  Query Match            10.2%;  Score 78.5;  DB 7;  Length 219;
  Best Local Similarity   29.9%;  Pred. No. 4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         25 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 83

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         84 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 130


RESULT 40
US-11-434-184-7220
; Sequence 7220, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
```

```
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7220
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(219)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-184-7220

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 219;
  Best Local Similarity   29.9%;  Pred. No. 4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         25 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 83

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |     |     | :    |: |:
Db         84 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 130


RESULT 41
US-11-434-203-7220
; Sequence 7220, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7220
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(219)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-203-7220

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 219;
  Best Local Similarity   29.9%;  Pred. No. 4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         25 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 83

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |     |     | :    |: |:
Db         84 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 130


RESULT 42
US-11-434-127-7220
; Sequence 7220, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7220
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(219)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-127-7220

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 219;
  Best Local Similarity   29.9%;  Pred. No. 4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         25 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 83

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |     |     | :    |: |:
Db         84 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 130


RESULT 43
US-11-434-199-7220
; Sequence 7220, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
```

```
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7220
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(219)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-199-7220

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 219;
  Best Local Similarity   29.9%;  Pred. No. 4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         25 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 83

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         84 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 130


RESULT 44
US-11-434-137-6972
; Sequence 6972, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6972
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(234)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-137-6972

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 45
US-11-434-137-10774
; Sequence 10774, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10774
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-10774

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || |:| | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 46
US-11-434-184-6972
; Sequence 6972, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6972
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
```

```
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(234)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-184-6972

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 47
US-11-434-184-10774
; Sequence 10774, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10774
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-10774

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 48
US-11-434-203-6972
; Sequence 6972, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6972
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(234)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-203-6972

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 49
US-11-434-203-10774
; Sequence 10774, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10774
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-10774

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
```

```
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 50
US-11-434-127-6972
; Sequence 6972, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6972
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(234)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-127-6972

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 51
US-11-434-127-10774
; Sequence 10774, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10774
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-10774

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 52
US-11-434-199-6972
; Sequence 6972, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6972
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(234)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-199-6972

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142
```

```
RESULT 53
US-11-434-199-10774
; Sequence 10774, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 10774
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-10774

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 234;
  Best Local Similarity   29.9%;  Pred. No. 4.3;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 54
US-11-434-137-6970
; Sequence 6970, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6970
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-6970

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 258;
  Best Local Similarity   29.9%;  Pred. No. 4.8;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         21 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 79

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         80 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 126


RESULT 55
US-11-434-184-6970
; Sequence 6970, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6970
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-6970

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 258;
  Best Local Similarity   29.9%;  Pred. No. 4.8;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         21 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 79

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         80 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 126


RESULT 56
US-11-434-203-6970
; Sequence 6970, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
```

```
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6970
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-6970

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 258;
  Best Local Similarity   29.9%;  Pred. No. 4.8;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         21 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 79

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         80 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 126


RESULT 57
US-11-434-127-6970
; Sequence 6970, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6970
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-6970

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 258;
  Best Local Similarity   29.9%;  Pred. No. 4.8;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         21 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 79

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         80 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 126


RESULT 58
US-11-434-199-6970
; Sequence 6970, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6970
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-6970

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 258;
  Best Local Similarity   29.9%;  Pred. No. 4.8;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         21 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 79

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         80 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 126


RESULT 59
US-11-434-137-758
; Sequence 758, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 758
```

```
;   LENGTH: 392
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-758

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 392;
  Best Local Similarity   29.9%;  Pred. No. 7.7;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 60
US-11-434-184-758
; Sequence 758, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 758
;   LENGTH: 392
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-758

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 392;
  Best Local Similarity   29.9%;  Pred. No. 7.7;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 61
US-11-434-203-758
; Sequence 758, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 758
;   LENGTH: 392
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-758

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 392;
  Best Local Similarity   29.9%;  Pred. No. 7.7;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 62
US-11-434-127-758
; Sequence 758, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 758
;   LENGTH: 392
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-758

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 392;
  Best Local Similarity   29.9%;  Pred. No. 7.7;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
```

```
                | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 63
US-11-434-199-758
; Sequence 758, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 758
;   LENGTH: 392
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-758

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 392;
  Best Local Similarity   29.9%;  Pred. No. 7.7;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
                | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 64
US-11-434-137-9592
; Sequence 9592, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9592
;   LENGTH: 454
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(454)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-137-9592

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 454;
  Best Local Similarity   29.9%;  Pred. No. 9.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
                | |      ::   |||: | : : |    |    | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 65
US-11-434-184-9592
; Sequence 9592, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9592
;   LENGTH: 454
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(454)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-184-9592

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 454;
  Best Local Similarity   29.9%;  Pred. No. 9.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
                | |      ::   |||: | : : |    |    | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 66
US-11-434-203-9592
```

```
; Sequence 9592, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9592
;   LENGTH: 454
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(454)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-203-9592

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 454;
  Best Local Similarity   29.9%;  Pred. No. 9.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 67
US-11-434-127-9592
; Sequence 9592, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9592
;   LENGTH: 454
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(454)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-127-9592

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 454;
  Best Local Similarity   29.9%;  Pred. No. 9.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 68
US-11-434-199-9592
; Sequence 9592, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9592
;   LENGTH: 454
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(454)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-199-9592

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 454;
  Best Local Similarity   29.9%;  Pred. No. 9.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 69
US-11-434-137-764
; Sequence 764, Application US/11434137
; GENERAL INFORMATION:
```

```
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 764
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-764

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 467;
  Best Local Similarity   29.9%;  Pred. No. 9.4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        257 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 315

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        316 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 362


RESULT 70
US-11-434-184-764
; Sequence 764, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 764
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-764

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 467;
  Best Local Similarity   29.9%;  Pred. No. 9.4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        257 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 315

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        316 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 362


RESULT 71
US-11-434-203-764
; Sequence 764, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 764
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-764

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 467;
  Best Local Similarity   29.9%;  Pred. No. 9.4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        257 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 315

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        316 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 362


RESULT 72
US-11-434-127-764
; Sequence 764, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
```

```
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 764
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-764

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 467;
  Best Local Similarity   29.9%;  Pred. No. 9.4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   | |    |:|     || || | :
Db        257 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 315

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |     |     | :    |: |:
Db        316 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 362


RESULT 73
US-11-434-199-764
; Sequence 764, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 764
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-764

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 467;
  Best Local Similarity   29.9%;  Pred. No. 9.4;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   | |    |:|     || || | :
Db        257 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 315

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |     |     | :    |: |:
Db        316 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 362


RESULT 74
US-11-434-137-9594
; Sequence 9594, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9594
;   LENGTH: 1389
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-137-9594

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 1389;
  Best Local Similarity   29.9%;  Pred. No. 32;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   | |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |     |     | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 75
US-11-434-184-9594
; Sequence 9594, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9594
;   LENGTH: 1389
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-184-9594

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 1389;
```

```
  Best Local Similarity   29.9%;  Pred. No. 32;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 76
US-11-434-203-9594
; Sequence 9594, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9594
;   LENGTH: 1389
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-203-9594

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 1389;
  Best Local Similarity   29.9%;  Pred. No. 32;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 77
US-11-434-127-9594
; Sequence 9594, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9594
;   LENGTH: 1389
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-127-9594

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 1389;
  Best Local Similarity   29.9%;  Pred. No. 32;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 78
US-11-434-199-9594
; Sequence 9594, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9594
;   LENGTH: 1389
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
US-11-434-199-9594

  Query Match             10.2%;  Score 78.5;  DB 7;  Length 1389;
  Best Local Similarity   29.9%;  Pred. No. 32;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db        244 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 302

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db        303 VVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFE 349


RESULT 79
US-11-434-137-7202
```

```
; Sequence 7202, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7202
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(242)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-137-7202

  Query Match             10.0%;  Score 76.5;  DB 7;  Length 242;
  Best Local Similarity   29.9%;  Pred. No. 7.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVCETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 80
US-11-434-184-7202
; Sequence 7202, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7202
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(242)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-184-7202

  Query Match             10.0%;  Score 76.5;  DB 7;  Length 242;
  Best Local Similarity   29.9%;  Pred. No. 7.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVCETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 81
US-11-434-203-7202
; Sequence 7202, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7202
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(242)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-203-7202

  Query Match             10.0%;  Score 76.5;  DB 7;  Length 242;
  Best Local Similarity   29.9%;  Pred. No. 7.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |       ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVCETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 82
US-11-434-127-7202
; Sequence 7202, Application US/11434127
; GENERAL INFORMATION:
```

```
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7202
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(242)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-127-7202

  Query Match             10.0%;  Score 76.5;  DB 7;  Length 242;
  Best Local Similarity   29.9%;  Pred. No. 7.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVCETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 83
US-11-434-199-7202
; Sequence 7202, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7202
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Streptococcus agalactiae
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(242)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-11-434-199-7202

  Query Match             10.0%;  Score 76.5;  DB 7;  Length 242;
  Best Local Similarity   29.9%;  Pred. No. 7.1;
  Matches   32;  Conservative   15;  Mismatches   57;  Indels    3;  Gaps    3;

Qy          7 NLGEAYEYPTFIQDLRNELAKGTPVC-QLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:||  :    | :|  :| ||| |  : ||   |  |    |:|     || || | :
Db         37 NVGETPKAEDSIGNL-PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVK 95

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATS-KLFPGVTNRVTLTFD 111
              | |      ::   |||: | : : |    |    | :    |: |:
Db         96 VVDPRTDADKNDPAGKDQQVNVCETPKAEDSIGNLPDLPKGTTVAFE 142


RESULT 84
US-60-836-986-5988
; Sequence 5988, Application US/60836986
; GENERAL INFORMATION:
;  APPLICANT: Hood, Leroy
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Johnson, Richard
;  APPLICANT:  Marelli, Marcello
;  APPLICANT:  Li, Xiaojun
;  TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 460092.405P1
;  CURRENT APPLICATION NUMBER: US/60/836,986
;  CURRENT FILING DATE:  2006-08-09
;  NUMBER OF SEQ ID NOS: 32934
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5988
;   LENGTH: 1274
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-836-986-5988

  Query Match             9.8%;  Score 75.5;  DB 8;  Length 1274;
  Best Local Similarity   21.7%;  Pred. No. 56;
  Matches   38;  Conservative   24;  Mismatches   66;  Indels   47;  Gaps    8;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADD----------KRFVLV 50
              |  :|: ::| : | :|  |  |   :  |    || :                |:
Db       1074 SMEMGQEHQYHSKIDELIEETVK-EMITLLVAKFVTILEGVLAKLSRYDEGTLFSSFLSF 1132

Qy         51 DITTTSK--KTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTL 108
                :   ||     |  :|| | ||   :   |     |  |||      :::      :
Db       1133 TVKAASKYVDVPKPGMDVADAYVTFVRHSQD-----VLRDKV----NEEMY------IER 1177

Qy        109 TFDGSYQKLVNAA---KVDRKDLELGVYKL-----------EFSIEAIWGKTQN 148
               ||  |   :|       || ||:| :|:|           :| :: :   | |
Db       1178 LFDQWYNSSMNVICTWLTDRMDLQLHIYQLKTLIRMVKKTYRDFRLQGVLDSTLN 1232


RESULT 85
US-60-836-986-5989
; Sequence 5989, Application US/60836986
; GENERAL INFORMATION:
;  APPLICANT: Hood, Leroy
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Johnson, Richard
;  APPLICANT:  Marelli, Marcello
;  APPLICANT:  Li, Xiaojun
;  TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 460092.405P1
;  CURRENT APPLICATION NUMBER: US/60/836,986
;  CURRENT FILING DATE:  2006-08-09
;  NUMBER OF SEQ ID NOS: 32934
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5989
;   LENGTH: 1314
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-836-986-5989

  Query Match             9.8%;  Score 75.5;  DB 8;  Length 1314;
  Best Local Similarity   21.7%;  Pred. No. 58;
  Matches   38;  Conservative   24;  Mismatches   66;  Indels   47;  Gaps    8;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADD--------------KRFVLV 50
              |  :|: ::| : | :|  |  |   :  |      || :                 |:
Db       1114 SMEMGQEHQYHSKIDELIEETVK-EMITLLVAKFVTILEGVLAKLSRYDEGTLFSSFLSF 1172

Qy         51 DITTTSK--KTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTL 108
               :   ||      |  :|| | ||   :   |     |  |||      :::      :
Db       1173 TVKAASKYVDVPKPGMDVADAYVTFVRHSQD-----VLRDKV----NEEMY------IER 1217

Qy        109 TFDGSYQKLVNAA---KVDRKDLELGVYKL------------EFSIEAIWGKTQN 148
              ||  |   :|       || ||:| :|:|            :| :: :   | |
Db       1218 LFDQWYNSSMNVICTWLTDRMDLQLHIYQLKTLIRMVKKTYRDFRLQGVLDSTLN 1272


RESULT 86
US-60-836-986-5987
; Sequence 5987, Application US/60836986
; GENERAL INFORMATION:
;  APPLICANT: Hood, Leroy
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Johnson, Richard
;  APPLICANT:  Marelli, Marcello
;  APPLICANT:  Li, Xiaojun
;  TITLE OF INVENTION: ORGAN-SPECIFIC PROTEINS AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 460092.405P1
;  CURRENT APPLICATION NUMBER: US/60/836,986
;  CURRENT FILING DATE:  2006-08-09
;  NUMBER OF SEQ ID NOS: 32934
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5987
;   LENGTH: 1353
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-836-986-5987

  Query Match             9.8%;  Score 75.5;  DB 8;  Length 1353;
  Best Local Similarity   21.7%;  Pred. No. 60;
  Matches   38;  Conservative   24;  Mismatches   66;  Indels   47;  Gaps    8;

Qy          5 SFNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADD--------------KRFVLV 50
              |  :|: ::| : | :|  |  |   :  |      || :                 |:
Db       1153 SMEMGQEHQYHSKIDELIEETVK-EMITLLVAKFVTILEGVLAKLSRYDEGTLFSSFLSF 1211

Qy         51 DITTTSK--KTVKVAIDVTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTL 108
               :   ||      |  :|| | ||   :   |     |  |||      :::      :
Db       1212 TVKAASKYVDVPKPGMDVADAYVTFVRHSQD-----VLRDKV----NEEMY------IER 1256

Qy        109 TFDGSYQKLVNAA---KVDRKDLELGVYKL------------EFSIEAIWGKTQN 148
              ||  |   :|       || ||:| :|:|            :| :: :   | |
Db       1257 LFDQWYNSSMNVICTWLTDRMDLQLHIYQLKTLIRMVKKTYRDFRLQGVLDSTLN 1311


RESULT 87
US-11-434-137-8456
; Sequence 8456, Application US/11434137
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 8456
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-137-8456

  Query Match             9.6%;  Score 73.5;  DB 7;  Length 341;
  Best Local Similarity   24.3%;  Pred. No. 20;
  Matches   25;  Conservative   20;  Mismatches   35;  Indels   23;  Gaps    5;

Qy         49 LVDITTTSKKTVKVAIDVTDVYVVGYQDKW---------DG-----KDRAVFLDKVPTVA 94
              |:   | ||:|| ::: :|:      |  |         :|     :|   :   :|
Db        247 LIATVTKSKETVDISVSLTEA-----QSSWISLTNSEIGEGGITLTQDSPTYTATLPAEI 301

Qy         95 TSKLFP-GVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLE 136
              |  |   |||  |::| ||   : |: : :   ||    :|::
Db        302 TESLLTLGVTKGVSVTIDG---QPVDLSPLTSTDLSYITFKIQ 341


RESULT 88
US-11-434-184-8456
; Sequence 8456, Application US/11434184
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,184
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 8456
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-184-8456

  Query Match             9.6%;  Score 73.5;  DB 7;  Length 341;
  Best Local Similarity   24.3%;  Pred. No. 20;
  Matches   25;  Conservative   20;  Mismatches   35;  Indels   23;  Gaps    5;

Qy         49 LVDITTTSKKTVKVAIDVTDVYVVGYQDKW---------DG-----KDRAVFLDKVPTVA 94
              |:   | ||:|| ::: :|:      |  |         :|     :|   :   :|
Db        247 LIATVTKSKETVDISVSLTEA-----QSSWISLTNSEIGEGGITLTQDSPTYTATLPAEI 301
```

```
Qy          95 TSKLFP-GVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLE 136
               |  |   |||  |::| ||   : |: : :   ||    :|::
Db         302 TESLLTLGVTKGVSVTIDG---QPVDLSPLTSTDLSYITFKIQ 341


RESULT 89
US-11-434-203-8456
; Sequence 8456, Application US/11434203
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,203
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 8456
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-203-8456

  Query Match             9.6%;  Score 73.5;  DB 7;  Length 341;
  Best Local Similarity   24.3%;  Pred. No. 20;
  Matches   25;  Conservative   20;  Mismatches   35;  Indels   23;  Gaps    5;

Qy          49 LVDITTTSKKTVKVAIDVTDVYVVGYQDKW---------DG-----KDRAVFLDKVPTVA 94
               |:   | ||:|| ::: :|:      |  |          :|     :|   :   :|
Db         247 LIATVTKSKETVDISVSLTEA-----QSSWISLTNSEIGEGGITLTQDSPTYTATLPAEI 301

Qy          95 TSKLFP-GVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLE 136
               |  |   |||  |::| ||   : |: : :   ||    :|::
Db         302 TESLLTLGVTKGVSVTIDG---QPVDLSPLTSTDLSYITFKIQ 341


RESULT 90
US-11-434-127-8456
; Sequence 8456, Application US/11434127
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,127
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 8456
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-127-8456

  Query Match             9.6%;  Score 73.5;  DB 7;  Length 341;
  Best Local Similarity   24.3%;  Pred. No. 20;
  Matches   25;  Conservative   20;  Mismatches   35;  Indels   23;  Gaps    5;

Qy          49 LVDITTTSKKTVKVAIDVTDVYVVGYQDKW---------DG-----KDRAVFLDKVPTVA 94
               |:   | ||:|| ::: :|:      |  |          :|     :|   :   :|
Db         247 LIATVTKSKETVDISVSLTEA-----QSSWISLTNSEIGEGGITLTQDSPTYTATLPAEI 301

Qy          95 TSKLFP-GVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLE 136
               |  |   |||  |::| ||   : |: : :   ||    :|::
Db         302 TESLLTLGVTKGVSVTIDG---QPVDLSPLTSTDLSYITFKIQ 341


RESULT 91
US-11-434-199-8456
; Sequence 8456, Application US/11434199
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,199
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 8456
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-199-8456

  Query Match             9.6%;  Score 73.5;  DB 7;  Length 341;
  Best Local Similarity   24.3%;  Pred. No. 20;
  Matches   25;  Conservative   20;  Mismatches   35;  Indels   23;  Gaps    5;

Qy          49 LVDITTTSKKTVKVAIDVTDVYVVGYQDKW---------DG-----KDRAVFLDKVPTVA 94
               |:   | ||:|| ::: :|:      |  |          :|     :|   :   :|
Db         247 LIATVTKSKETVDISVSLTEA-----QSSWISLTNSEIGEGGITLTQDSPTYTATLPAEI 301

Qy          95 TSKLFP-GVTNRVTLTFDGSYQKLVNAAKVDRKDLELGVYKLE 136
               |  |   |||  |::| ||   : |: : :   ||    :|::
Db         302 TESLLTLGVTKGVSVTIDG---QPVDLSPLTSTDLSYITFKIQ 341


RESULT 92
US-10-805-394A-6425
; Sequence 6425, Application US/10805394A
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
```

```
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/10/805,394A
;  CURRENT FILING DATE:  2004-03-22
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6425
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-805-394A-6425

  Query Match             9.5%;  Score 73;  DB 6;  Length 372;
  Best Local Similarity   25.2%;  Pred. No. 25;
  Matches   37;  Conservative   21;  Mismatches   47;  Indels   42;  Gaps    7;

Qy         12 YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADD-------KRFVLVDITTTSKKTVKVAI 64
              |:    | |:  |:|       | :   ::||        :| :| |::      : | :
Db        114 YQVRVPISDVDKEVA------ALSLAFNSMADQLEHTEELRRNMLSDLSHEMNTPLSVLL 167

Qy         65 DVTDVYVVGYQD---KWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
                 ||| | ||   :||    ||| :::          | :|:|   |      |: |
Db        168 ----VYVDGLQDGMVEWDADTHAVFAEQL----------GRLSRLTSDLDD-----VSRA 208

Qy        122 KVDRKDLELGVYKLEFSIEAIWGKTQN 148
              :  | |       | :|  || |   |
Db        209 QEHRFD-------LVYSTVAIGGLIHN 228


RESULT 93
US-11-508-066-42
; Sequence 42, Application US/11508066
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
;  TITLE OF INVENTION:  REGULATORY PROTEINS
;  FILE REFERENCE: BGI-123CPCNDV2
;  CURRENT APPLICATION NUMBER: US/11/508,066
;  CURRENT FILING DATE:  2006-08-21
;  PRIOR APPLICATION NUMBER: 11/006098
;  PRIOR FILING DATE: 2005-12-05
;  PRIOR APPLICATION NUMBER: 09/602,874
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 60/142690
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: 60/151251
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19930476.9
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: DE 19931419.5
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: DE 19931420.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128
;  PRIOR FILING DATE: 1999-07-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 362
; SEQ ID NO 42
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-11-508-066-42

  Query Match             9.5%;  Score 73;  DB 7;  Length 372;
  Best Local Similarity   25.2%;  Pred. No. 25;
  Matches   37;  Conservative   21;  Mismatches   47;  Indels   42;  Gaps    7;

Qy         12 YEYPTFIQDLRNELAKGTPVCQLPVTLQTIADD-------KRFVLVDITTTSKKTVKVAI 64
              |:    | |:  |:|       | :   ::||        :| :| |::      : | :
Db        114 YQVRVPISDVDKEVA------ALSLAFNSMADQLEHTEELRRNMLSDLSHEMNTPLSVLL 167

Qy         65 DVTDVYVVGYQD---KWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAA 121
                 ||| | ||   :||    ||| :::          | :|:|   |      |: |
Db        168 ----VYVDGLQDGMVEWDADTHAVFAEQL----------GRLSRLTSDLDD-----VSRA 208

Qy        122 KVDRKDLELGVYKLEFSIEAIWGKTQN 148
              :  | |       | :|  || |   |
Db        209 QEHRFD-------LVYSTVAIGGLIHN 228


RESULT 94
US-11-027-891A-5266
; Sequence 5266, Application US/11027891A
; GENERAL INFORMATION:
;  APPLICANT: Doucette-Stamm, Lynn
;  APPLICANT:  Bush, David
;  APPLICANT:  Zeng, Qiandong
;  APPLICANT:  Opperman, Timothy
;  APPLICANT:  Houseweart, Chad Eric
;  TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE: 3687.1000-025
;  CURRENT APPLICATION NUMBER: US/11/027,891A
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: US 10/640,833
;  PRIOR FILING DATE: 2003-08-14
;  PRIOR APPLICATION NUMBER: US 09/583,110
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/107,433
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/085,131
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: US 60/051,553
;  PRIOR FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 5324
; SEQ ID NO 5266
;   LENGTH: 2172
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-11-027-891A-5266

  Query Match             9.5%;  Score 73;  DB 7;  Length 2172;
  Best Local Similarity   24.1%;  Pred. No. 1.8e+02;
  Matches   32;  Conservative   24;  Mismatches   61;  Indels   16;  Gaps    5;

Qy          6 FNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:  :   |   |: :| :   || : :: :  : :|  |:     |    |       |
Db       1549 FSFDKVETYAVRIRMVRADNKLGTSITEVQIFAKQVAAAKQ-GQTRIQVDGKDLANFNPD 1607

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDR 125
              :|| |:    :  ||        ||| |  |    |:   |   :|   ::: || :
Db       1608 LTDYYL----ESVDG--------KVPAVTASVSNNGLATVVPSVREGEPVRVI--AKAEN 1653

Qy        126 KDLELGVYKLEFS 138
               |: || |:| |:
Db       1654 GDI-LGEYRLHFT 1665
```

```
RESULT 95
US-11-027-879A-5266
; Sequence 5266, Application US/11027879A
; GENERAL INFORMATION:
;  APPLICANT: Doucette-Stamm, Lynn
;  APPLICANT:  Bush, David
;  APPLICANT:  Zeng, Qiandong
;  APPLICANT:  Opperman, Timothy
;  APPLICANT:  Houseweart, Chad Eric
;  TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE: 3687.1000-021
;  CURRENT APPLICATION NUMBER: US/11/027,879A
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: US 10/640,833
;  PRIOR FILING DATE: 2003-08-14
;  PRIOR APPLICATION NUMBER: US 09/583,110
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/107,433
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/085,131
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: US 60/051,553
;  PRIOR FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 5324
; SEQ ID NO 5266
;   LENGTH: 2172
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-11-027-879A-5266

  Query Match             9.5%;  Score 73;  DB 7;  Length 2172;
  Best Local Similarity   24.1%;  Pred. No. 1.8e+02;
  Matches   32;  Conservative   24;  Mismatches   61;  Indels   16;  Gaps    5;

Qy          6 FNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:  :   |   |: :| :   || : :: :  : :|  |:     |    |       |
Db       1549 FSFDKVETYAVRIRMVRADNKLGTSITEVQIFAKQVAAAKQ-GQTRIQVDGKDLANFNPD 1607

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDR 125
              :|| |:    :  ||        ||| |  |    |:  |    :|  :::  || :
Db       1608 LTDYYL----ESVDG--------KVPAVTASVSNNGLATVVPSVREGEPVRVI--AKAEN 1653

Qy        126 KDLELGVYKLEFS 138
              |: || |:| |:
Db       1654 GDI-LGEYRLHFT 1665


RESULT 96
US-11-027-892A-5266
; Sequence 5266, Application US/11027892A
; GENERAL INFORMATION:
;  APPLICANT: Doucette-Stamm, Lynn
;  APPLICANT:  Bush, David
;  APPLICANT:  Zeng, Qiandong
;  APPLICANT:  Opperman, Timothy
;  APPLICANT:  Houseweart, Chad Eric
;  TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE: 3687.1000-009
;  CURRENT APPLICATION NUMBER: US/11/027,892A
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: US 10/640,833
;  PRIOR FILING DATE: 2003-08-14
;  PRIOR APPLICATION NUMBER: US 09/583,110
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/107,433
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/085,131
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: US 60/051,553
;  PRIOR FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 5324
; SEQ ID NO 5266
;   LENGTH: 2172
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-11-027-892A-5266

  Query Match             9.5%;  Score 73;  DB 7;  Length 2172;
  Best Local Similarity   24.1%;  Pred. No. 1.8e+02;
  Matches   32;  Conservative   24;  Mismatches   61;  Indels   16;  Gaps    5;

Qy          6 FNLGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAID 65
              |:  :   |   |: :| :   || : :: :  : :|  |:     |    |       |
Db       1549 FSFDKVETYAVRIRMVRADNKLGTSITEVQIFAKQVAAAKQ-GQTRIQVDGKDLANFNPD 1607

Qy         66 VTDVYVVGYQDKWDGKDRAVFLDKVPTVATSKLFPGVTNRVTLTFDGSYQKLVNAAKVDR 125
              :|| |:    :  ||        ||| |  |    |:  |    :|  :::  || :
Db       1608 LTDYYL----ESVDG--------KVPAVTASVSNNGLATVVPSVREGEPVRVI--AKAEN 1653

Qy        126 KDLELGVYKLEFS 138
              |: || |:| |:
Db       1654 GDI-LGEYRLHFT 1665


RESULT 97
PCT-US06-18535-4363
; Sequence 4363, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4363
;   LENGTH: 288
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (94)..(94)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (136)..(136)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (170)..(170)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (210)..(210)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (228)..(228)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
PCT-US06-18535-4363

  Query Match             9.4%;  Score 72.5;  DB 1;  Length 288;
  Best Local Similarity   24.3%;  Pred. No. 21;
  Matches   35;  Conservative   24;  Mismatches   64;  Indels   21;  Gaps    7;

Qy          8 LGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADD--KRFVLV---DITTTSKKTVKV 62
              ||:|  |    :| |: |:  |    ||      |  ::  ||         | :|   ||
Db         48 LGKATEKD--LQQLKAEIMDGLQSVQLNAEHSTSVEEEVKRIKAEHNDXATPSSTARVKG 105

Qy         63 AIDVTDVYVVGY--QDKW----------DGKDRAVFLDKVPTVATSKLFPGVTNRVTLTF 110
               ::||  :  ||  : ||          |   :  ::: :|::   :: |     : |:
Db        106 KLNVTRAFGAGYLKEPKWNSMLLGCFKIDYXGKGPYINCIPSLHHHRIGPN-DKFLVLSS 164
```

```
Qy        111 DGSYQK-LVNAAKVDRKDLELGVY 133
              || ||    |   ||  ::    |
Db        165 DGLYQXYFTNKEVVDEVEMFTAAY 188


RESULT 98
US-11-431-855-4363
; Sequence 4363, Application US/11431855
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4363
;   LENGTH: 288
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (94)..(94)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (136)..(136)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (170)..(170)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (210)..(210)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (228)..(228)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-431-855-4363

  Query Match             9.4%;  Score 72.5;  DB 7;  Length 288;
  Best Local Similarity   24.3%;  Pred. No. 21;
  Matches   35;  Conservative   24;  Mismatches   64;  Indels   21;  Gaps    7;

Qy          8 LGEAYEYPTFIQDLRNELAKGTPVCQLPVTLQTIADD--KRFVLV---DITTTSKKTVKV 62
              ||:| |    :| |: |:  |    ||      |  ::  ||         | :|   ||
Db         48 LGKATEKD--LQQLKAEIMDGLQSVQLNAEHSTSVEEEVKRIKAEHNDXATPSSTARVKG 105

Qy         63 AIDVTDVYVVGY--QDKW----------DGKDRAVFLDKVPTVATSKLFPGVTNRVTLTF 110
               ::||  :  ||  : ||          |   :  ::: :|::   :: |     : |:
Db        106 KLNVTRAFGAGYLKEPKWNSMLLGCFKIDYXGKGPYINCIPSLHHHRIGPN-DKFLVLSS 164

Qy        111 DGSYQK-LVNAAKVDRKDLELGVY 133
              || ||    |   ||  ::    |
Db        165 DGLYQXYFTNKEVVDEVEMFTAAY 188


RESULT 99
PCT-US06-18535-10164
; Sequence 10164, Application PC/TUS0618535
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)A
;  CURRENT APPLICATION NUMBER: PCT/US06/18535
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10164
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Cryphonectria parasitica
PCT-US06-18535-10164

  Query Match             9.4%;  Score 72.5;  DB 1;  Length 369;
  Best Local Similarity   31.9%;  Pred. No. 28;
  Matches   22;  Conservative    6;  Mismatches   18;  Indels   23;  Gaps    3;

Qy         19 QDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVV------ 72
              ||  |    |||   :|:|  |:              || |  ||   ||||::
Db        296 QDYENGSPTGTPTTGVPITGLTV-------------SKVTGSVASSATDVYILCGKGSC 341

Qy         73 -GYQDKWDG 80
               |:  || |
Db        342 SGW--KWSG 348


RESULT 100
US-11-431-855-10164
; Sequence 10164, Application US/11431855
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark et. al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53708)C
;  CURRENT APPLICATION NUMBER: US/11/431,855
;  CURRENT FILING DATE:  2006-05-10
;  NUMBER OF SEQ ID NOS: 33637
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10164
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Cryphonectria parasitica
US-11-431-855-10164

  Query Match             9.4%;  Score 72.5;  DB 7;  Length 369;
  Best Local Similarity   31.9%;  Pred. No. 28;
  Matches   22;  Conservative    6;  Mismatches   18;  Indels   23;  Gaps    3;

Qy         19 QDLRNELAKGTPVCQLPVTLQTIADDKRFVLVDITTTSKKTVKVAIDVTDVYVV------ 72
              ||  |    |||   :|:|  |:              || |  ||   ||||::
Db        296 QDYENGSPTGTPTTGVPITGLTV-------------SKVTGSVASSATDVYILCGKGSC 341

Qy         73 -GYQDKWDG 80
               |:  || |
Db        342 SGW--KWSG 348


Search completed: September 18, 2006, 19:31:14
Job time : 54.6089 secs
```